

```
Human butyrophilin (BTF5) mRNA, complete cds
NCBI Description
                   308162
Seq. No.
                   uC-zmflmo17075b01b2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4210948
BLAST score
                   304
                   6.0e-28
E value
                   82
Match length
                   73
% identity
                   (AF085275) DnaJ protein [Hevea brasiliensis]
NCBI Description
                   308163
Seq. No.
Seq. ID
                   uC-zmflmo17075d03b2
Method
                   BLASTX
NCBI GI
                   g4204303
BLAST score
                   219
E value
                   1.0e-17
Match length
                   45
% identity
                   87
                   (AC003027) lcl_prt_seq No definition line found
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   308164
Seq. ID
                   uC-zmflmo17075e10b2
Method
                   BLASTX
NCBI GI
                   g82696
BLAST score
                   347
                   6.0e-33
E value
                   78
Match length
                   85
% identity
NCBI Description
                   glycine-rich protein - maize >gi 22293_emb_CAA43431_
                   (X61121) glycine-rich protein [Zea mays]
                   308165
Seq. No.
                   uC-zmflmo17075f09b2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g135449
BLAST score
                   420
E value
                   2.0e-41
Match length
                   128
% identity
                   63
NCBI Description
                   TUBULIN BETA-1 CHAIN >gi 100932 pir S14701 tubulin beta-1
                   chain - maize >gi_295851_emb_CA\overline{A}370\overline{60}_ (X52878) beta 1
                   tubulin [Zea mays]
Seq. No.
                   308166
                   uC-zmflmo17075g11a1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3132824
BLAST score
                   48
```

NCBI GI g3132824
BLAST score 48
E value 6.0e-18
Match length 118
% identity 86

NCBI Description Zea mays putative cytosine-5 DNA methyltransferase (ZMET1)

gene, complete cds

NCBI Description

```
Seq. No.
Seq. ID
                   uC-zmflmo17075h03b2
Method
                   BLASTX
NCBI GI
                   g3080427
BLAST score
                   514
E value
                   2.0e-52
Match length
                   133
                   74
% identity
NCBI Description
                   (AL022604) putative protein [Arabidopsis thaliana]
Seq. No.
                   308168
Seq. ID
                   uC-zmflmo17076c06b1
Method
                   BLASTX
NCBI GI
                   g1313909
BLAST score
                   258
E value
                   3.0e-22
Match length
                   90
% identity
                   61
                   (D84508) CDPK-related protein kinase [Zea mays]
NCBI Description
Seq. No.
Seq. ID
                   uC-zmflmo17076c09b1
Method
                   BLASTX
NCBI GI
                   q4038592
BLAST score
                   200
E value
                   4.0e-21
Match length
                   86
% identity
                   64
NCBI Description
                   (Y10403) RNA-directed RNA polymerase [Lycopersicon
                   esculentum]
Seq. No.
                   308170
Seq. ID
                   uC-zmflmo17076e04b1
Method
                   BLASTX
NCBI GI
                   g112994
                            J. . . .
BLAST score
                   415 -
E value
                   8.0e-41
Match length
                  85
% identity
                   96
NCBI Description
                  GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN
                   >gi 82685 pir S04536 embryonic abundant protein,
                   glycine-rich - maize >gi_22313_emb_CAA31077_ (X12564)
                  ABA-inducible gene protein [Zea mays]
                  >gi_226091_prf__1410284A abscisic acid inducible gene [Zea
                  mays]
Seq. No.
                   308171
Seq. ID
                  uC-zmflmo17076f08b1
Method
                  BLASTX
                   g4204289
NCBI GI
BLAST score
                  167
E value
                   2.0e-11
Match length
                  116
% identity
                   41
```

[Arabidopsis thaliana]

(AC003027) lcl prt_seq No definition line found



```
Seq. No.
                   308172
Seq. ID
                   uC-zmflmo17076g02b1
Method
                   BLASTX
NCBI GI
                   g2244899
BLAST score
                   265
E value
                   1.0e-23
Match length
                   135
% identity
                   50
                   (Z97338) similar to UFD1 protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   308173
Seq. ID
                   uC-zmflmo17076h04b1
Method
                   BLASTN
NCBI GI
                   q22332
BLAST score
                   124
E value
                   3.0e-63
Match length
                   303
% identity
                   86
NCBI Description Z.mays HRGP gene
Seq. No.
                   308174
Seq. ID
                   uC-zmflmo17077e02b1
Method
                   BLASTX
NCBI GI
                   g3212849
BLAST score
                   314
E value
                   7.0e-29
Match length
                   92
% identity
                   63
NCBI Description
                   (AC004005) unknown protein [Arabidopsis thaliana]
Seq. No.
                   308175
Seq. ID
                   uC-zmflmo17077e05b1
Method
                   BLASTX
NCBI GI
                   g1167955
BLAST score
                   148
E value
                   2.0e-09
Match length
                   41
% identity
                   66
NCBI Description
                   (U43497) putative 32.7 kDa jasmonate-induced protein
                   [Hordeum vulgare] >gi_2465428 (AF021257) 32 kDa protein
                   [Hordeum vulgare]
                   308176
Seq. No.
Seq. ID
                   uC-zmflmo17077f07b1
Method
                   BLASTX
                   g1169382
                   268
                   3.0e-28
                   113
% identity
                   61
```

NCBI GI BLAST score E value Match length

NCBI Description DNAJ PROTEIN HOMOLOG 2 >gi 542196 pir S42031 LDJ2 protein

- leek >gi_454303_emb_CAA5 $\overline{4}$ 720_ (\overline{X} 776 $\overline{32}$) LDJ2 [Allium

porrum]

Seq. No.

308177

Seq. ID uC-zmflmo17077h04b1

Method BLASTN



```
NCBI GI
                  g257040
BLAST score
                  181
E value
                  3.0e-97
Match length
                  311
% identity
                  93
NCBI Description
                  hydroxyproline-rich glycoprotein [maize, Genomic, 1703 nt]
                  308178
Seq. No.
                  uC-zmflmo17078c09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1905934
BLAST score
                  314
E value
                  1.0e-38
Match length
                  112
% identity
                  82
NCBI Description
                  (U32110) MADS box protein [Sorghum bicolor]
                  308179
Seq. No.
Seq. ID
                  uC-zmflmo17078c11b1
Method
                  BLASTX
NCBI GI
                  q1326382
BLAST score
                  158
E value
                  1.0e-10
Match length
                  54
% identity
                  48
NCBI Description
                  (U58751) coded for by C. elegans cDNA yk21d11.3; coded for
                  by C. elegans cDNA yk3h4.3; coded for by C. elegans cDNA
                  yk12d7.3; coded for by C. elegans cDNA yk21d11.5; coded for
                  by C. elegans cDNA cm2f6; coded for by C. elegans cDNA
                  yk46e12.5;
Seq. No.
                  308180
Seq. ID
                  uC-zmflmo17078e07b1
Method
                  BLASTX
NCBI GI
                  g2696804
BLAST score
                  616
E value
                  3.0e-64
Match length
                  122
% identity
                  96
NCBI Description
                  (AB009665) water channel protein [Oryza sativa]
                  308181
Seq. No.
Seq. ID
                  uC-zmflmo17078f02b1
Method
                  BLASTX
                  g4406764
                  148
                  1.0e-09
```

NCBI GI BLAST score E value Match length 90 % identity 34

(AC006836) putative uridylyl transferase [Arabidopsis NCBI Description

thaliana]

Seq. No. 308182

Seq. ID uC-zmflmo17078f05b1

Method BLASTX NCBI GI g4200165 BLAST score 234

```
E value
                       2.0e-19
    Match length
                       62
     % identity
                       74
    NCBI Description
                       (Y16262) neutral invertase [Daucus carota]
     Seq. No.
                       308183
                       uC-zmflmo17078h03a1
     Seq. ID
    Method
                       BLASTN
NCBI GI
                       q22312
    BLAST score
                       53
                       2.0e-21
    E value
    Match length
                       97
     % identity
                       89
    NCBI Description
                       Maize ABA-inducible gene for glycine-rich protein ( ABA =
                       abscisic acid)
    Seq. No.
                       308184
    Seq. ID
                       uC-zmflmo17078h03b1
    Method
                       BLASTX
    NCBI GI
                       g112994
    BLAST score
                       422
    E value
                       1.0e-41
    Match length
                       85
    % identity
                       96
    NCBI Description
                       GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN
                       >gi 82685 pir S04536 embryonic abundant protein,
                       glycine-rich - maize >gi 22313 emb CAA31077 (X12564)
                       ABA-inducible gene protein [Zea mays]
                       >gi_226091_prf__1410284A abscisic acid inducible gene [Zea
                       mays]
    Seq. No.
                       308185
    Seq. ID
                       uC-zmflmo17078h07b1
    Method
                       BLASTX
    NCBI GI
                       g2984709
    BLAST score
                       381
    E value
                       9.0e-37
    Match length
                       133
    % identity
    NCBI Description
                       (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]
    Seq. No.
                       308186
    Seq. ID
                       uC-zmflmo17078h10b1
    Method
                       BLASTX
    NCBI GI
                       q4572679
    BLAST score
                       305
    E value
                       7.0e-28
    Match length
                       108
    % identity
                       59
    NCBI Description
                       (AC006954) RSZp22 splicing factor; contains RNA recognition
                       motif [Arabidopsis thaliana]
```

Seq. No. 308187

Seq. ID uC-zmflmo17079a01b1

Method BLASTX
NCBI GI g2369714
BLAST score 312

```
89
```

```
E value
                   6.0e-29
                                          `~
Match length
% identity
                  72
NCBI Description
                  (Z97178) elongation factor 2 [Beta vulgaris]
Seq. No.
                  308188
Seq. ID
                  uC-zmflmo17079a05b1
Method
                  BLASTX
NCBI GI
                  g2244780
BLAST score
                  174
E value
                  1.0e-12
Match length
                  86
                  47
% identity
NCBI Description
                  (Z97335) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  308189
Seq. ID
                  uC-zmflmo17079a10b1
Method
                  BLASTX
NCBI GI
                  g2984709
BLAST score
                  198
E value
                  1.0e-25
Match length
                  98
% identity
NCBI Description
                  (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]
Seq. No.
                  308190 .
Seq. ID
                  uC-zmflmo17079b02b1
Method
                  BLASTX
NCBI GI
                  g2961285
BLAST score
                  157
E value
                  1.0e-10
Match length
                  52
% identity
NCBI Description
                  (Y16848) cinnamyl alcohol dehydrogenase-like protein,
                  subunit b [Arabidopsis thaliana]
Seq. No.
                  308191
Seq. ID
                  uC-zmflmo17079c09b1
Method
                  BLASTN
NCBI GI
                  g575730
BLAST score
                  88
                  4.0e-42
E value
Match length
                  188
% identity
                  88
NCBI Description
                  Z.mays mRNA for transmembrane protein
Seq. No.
                  308192
Seq. ID
                  uC-zmflmo17079d04b1
Method
```

BLASTX NCBI GI g3212848 BLAST score 174 E value 4.0e-13 Match length 67 57 % identity

NCBI Description (AC004005) putative inositol polyphosphate-5-phosphatase

[Arabidopsis thaliana]

```
Seq. No.
                  308193
Seq. ID
                  uC-zmflmo17079g06a1
Method
                  BLASTN
NCBI GI
                  g416146
BLAST score
                  228
E value
                  1.0e-125
Match length
                  275
                  96
% identity
NCBI Description Zea mays beta-6 tubulin (tub6) gene and mRNA, complete cds
Seq. No.
                  308194
Seq. ID
                  uC-zmflmo17083b01a1
Method
                  BLASTN
NCBI GI
                  g758354
BLAST score
                  94
                  1.0e-45
E value
Match length
                  153
% identity
                  91
NCBI Description Z.mays mRNA for plasma membrane H+ ATPase
Seq. No.
                  308195
Seq. ID
                  uC-zmflmo17083d10a1
Method
                  BLASTN
NCBI GI
                  g1060934
BLAST score
                  50
                  2.0e-19
E value
Match length
                  123
% identity
                  86
NCBI Description Maize mRNA for mLIP15 (DNA-binding factor), complete cds
Seq. No.
                  308196
Seq. ID
                  uC-zmflmo17083e11a1
Method
                  BLASTN
NCBI GI
                  q1244659
BLAST score
                  72
                  2.0e-32
E value
Match length
                  166
% identity
                  93
NCBI Description Zea mays copia-type retroelement PREM-2, partial sequence
Seq. No.
                  308197
                  uC-zmflmo17084b02a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4583431
BLAST score
                  236
E value
                  2.0e-20
Match length
                  54
% identity
                  83
NCBI Description (AF126489) rough sheath2 protein [Zea mays]
                  308198
Seq. No.
Seq. ID
                  uC-zmflmo17084f11a1
```

BLAST score 219 E value 6.0e-18

BLASTX g3779218

Match length 67

Method

NCBI GI BLAST score



% identity NCBI Description (AF030879) protein kinase CPK1 [Solanum tuberosum] Seq. No. 308199 uC-zmflmo17084q10a1 Seq. ID Method BLASTN NCBI GI q2832242 BLAST score 65 E value 4.0e-28 Match length 109 % identity 90 NCBI Description Zea mays 22-kDa alpha zein gene cluster, complete sequence 308200 Seq. No.

Seq. ID uC-zmflmo17085a02a1

Method BLASTX NCBI GI g2129587 BLAST score 321 E value 1.0e-29 Match length 125 % identity 45

gamma-qlutamyltransferase (EC 2.3.2.2) - Arabidopsis NCBI Description

thaliana >gi 928934 emb CAA89206 (Z49240) gamma-glutamyl

transpeptidase [Arabidopsis thaliana]

>gi 1585436 prf 2124427C gamma-Glu transpeptidase

[Arabidopsis thaliana]

308201 Seq. No.

Seq. ID uC-zmflmo17085d06a1

Method BLASTN NCBI GI q575425 BLAST score 58 6.0e-24 E value Match length 96 % identity 100

NCBI Description Z.mays mRNA for sugar-starvation induced protein

Seq. No. 308202

uC-zmflmo17085h12a1 Seq. ID

Method BLASTN g22091 NCBI GI BLAST score 268 E value 1.0e-149 Match length 325 % identity 96

NCBI Description Z.diploperennis gene for hydroxyproline-rich glycoprotein

Seq. No. 308203

uC-zmflmo17086b09a1 Seq. ID

Method BLASTX NCBI GI q4468813 BLAST score 143 2.0e-09 E value Match length 52 % identity 50

NCBI Description (AL035601) putative protein [Arabidopsis thaliana]

```
Seq. No.
                   308204
Seq. ID
                   uC-zmflmo17086f07a1
Method
                   BLASTN
NCBI GI
                   q1743387
BLAST score
                   40
E value
                   3.0e-13
Match length
                   99
% identity
                   88
NCBI Description
                  S.bicolor mRNA for pSbaNS5 protein
Seq. No.
                   308205
Seq. ID
                   uC-zmflmo17086g10a1
Method
                   BLASTN
NCBI GI
                   q1143704
BLAST score
                   119
E value
                   1.0e-60
Match length
                   159
% identity
                   94
NCBI Description Z.mays mRNA for homeobox 2a protein
Seq. No.
                   308206
Seq. ID
                  uC-zmflmo17087q08a1
Method
                   BLASTN
NCBI GI
                   g2921303
BLAST score
                   176
E value
                   2.0e-94
Match length
                   228
% identity
                   94
NCBI Description
                  Zea mays herbicide safener binding protein (SBP1) mRNA,
                   complete cds
Seq. No.
                   308207
Seq. ID
                   uC-zmflmo17090a05a1
Method
                  BLASTX
NCBI GI
                   g4454482
BLAST score
                  159
E value
                   1.0e-15
Match length
                  72
% identity
                   49
NCBI Description
                  (AC006234) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  308208
Seq. ID
                  uC-zmflmo17090e02a1
Method
                  BLASTN
NCBI GI
                  g3452302
BLAST score
                  108
E value
                  8.0e-54
Match length
                  288
% identity
                  89
NCBI Description
                  Zea mays retrotransposon Milt 3' LTR, partial sequence
```

Seq. No. 308209

Seq. ID uC-zmflmo17092f04a1

Method BLASTX
NCBI GI g3645898
BLAST score 284
E value 1.0e-25

Match length

% identity

106 47

```
Match length
% identity
                   63
NCBI Description
                   (U68408) in-frame stop codon; possibly a post-transposition
                  mutation [Zea mays]
                   308210
Seq. No.
Seq. ID
                   uC-zmflmo17095b07b3
Method
                   BLASTX .
                   g2760349
NCBI GI
BLAST score
                   621
E value
                   7.0e-65
Match length
                  135
% identity
                   20
NCBI Description
                  (U84969) ubiquitin [Arabidopsis thaliana]
                   308211
Seq. No.
Seq. ID
                  uC-zmflmo17095b08b3
Method
                  BLASTX
NCBI GI
                   q82512
BLAST score
                   662
E value
                  1.0e-69
                                                                       .--
Match length
                  142
                   42
% identity
NCBI Description
                  ubiquitin precursor - rice (fragment)
                  >gi_218189_dbj_BAA02241_ (D12776) poly-ubiquitin [Oryza
                   sativa]
                   308212
Seq. No.
Seq. ID
                  uC-zmflmo17095c12b2
Method
                  BLASTX
NCBI GI
                  g451193
BLAST score
                  172
E value
                  2.0e-12
Match length
                   63
                  57
% identity
NCBI Description
                  (L28008) wali7 [Triticum aestivum]
                  >gi_1090845_prf__2019486B wali7 gene [Triticum aestivum]
Seq. No.
                  308213
Seq. ID
                  uC-zmflmo17095d04b3
Method
                  BLASTN
NCBI GI-
                  g22332
BLAST score
                  149
E value
                  3.0e-78
Match length
                  288
% identity
                  88
NCBI Description
                  Z.mays HRGP gene
Seq. No.
                  308214
Seq. ID
                  uC-zmflmo17095d12b3
Method
                  BLASTX
NCBI GI
                  q3256066
BLAST score
                  229
E value
                  4.0e-19
```

43801

NCBI Description (Y13987) chloroplast NAD-MDH [Arabidopsis thaliana]

```
Seq. No.
                    308215
                    uC-zmflmo17095f08b3
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    q82496
                    227
 BLAST score
 E value
                    4.0e-19
Match length
                    73
                    66<sup>°</sup>
 % identity
                   phenylalanine ammonia-lyase (EC 4.3.1.5) - rice
 NCBI Description
 Seq. No.
                    308216
                    uC-zmflmo17095f11b3
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g3821254
 BLAST score
                    232
                    2.0e-19
 E value
 Match length
                    85
 % identity
                    58
 NCBI Description
                   (AJ007789) geranylgeranyl reductase [Nicotiana tabacum]
                    308217
 Seq. No.
 Seq. ID
                    uC-zmflmo17095g08b3
 Method
                    BLASTX
                    g1352268
 NCBI GI
 BLAST score
                    141
                    3.0e-09
• E value
 Match length
                    58
 % identity
                    53
                    DEOXYHYPUSINE SYNTHASE >gi 1019423 (U22400) deoxyhypusine
 NCBI Description
                    synthase [Neurospora crassa]
                    308218
 Seq. No.
 Seq. ID
                    uC-zmflmo17097c06b1
 Method
                    BLASTX
 NCBI GI
                    q2827536
 BLAST score
                    189
 E value
                    2.0e-14
 Match length
                    73
 % identity
                    47
 'NCBI Description
                   (AL021633) hypothetical protein [Arabidopsis thaliana]
 Seq. No.
                    308219
 Seq. ID
                    uC-zmflmo17097d02b1
 Method
                    BLASTX
 NCBI GI
                    q464980
 BLAST score
                    142
 E value
                    1.0e-08
 Match length
                    43
 % identity
                    79
                   UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN
 NCBI Description
                    LIGASE) (UBIQUITIN CARRIER PROTEIN) >qi 166422 (L06967)
                    ubiquitin carrier protein [Medicago sativa]
 Seq. No.
                    308220
 Seq. ID
                    uC-zmflmo17097e03b1
 Method
                    BLASTX
```

NCBI GI

```
g4375829
NCBI GI
BLAST score
                  307
E value
                  4.0e-28
Match length
                  118
% identity
                  51
                   (AJ011977) RNA-directed RNA polymerase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  308221
Seq. ID
                  uC-zmflmo17099d03b1
Method
                  BLASTN
NCBI GI
                  g257040
BLAST score
                  287
E value
                  1.0e-160
Match length
                  525
% identity
                  30
NCBI Description
                  hydroxyproline-rich glycoprotein [maize, Genomic, 1703 nt]
Seq. No.
                  308222
Seq. ID
                  uC-zmflmo17099d04b1
Method
                  BLASTN
NCBI GI
                  q3057121
BLAST score
                  34
E value
                  2.0e-09
Match length
                  54
% identity
                  91
NCBI Description
                  Zea mays starch synthase DULL1 (dull1) gene, partial cds
Seq. No.
                  308223
                  uC-zmflmo17099e03b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4539330
BLAST score
                  463
                  3.0e-46
E value
Match length
                  135
% identity
                  64
NCBI Description
                   (AL035679) putative receptor-like protein kinase (fragment)
                   [Arabidopsis thaliana]
Seq. No.
                  308224
Seq. ID
                  uC-zmflmo17099g01b1
Method
                  BLASTX
NCBI GI
                  q729762
BLAST score
                  171
                  4.0e-16
E value
Match length
                  104
% identity
                  52
NCBI Description
                  17.0 KD CLASS II HEAT SHOCK PROTEIN (HSP 18)
                  >gi_477225_pir__A48425 heat shock protein HSP18 - maize
                  >gi 300079 bbs 130952 (S59777) HSP18=18 kda heat shock
                  protein [Zea mays, Oh43, clone cMHSP18-1, Peptide, 154 aa]
                   [Zea mays]
Seq. No.
                  308225
Seq. ID
                  uC-zmflmo17099g07b1
Method
                  BLASTX
```

g1915974

NCBI GI

E value

BLAST score

Match length

g3287695

1.0e-23

265

125

```
BLAST score
E value
                  1.0e-14
Match length
                  169
% identity
                  32
NCBI Description
                  (U62329) fructokinase [Lycopersicon esculentum] >gi 2102693
                   (U64818) fructokinase [Lycopersicon esculentum]
Seq. No.
                  308226
Seq. ID
                  uC-zmflmo17099q11b1
Method
                  BLASTX
NCBI GI
                  g3881189
BLAST score
                  329
E value
                  9.0e-31
Match length
                  91
% identity
NCBI Description
                  (Z99281) similar to ADP-ribosylation factor; cDNA EST
                  EMBL: C08179 comes from this gene; cDNA EST EMBL: C08337
                  comes from this gene; cDNA EST EMBL: C09829 comes from this
                  gene; cDNA EST yk291b4.5 comes from this gene; cDNA EST yk4
Seq. No.
                  308227
Seq. ID
                  uC-zmflmo17099h10b1
Method
                  BLASTX
NCBI GI
                  g2058273
BLAST score
                  474
E value
                  2.0e-47
Match length
                  113
% identity
NCBI Description (D83527) YK426 [Oryza sativa]
Seq. No.
                  308228
Seq. ID
                  uC-zmflmo17100a09b1
Method
                  BLASTX
NCBI GI
                  g2262105
BLAST score
                  470
E value
                  4.0e-47
Match length
                  144
% identity
                  60
                  (AC002343) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  308229
                  uC-zmflmo17100c07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2660688
BLAST score
                  222
                  5.0e-18
E value
Match length
                  88
% identity
                  43
NCBI Description (U85247) Naglu [Mus musculus]
                  308230
Seq. No.
                  uC-zmflmo17100c09b1
Seq. ID
Method
                  BLASTX
```

43804



% identity

NCBI Description (AC003979) Similar to hypothetical protein C34B7.2

gb 1729503 from C. elegans cosmid gb Z83220. [Arabidopsis

thaliana]

Seq. No.

308231

Seq. ID

uC-zmflmo17100c10b1

Method NCBI GI BLASTX q3287695

BLAST score E value

203

Match length

4.0e-16 97

% identity

45

NCBI Description

(AC003979) Similar to hypothetical protein C34B7.2

gb 1729503 from C. elegans cosmid gb_Z83220. [Arabidopsis

thaliana]

Seq. No.

308232

Seq. ID

uC-zmflmo17100c12b1

Method NCBI GI BLASTN g22332 258

BLAST score E value

1.0e-143

Match length

373

% identity

92

NCBI Description Z.mays HRGP gene

Seq. No.

308233

Seq. ID

uC-zmflmo17100g03b1

Method NCBI GI BLASTX g2160185

BLAST score

284

E value

2.0e-25

Match length % identity

102 58

NCBI Description

(AC000132) Similar to S. pombe ISP4 (gb_D83992).

[Arabidopsis thaliana]

Seq. No.

308234

Seq. ID

uC-zmflmo17100g08b1

Method NCBI GI BLASTX g135417

BLAST score

316

E value

3.0e-29

Match length

60 95

% identity NCBI Description

TUBULIN ALPHA-3 CHAIN >gi 100946 pir JN0105 tubulin

alpha-3 chain - maize >gi 22150 emb CAA44861 (X63176) Alpha-tubulin #3 [Zea mays] >gi 485377 (M60171) alpha-3

tubulin [Zea mays]

Seq. No.

308235

Seq. ID

uC-zmflmo17101b05b1

Method NCBI GI BLASTN

BLAST score

g507844

35

E value

5.0e-10



Match length 259 79 % identity 🚓

NCBI Description Zea mays A188 retrotransposon gag gene, complete cds

Seq. No.

308236

Seq. ID

uC-zmflmo17101b08b1

Method NCBI GI BLAST score BLASTX g3355533 189

E value Match length % identity

4.0e-14 130 31

NCBI Description

(AL021331) dJ366N23.1 (putative C. elegans UNC-93 (protein

1, C46F11.1) LIKE protein) [Homo sapiens]

Seq. No.

308237

Seq. ID uC-zmflmo17101e07b1

Method BLASTN NCBI GI g22332 BLAST score 238 E value 1.0e-131 Match length 317 % identity 94

NCBI Description Z.mays HRGP gene

Seq. No.

308238

Seq. ID uC-zmflmo17101f11b1

Method BLASTX NCBI GI g1507699 BLAST score 151 1.0e-09 E value Match length 105 % identity 35

NCBI Description (L81119) COL2 [Arabidopsis thaliana] >gi 1507701 (L81120)

COL2 [Arabidopsis thaliana]

Seq. No. 308239

Seq. ID uC-zmflmo17102g04a1

Method BLASTX NCBI GI q4454019 BLAST score 224 E value 2.0e-18 Match length 93 % identity 47

NCBI Description (AL035396) SRG1-like protein [Arabidopsis thaliana]

Seq. No. 308240

Seq. ID uC-zmflmo17103b12b1

Method BLASTX NCBI GI g3551247 BLAST score 229 E value 5.0e-19 Match length 60

% identity 73

NCBI Description (AB012703) 181 [Daucus carota]

Seq. No. 308241

```
Seq. ID
                   uC-zmflmo17103c01b1
Method
                   BLASTX
NCBI GI
                   g2369714
BLAST score
                   235
E value
                   1.0e-30
Match length
                   136
% identity
                   53
NCBI Description
                  (Z97178) elongation factor 2 [Beta vulgaris]
Seq. No.
                   308242
Seq. ID
                   uC-zmflmo17103c02b1
Method
                   BLASTX
NCBI GI
                   g3377797
BLAST score
                   322
E value
                   1.0e-35
Match length
                   125
% identity
                   (AF075597) Similar to 60S ribosome protein L19; coded for
NCBI Description
                   by A. thaliana cDNA T04719; coded for by A. thaliana cDNA
                   H36046; coded for by A. thaliana cDNA T44067; coded for by
                   A. thaliana cDNA T14056; coded for by A. thaliana cDNA
                  R90691 [Ara
Seq. No.
                   308243
Seq. ID
                  uC-zmflmo17103e02b1
Method
                  BLASTX
NCBI GI
                   g4503527
BLAST score
                   160
E value
                   9.0e-11
Match length
                  113
% identity
                   40
NCBI Description
                  UNKNOWN >gi 1778051 (U62583) Prt1 homolog [Homo sapiens]
                  308244
Seq. No.
Seq. ID
                  uC-zmflmo17103e04b1
Method
                  BLASTN
NCBI GI
                  g3273244
BLAST score
                  63
                  3.0e-27
E value
Match length
                  158
% identity
                  86
NCBI Description Oryza sativa DNA for NLS receptor, complete cds
Seq. No.
                  308245
Seq. ID
                  uC-zmflmo17103e12b1
Method
                  BLASTX
NCBI GI
                  g1703129
BLAST score
                  682
E value
                  6.0e-72
Match length
                  128
% identity
                  99
NCBI Description
                  ACTIN 11 >gi_2129522 pir S68109 actin 11 - Arabidopsis
```

thaliana >gi_1002533 (U27981) actin-11 [Arabidopsis

thaliana]

Seq. No.

308246

Seq. ID

uC-zmflmo17103g06b1

Method BLASTX
NCBI GI g3142300
BLAST score 148
E value 3.0e-09
Match length 75
% identity 49

NCBI Description (AC002411) Contains similarity to pre-mRNA processing

protein PRP39 gb_L29224 from S. cerevisiae. ESTs gb_R64908 and gb T88158, gb N38703 and gb AA651043 come from this

gene. [Arabidopsis thaliana]

Seq. No. 308247

Seq. ID uC-zmflmo17103g10b1

Method BLASTN
NCBI GI g4007864
BLAST score 197
E value 1.0e-107
Match length 266
% identity 86

NCBI Description Zea mays HRGP gene, AC1503 line

Seq. No. 308248

Seq. ID uC-zmflmo17103g11b1

Method BLASTN
NCBI GI g1310676
BLAST score 41
E value 8.0e-14
Match length 85

% identity 8

NCBI Description H.vulgare mRNA for serpin

Seq. No. 308249

Seq. ID uC-zmflmo17103h10b1

Method BLASTX
NCBI GI g1839597
BLAST score 303
E value 9.0e-28
Match length 78

% identity 73

NCBI Description (S82324) calcium/calmodulin-dependent protein kinase

homolog CaM kinase homolog MCK1 [Zea mays=maize, cv. Merit,

Jr.

root caps, Peptide, 625 aa] [Zea mays]

Seq. No. 308250

Seq. ID uC-zmflmo17104a02b1

Method BLASTX
NCBI GI g3252807
BLAST score 231
E value 3.0e-19
Match length 131
% identity 43

NCBI Description (AC004705) hypothetical protein [Arabidopsis thaliana]

Seq. No. 308251

Seq. ID uC-zmflmo17104g03b1

Method BLASTN NCBI GI g2425065

43808



BLAST score 70 E value 2.0e-31 Match length 104 % identity 91

NCBI Description Zea mays cysteine proteinase Mir3 (mir3) mRNA, complete cds

Seq. No. 308252

Seq. ID uC-zmflmo17105b11b1

Method BLASTX
NCBI GI g3600033
BLAST score 320
E value 3.0e-38
Match length 108
% identity 75

NCBI Description (AF080119) contains similarity to the N terminal domain of

the El protein (Pfam: El_N.hmm, score: 12.36) [Arabidopsis

thaliana]

Seq. No. 308253

Seq. ID uC-zmflmo17105c07b1

Method BLASTX
NCBI GI g1170029
BLAST score 195
E value 2.0e-15
Match length 57
% identity 68

NCBI Description GLUTAMATE-1-SEMIALDEHYDE 2,1-AMINOMUTASE PRECURSOR (GSA)

(GLUTAMATE-1-SEMIALDEHYDE AMINOTRANSFERASE) (GSA-AT)

>gi_100581_pir__A35789 glutamate-1-semialdehyde

2,1-aminomutase (EC 5.4.3.8) - barley >gi_506383 (M31545) glutamate 1-semialdehyde aminotransferase [Hordeum vulgare]

Seq. No. 308254

Seq. ID uC-zmflmo17105e01b1

Method BLASTX
NCBI GI g3033399
BLAST score 312
E value 1.0e-28
Match length 129
% identity 7

NCBI Description (AC004238) hypothetical protein [Arabidopsis thaliana]

Seq. No. 308255

Seq. ID uC-zmflmo17107b11a1

Method BLASTN
NCBI GI g22091
BLAST score 180
E value 6.0e-97
Match length 227
% identity 96

NCBI Description Z.diploperennis gene for hydroxyproline-rich glycoprotein

Seq. No. 308256

Seq. ID uC-zmflmo17107h07a1

MethodBLASTNNCBI GIg22091BLAST score252

```
E value
                  1.0e-140
Match length
                  288
                  97
% identity
                  Z.diploperennis gene for hydroxyproline-rich glycoprotein
NCBI Description
Seq. No.
                  308257
                  uC-zmflmo17108a03b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q70645
BLAST score
                  662
E value
                  1.0e-69
                  136
Match length
% identity
                  ubiquitin precursor - garden pea >gi 20589 emb CAA34886
NCBI Description
                  (X17020) polyubiquitin (AA 1-381) [Pisum sativum]
                  >qi 4115339 (L81142) ubiquitin [Pisum sativum]
                  >qi 226707 prf 1603402A poly-ubiquitin [Pisum sativum]
                  308258
Seq. No.
Seq. ID
                  uC-zmflmo17108a11a1
Method
                  BLASTN
```

Seq. ID uC-zmflmo1
Method BLASTN
NCBI GI g902583
BLAST score 106
E value 8.0e-53
Match length 203
% identity 87

NCBI Description Zea mays clone MubGl ubiquitin gene, complete cds

308259 Seq. No. Seq. ID uC-zmflmo17108c10b1 BLASTX Method NCBI GI q4102839 BLAST score 258 1.0e-22 E value 72 Match length % identity 64

NCBI Description (AF016713) LeOPT1 [Lycopersicon esculentum]

 Seq. No.
 308260

 Seq. ID
 uC-zmflmo17108d01b1

Method BLASTX
NCBI GI g3063456
BLAST score 153
E value 7.0e-10
Match length 98
% identity 36

NCBI Description (AC003981) F22013.18 [Arabidopsis thaliana]

Seq. No. 308261

Seq. ID uC-zmflmo17108d04a1

Method BLASTN
NCBI GI g22091
BLAST score 112
E value 2.0e-56
Match length 221
% identity 89

NCBI Description Z.diploperennis gene for hydroxyproline-rich glycoprotein

```
Seq. No.
                  308262
Seq. ID
                  uC-zmflmo17108d04b1
Method
                  BLASTN
NCBI GI
                  g257040
BLAST score
                  327
E value
                  0.0e + 00
Match length
                  351
% identity
                  25
NCBI Description hydroxyproline-rich glycoprotein [maize, Genomic, 1703 nt]
                  308263
Seq. No.
Seq. ID
                  uC-zmflmo17108d09b1
Method
                  BLASTX
NCBI GI
                  g3193292
BLAST score
                  201
                  5.0e-16
E value
Match length
                  77
                  49
% identity
                  (AF069298) similar to ATPases associated with various
NCBI Description
                  cellular activites (Pfam: AAA.hmm, score: 230.91)
                   [Arabidopsis thaliana]
Seq. No.
                  308264
Seq. ID
                  uC-zmflmo17108f05b1
Method
                  BLASTN
NCBI GI
                  g4007864
BLAST score
                  87
E value
                  1.0e-41
Match length
                  131
% identity
                  92
NCBI Description Zea mays HRGP gene, AC1503 line
Seq. No.
                  308265
Seq. ID
                  uC-zmflmo17108f12b1
Method
                  BLASTX
NCBI GI
                  g1122317
BLAST score
                  249
E value
                  6.0e-35
Match length
                  104
% identity
                  70
NCBI Description
                  (X94193) heat shock protein 17.9 [Pennisetum glaucum]
                  308266
Seq. No.
                  uC-zmflmo17108q04b1
Seq. ID
Method
                  BLASTX
                  g2792216
                  253
```

NCBI GI g2792210
BLAST score 253
E value 1.0e-21
Match length 129
% identity 44

NCBI Description (AF032686) NBS-LRR type resistance protein [Hordeum

vulgare]

Seq. No. 308267

Seq. ID uC-zmflmo17108g05a1

Method BLASTN

43811



```
NCBI GI
                   g4416300
BLAST score
                   41
                   9.0e-14
E value
Match length
                   53
% identity
                   48
```

NCBI Description Zea mays chromosome 4 22 kDa zein-associated intercluster

region, complete sequence

Seq. No. 308268

uC-zmflmo17108h08b1 Seq. ID

Method BLASTX NCBI GI g1684855 BLAST score 379 E value 1.0e-36 Match length 86 % identity 19

(U77939) ubiquitin-like protein [Phaseolus vulgaris] NCBI Description

Seq. No.

308269 uC-zmflmo17109a11a1 Seq. ID

Method BLASTX NCBI GI g3201617 BLAST score 179 E value 3.0e-13

Match length 68 % identity 44

NCBI Description (AC004669) hypothetical protein [Arabidopsis thaliana]

Seq. No. 308270

uC-zmflmo17109c04b1 Seq. ID

Method BLASTX NCBI GI g3860277 BLAST score 224 2.0e-18 E value Match length 104 % identity 47

NCBI Description (AC005824) putative ribosomal protein L10 [Arabidopsis

thaliana] >gi_4314394_gb_AAD15604_ (AC006232) putative

ribosomal protein L10A [Arabidopsis thaliana]

Seq. No. 308271

uC-zmflmo17109c11b1 Seq. ID

Method BLASTX NCBI GI q283045 BLAST score 216 E value 1.0e-17 Match length 85 55 % identity

NCBI Description hydroxyproline-rich glycoprotein - maize

>gi_22333_emb_CAA44844_ (X63134) hydroxyproline-rich

glycoprotein [Zea mays] >gi_228936_prf__1814452A Hyp-rich

glycoprotein [Zea mays]

Seq. No. 308272

. J. .

uC-zmflmo17109d11b1 Seq. ID

Method BLASTX NCBI GI q4006898

```
BLAST score
E value
                    6.0e-54
Match length
                   141
 % identity
                   74
                    (Z99708) splicing factor-like protein [Arabidopsis
NCBI Description
Seq. No.
                   308273
Seq. ID
                   uC-zmflmo17109e06a1
Method
                   BLASTX
NCBI GI
                   g3132310
BLAST score
                   186
E value
                   3.0e-14
Match length
                   38
% identity
                   97
NCBI Description
                   (AB012228) phosphoenolpyruvate carboxylase [Zea mays]
Seq. No.
                   308274
Seq. ID
                   uC-zmflmo17109f03b1
Method
                   BLASTX
NCBI GI
                <u>⊸</u>, g3152606
BLAST score
                   203
E value
                   9.0e-16
Match length
                   53
% identity
                   53
NCBI Description
                   (AC004482) putative ring zinc finger protein [Arabidopsis
                   thalianal
Seq. No.
                   308275
Seq. ID
                   uC-zmflmo17109q05b1
Method
                   BLASTX
NCBI GI
                   g82734
BLAST score
                   706
E value
                   9.0e-75
Match length
                   148
% identity
                   29
NCBI Description
                   ubiquitin precursor - maize (fragment)
                   >gi_226763_prf__1604470A poly-ubiquitin [Zea mays]
Seq. No.
                   308276
Seq. ID
                   uC-zmflmo17109q08b1
Method
                   BLASTX
NCBI GI
                   g2739367
BLAST score
                   241
E value
                   2.0e-20
Match length
                   92
% identity
                   25
```

NCBI Description

(AC002505) putative phosphatidylinositol-4-phosphate

5-kinase [Arabidopsis thaliana]

Seq. No. 308277

Seq. ID uC-zmflmo17109h04b1

Method BLASTX NCBI GI g320608 BLAST score 655 E value 8.0e-69 Match length 139



% identity NCBI Description ubiquitin precursor - wild oat >gi_15989_emb_CAA49200 (X69422) tetraubiquitin [Avena fatua] >gi 777758 (L41658) polyubiquitin [Saccharum sp.] Seq. No. 308278 Seq. ID uC-zmflmo17113a10b1 Method BLASTX NCBI GI q1709798 BLAST score 259 E value 1.0e-22 Match length 85 % identity 67 NCBI Description 26S PROTEASE REGULATORY SUBUNIT 6B HOMOLOG >gi 1155334 (U43398) POTATP1 [Solanum tuberosum] Seq. No. 308279 Seq. ID uC-zmflmo17113b08a1 Method BLASTX NCBI GI g480670 BLAST score 151 E value 6.0e-10 Match length 44 % identity 66 NCBI Description NADPH--ferrihemoprotein reductase (EC 1.6.2.4) - Jerusalem artichoke (fragment) Seq. No. 308280 Seq. ID uC-zmflmo17113c04b1 Method BLASTX g1890575 NCBI GI BLAST score 292 E value 2.0e-26 Match length 76 % identity 70 NCBI Description (X93174) xyloglucan endotransglycosylase (XET) [Hordeum vulgare] Seq. No. 308281 Seq. ID uC-zmflmo17113d05b1 Method BLASTX NCBI GI g1082285 BLAST score 184 E value 1.0e-13 Match length 98 % identity 44 NCBI Description protein kinase (EC 2.7.1.37) cdc2-related PITSLRE alpha 2-3 - human

Seq. No. 308282

Seq. ID uC-zmflmo17113g04b1 Method BLASTX

NCBI GI g3287696
BLAST score 267
E value 2.0e-23
Match length 103
% identity 48



(AC003979) Strong similarity to phosphoribosylanthranilate NCBI Description transferase gb D86180 from Pisum sativum. This ORF may be part of a larger gene that lies in the overlapping region. [Arabidopsis thaliana] Seq. No. 308283 Seq. ID uC-zmflmo17114d05a1 Method BLASTN NCBI GI g3452293 BLAST score 95 E value 5.0e-46 Match length 142 % identity 93 NCBI Description Zea mays retrotransposon Ji-1 5' LTR, partial sequence Seq. No. 308284 uC-zmflmo17115e07a1 Seq. ID Method BLASTX NCBI GI q2286200 BLAST score 266 E value 6.0e-25 Match length 84 % identity 75 NCBI Description (AF010578) polynucleotide phosphorylase [Pisum sativum] 308285 Seq. No. Seq. ID uC-zmflmo17115f03a1 Method BLASTN NCBI GI q1185553 BLAST score 73 E value 9.0e-33 Match length 144 % identity 44 NCBI Description Zea mays glyceraldehyde-3-phosphate dehydrogenase (gpc2) gene, complete cds Seq. No. 308286 Seq. ID uC-zmflmo17116b01b1 Method BLASTX NCBI GI q3420801 BLAST score 217 E value 1.0e-17 Match length 90 % identity 49 NCBI Description (AF081066) IAA-amino acid hydrolase homolog ILL3 [Arabidopsis thaliana] Seq. No. 308287

Seq. ID uC-zmflmo17116b04b1

Method BLASTX NCBI GI q4249386 BLAST score 467 E value 9.0e-47 Match length 104 % identity 88

(AC005966) Strong similarity to gb_AF061286 gamma-adaptin 1 NCBI Description from Arabidopsis thaliana. EST gb_H37393 comes from this



% identity

gene. [Arabidopsis thaliana]

```
308288
Seq. No.
Seq. ID
                  uC-zmflmo17116b07b1
Method
                  BLASTN
NCBI GI
                  q4007864
BLAST score
                  190
                  1.0e-102
E value
                  266
Match length
                  93
% identity
                  Zea mays HRGP gene, AC1503 line
NCBI Description
                  308289
Seq. No.
                  uC-zmflmo17116c02b1
Seq. ID
                  BLASTX
Method
NCBI GI
                   g2130442
BLAST score
                   185
E value
                   1.0e-13
                   123
Match length
% identity
                  hypothetical protein SPAC8A4.01c - fission yeast
NCBI Description
                   (Schizosaccharomyces pombe) (fragment)
                   >gi 1052534 emb_CAA91511_ (Z66569) unknown
                   [Schizosaccharomyces pombe]
                   308290
Seq. No.
Seq. ID
                   uC-zmflmo17116c06b1
                   BLASTN
Method
                   g22461
NCBI GI
BLAST score
                   105
                   4.0e-52
E value
                   169
Match length
% identity
                   91
NCBI Description
                  Maize RAB-17 gene
                   308291
Seq. No.
                   uC-zmflmo17116e07b1
Seq. ID
                   BLASTX
Method
                   g3875385
NCBI GI
BLAST score
                   223
                   6.0e-19
E value
                   105
Match length
% identity
                   53
                   (Z54284) similar to phosphatidylinositol biosynthetic
NCBI Description
                   protein; cDNA EST yk349e7.5 comes from this gene
                   [Caenorhabditis elegans]
                   308292
Seq. No.
                   uC-zmflmo17116f11a1
Seq. ID
                   BLASTN
Method
                   g342663
NCBI GI
                   53
BLAST score
E value
                   3.0e-21
                   53
Match length
```

NCBI Description Maize mitochondrial 18S ribosomal RNA gene

```
Seq. No.
                  uC-zmflmo17117c01b1
Seq. ID
                  BLASTN
Method
                  g1420923
NCBI GI
                  83
BLAST score
                  9.0e-39
E value
                  103
Match length
                   95
% identity
NCBI Description Zea mays repressor-like protein (in1) gene, complete cds
                   308294
Seq. No.
                  uC-zmflmo17117c07b1
Seq. ID
                   BLASTX
Method
                   g1946371
NCBI GI
                   152
BLAST score
                   3.0e-10
E value
                   65
Match length
                   46
% identity
                   (U93215) regulatory protein Viviparous-1 isolog
NCBI Description
                   [Arabidopsis thaliana]
                   308295
Seq. No.
                   uC-zmflmo17117c09b1
Seq. ID
                   BLASTX
Method
                   g112994
NCBI GI
                   421
BLAST score
                   2.0e-41
E value
                   84
Match length
% identity
                   GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN
NCBI Description
                   >gi_82685_pir__S04536 embryonic abundant protein,
                   glycine-rich - maize >gi_22313_emb_CAA31077_ (X12564)
                   ABA-inducible gene protein [Zea mays]
                   >gi_226091_prf__1410284A abscisic acid inducible gene [Zea
                   mays]
                   308296
Seq. No.
Seq. ID
                   uC-zmflmo17117d07b1
                   BLASTX
Method
                   g1703131
NCBI GI
                   175
BLAST score
                   8.0e-13
E value
                   43
Match length
 % identity
                   ACTIN 12 >gi_2129523_pir__S68110 actin 12 - Arabidopsis
NCBI Description
                   thaliana >gi_1002535 (U27982) actin-12 [Arabidopsis
                   thaliana]
 Seq. No.
                   308297
                   uC-zmflmo17117e06b1
 Seq. ID
                   BLASTN
 Method
                   g22435
 NCBI GI
 BLAST score
                   61
 E value
                   1.0e-25
 Match length
                   121
```

NCBI Description Z.mays PK1 gene for receptor-like protein kinase

89

% identity



```
308298
Seq. No.
                  uC-zmflmo17117h10b1
Seq. ID
Method
                  BLASTN
                  g22332
NCBI GI
                  286
BLAST score
                  1.0e-160
E value
                  380
Match length
                  94
% identity
NCBI Description Z.mays HRGP gene
                  308299
Seq. No.
                  uC-zmflmo17118c03a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g22342
BLAST score
                  37
                  1.0e-11
E value
Match length
                  61
% identity
                  90
                  Maize gene for heat shock protein 70 exon 2 and 3'-UT
NCBI Description
                   (hsp70; clone pMON 9502)
                  308300
Seq. No.
                  uC-zmflmo17118c03b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3962377
BLAST score
                  524
E value
                  2.0e-53
Match length
                  118
                  89
% identity
NCBI Description (AJ002551) heat shock protein 70 [Arabidopsis thaliana]
                   308301
Seq. No.
                  uC-zmflmo17118d11b1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g3821780
                   36
BLAST score
                   8.0e-11
E value
Match length
                   50
                   66
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                   308302
Seq. No.
                   uC-zmflmo17118d12b1
Seq. ID
                   BLASTX
Method
                   g4263722
NCBI GI
                   442
BLAST score
                   7.0e-51
E value
                   129
Match length
                   79
% identity
NCBI Description (AC006223) putative glucan synthase [Arabidopsis thaliana]
                   308303
Seq. No.
                   uC-zmflmo17118f04b1
Seq. ID
                   BLASTX
Method
```

g1890575

516

NCBI GI BLAST score

thaliana]

% identity

NCBI Description

```
1.0e-52
E value
Match length
                  119
% identity
                  76
NCBI Description
                   (X93174) xyloglucan endotransglycosylase (XET) [Hordeum
                  vulgare]
                  308304
Seq. No.
Seq. ID
                  uC-zmflmo17118g01b1
Method
                  BLASTX
NCBI GI
                  q3337367
BLAST score
                  333
                   4.0e-31
E value
                  123
Match length
                   52
% identity
                  (AC004481) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   308305
Seq. ID
                  uC-zmflmo17118g02b1
Method
                  BLASTN
NCBI GI
                   q22292
BLAST score
                   76
E value
                   1.0e-34
Match length
                   165
                   93
% identity
                  Z.mays mRNA for glycine-rich protein
NCBI Description
Seq. No.
                   308306
Seq. ID
                   uC-zmflmo17118g04b1
Method
                   BLASTX
NCBI GI
                   g2244787
BLAST score
                   383
E value
                   5.0e-37
                   134
Match length
% identity
                   57
                   (Z97335) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   308307
Seq. No.
                   uC-zmflmo17118h03b1
Seq. ID
Method
                   BLASTX
                   g4455327
NCBI GI
BLAST score
                   156
                   2.0e-10
E value
                   81
Match length
                   42
% identity
                   (AL035525) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   308308
Seq. No.
                   uC-zmflmo17121a03a1
Seq. ID
                   BLASTX
Method
                   g2262101
NCBI GI
BLAST score
                   172
                   3.0e-12
E value
Match length
                   59
```

(AC002343) kinesin heavy chain isolog [Arabidopsis



```
Seq. No.
Seq. ID
                  uC-zmflmo17121c04a1
Method
                  BLASTN
                  q22091
NCBI GI
                  181
BLAST score
                  2.0e-97
E value
Match length
                  230
                  95
% identity
NCBI Description Z.diploperennis gene for hydroxyproline-rich glycoprotein
                  308310
Seq. No.
                  uC-zmflmo17122a03a1
Seq. ID
Method
                  BLASTX
                  g1805254
NCBI GI
BLAST score
                  323
                  5.0e-30
E value
Match length
                  72
                  81
% identity
                  (U62622) monogalactosyldiacylglycerol synthase [Cucumis
NCBI Description
                  sativus]
                  308311
Seq. No.
                  uC-zmflmo17122a07b1
Seq. ID
Method
                  BLASTX
                  g1350548
NCBI GI
BLAST score
                  226
                  2.0e-18
E value
Match length
                   65
                   58
% identity
NCBI Description (L47609) heat shock-like protein [Picea glauca]
                   308312
Seq. No.
                   uC-zmflmo17122a11b1
Seq. ID
Method
                   BLASTN
                   q414704
NCBI GI
BLAST score
                   46
                   1.0e-16
E value
Match length
                   74
% identity
                   91
NCBI Description O.sativa mRNA for cytochrome b5
Seq. No.
                   308313
                   uC-zmflmo17122a12b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2281449
                   270
BLAST score
                   7.0e-24
E value
                   90
Match length
% identity
                   66
                   (U90214) leucine zipper transcription factor TGA2.1
NCBI Description
                   [Nicotiana tabacum]
Seq. No.
                   308314
```

Seq. ID uC-zmflmo17122b03b1

Method BLASTX
NCBI GI g1001607
BLAST score 185

NCBI GI

E value

BLAST score

g2827643 206

3.0e-16



```
3.0e-14
E value
                  66
Match length
                  45
% identity
                  (D64000) hypothetical protein [Synechocystis sp.]
NCBI Description
                  308315
Seq. No.
                  uC-zmflmo17122c07b1
Seq. ID
                  BLASTX
Method
                  g2160782
NCBI GI
                  443
BLAST score
                  5.0e-44
E value
                  126
Match length
                   71
% identity
                  (AF001505) putative ammonium transporter OsAMT1p [Oryza
NCBI Description
                   sativa]
                   308316
Seq. No.
                   uC-zmflmo17122c09a1
Seq. ID
                   BLASTN
Method
                   g12479
NCBI GI
                   94
BLAST score
                   3.0e-45
E value
                   160
Match length
                   96
% identity
                   Zea mays chloroplast trnC gene, rpoB gene, rpoCl gene,
NCBI Description
                   rpoC2 gene and rps2 gene for transfer RNA-Cys, RNA
                   polymerase subunits beta, beta-1, beta-2 and ribosomal
                   protein S2 respectively
                   308317
Seq. No.
                   uC-zmflmo17122c09b1
Seq. ID
                   BLASTX
Method
                   g3063700
NCBI GI
                   150
BLAST score
                   1.0e-09
E value
                   73
Match length
                   41
 % identity
                   (AL022537) putative protein [Arabidopsis thaliana]
NCBI Description
                   308318
 Seq. No.
                   uC-zmflmo17122d04b1
 Seq. ID
                   BLASTX
 Method
                   g135411
 NCBI GI
 BLAST score
                   684
                   3.0e-72
 E value
                   131
 Match length
                   97
 % identity
                   TUBULIN ALPHA-2 CHAIN >gi_82732_pir__S15772 tubulin alpha-2
 NCBI Description
                   chain - maize >gi_22148_emb_CAA33733_ (X15704)
                   alpha2-tubulin [Zea mays]
                    308319
 Seq. No.
                    uC-zmflmo17122e02b1
 Seq. ID
 Method
                   BLASTX
```

43821



```
Match length
% identity
                  (AL021636) predicted protein [Arabidopsis thaliana]
NCBI Description
                  >gi_3549641_emb_CAA06432_ (AJ005195) receiver-like protein
                  4 [Arabidopsis thaliana]
                  308320
Seq. No.
                  uC-zmflmo17122e07b1
Seq. ID
                  BLASTN
Method
                  q3510343
NCBI GI
                  46
BLAST score
                  9.0e-17
E value
                  90
Match length
                  88
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MJC20, complete sequence [Arabidopsis thaliana]
                  308321
Seq. No.
                  uC-zmflmo17122h03b1
Seq. ID
                  BLASTN
Method
                  g22312
NCBI GI
                  36
BLAST score
                  3.0e-11
E value
Match length
                   68
                   88
% identity
                  Maize ABA-inducible gene for glycine-rich protein ( ABA =
NCBI Description
                  abscisic acid)
                   308322
Seq. No.
                   uC-zmflmo17122h07b1
Seq. ID
                   BLASTN
Method
                   g169843
NCBI GI
                   42
BLAST score
                   1.0e-14
E value
                   86
Match length
                   87
% identity
                   Saccharum sp. phosphoenolpyruvate carboxylase (SCPEPCD1)
NCBI Description
                   gene, complete cds
                   308323
Seq. No.
                   uC-zmflmo17123d12a1
Seq. ID
                   BLASTX
Method
                   a548702
NCBI GI
BLAST score
                   239
                   4.0e-20
E value
                   80
Match length
                   51
 % identity
                   DNA-DIRECTED RNA POLYMERASE II 14.5 KD POLYPEPTIDE (RPB9)
NCBI Description
                   (RPB14.5) >gi_543001_pir__S41621 DNA-directed RNA
                   polymerase (EC 2.7.7.6) II 14.5K chain - human
                   >gi_397150_emb_CAA80649_ (Z23102) RNA Polymerase II subunit
                   14.5 kD [Homo sapiens] >gi_1905901 (AD001527) HUMAN
                   DNA-DIRECTED RNA POLYMERASE II 14.5 KD SUBUNIT [Homo
                   sapiens]
```

308324

uC-zmflmo17125a03b1

Seq. No.

Seq. ID



```
BLASTX
Method
                   g4510345
NCBI GI
BLAST score
                   155
                   2.0e-10
E value
Match length
                   86
% identity
                   40
                   (AC006921) unknown protein [Arabidopsis thaliana]
NCBI Description
                   308325
Seq. No.
                   uC-zmflmo17125c11b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g854731
BLAST score
                   763
                   2.0e-81
E value
                   147
Match length
% identity
                   99
                   (U19183) acetyl-coenzyme A carboxylase [Zea mays]
NCBI Description
                   308326
Seq. No.
                   uC-zmflmo17125d07b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3779024
                   503
BLAST score
                   4.0e-51
E value
                   129
Match length
                   70
% identity
                   (AC005171) unknown protein [Arabidopsis thaliana]
NCBI Description
                   308327
Seq. No.
                   uC-zmflmo17125d10a1
Seq. ID
                   BLASTX
Method
                   q4249391
NCBI GI
BLAST score
                   154
                   7.0e-11
E value
Match length
                   75
% identity
                   51
                   (AC005966) Similar to gi_3249076 T13D8.16 beta glucosidase
NCBI Description
                   from Arabidopsis thaliana BAC gb_AC004473. [Arabidopsis
                   thaliana]
 Seq. No.
                   308328
                   uC-zmflmo17125d11b1
 Seq. ID
Method
                   BLASTX
                   q2129656
 NCBI GI
                   175
 BLAST score
                   7.0e-13
 E value
                   81
 Match length
 % identity
                   43
                   OBP33pep protein - Arabidopsis thaliana (fragment)
 NCBI Description
                   >gi 1022801 (U37699) OBP33pep [Arabidopsis thaliana]
                   308329
 Seq. No.
                   uC-zmflmo17125e09b1
 Seq. ID
                   BLASTN
 Method
                   g22332
 NCBI GI
 BLAST score
                   63
```

7.0e-27

E value



```
Match length
                  89
% identity
NCBI Description
                  Z.mays HRGP gene
Seq. No.
                   308330
                  uC-zmflmo17125g04b1
Seq. ID
                  BLASTX
Method
```

g3152606 NCBI GI BLAST score 168 E value 1.0e-19 Match length 101 48 % identity

(AC004482) putative ring zinc finger protein [Arabidopsis NCBI Description

thaliana]

308331

Seq. No. uC-zmflmo17126a11b1 Seq. ID Method BLASTN NCBI GI g2832242 BLAST score 72

2.0e-32 E value Match length 219 % identity 84

Zea mays 22-kDa alpha zein gene cluster, complete sequence NCBI Description

Seq. No. 308332

uC-zmflmo17126d06b1 Seq. ID

Method BLASTX NCBI GI g4335745 BLAST score 227 1.0e-18 E value Match length 90 % identity 48

(AC006284) putative hydrolase (contains an NCBI Description

esterase/lipase/thioesterase active site serine domain

_*<u>*</u>

(prosite: PS50187) [Arabidopsis thaliana]

308333 Seq. No.

uC-zmflmo17126d08b1 Seq. ID

BLASTN Method g4007864 NCBI GI BLAST score 417 0.0e + 00E value 494 Match length % identity 30

NCBI Description Zea mays HRGP gene, AC1503 line

308334 Seq. No.

uC-zmflmo17126e11b1 Seq. ID

Method BLASTX NCBI GI q4220524 208 BLAST score 2.0e-16 E value 54 Match length 70 % identity

NCBI Description (AL035356) putative protein [Arabidopsis thaliana]



```
Seq. No.
                  uC-zmflmo17126f08b1
Seq. ID
                  BLASTN
Method
                  q416146
NCBI GI
                  216
BLAST score
                  1.0e-118
E value
Match length
                  243
                  98
% identity
NCBI Description Zea mays beta-6 tubulin (tub6) gene and mRNA, complete cds
                  308336
Seq. No.
                  uC-zmflmo17126f12b1
Seq. ID
                  BLASTX
Method
                   g1172811
NCBI GI
                  165
BLAST score
                   2.0e-11
E value
                   31
Match length
                   97
% identity
                  60S RIBOSOMAL PROTEIN L10-1 (PUTATIVE TUMOR SUPRESSOR SC34)
NCBI Description
                   >gi_1076751_pir__S49575 ribosomal protein L10.e, cytosolic
                   - rice >gi 575355 emb_CAA57339_ (X81691) putative tumor
                   suppresser [Oryza sativa]
                   308337
Seq. No.
                   uC-zmflmo17127a12b1
Seq. ID
                   BLASTX
Method
                   g537313
NCBI GI
                   177
BLAST score
                   6.0e-13
E value
                   54
Match length
                   65
% identity
                   (L36159) unknown protein [Medicago sativa]
NCBI Description
                   308338
Seq. No.
                   uC-zmflmo17127d05b1
Seq. ID
                   BLASTX
Method
                   q82696
NCBI GI
BLAST score
                   403
                   2.0e-39
E value
                   86
Match length
                   92
 % identity
                   glycine-rich protein - maize >gi_22293_emb_CAA43431_
NCBI Description
                   (X61121) glycine-rich protein [Zea mays]
                   308339
 Seq. No.
                   uC-zmflmo17127e05b1
 Seq. ID
                   BLASTX
 Method
                   g2181188
 NCBI GI
 BLAST score
                   245
```

1.0e-20 E value 163 Match length % identity 36

(Y12530) serine /threonine kinase [Brassica oleracea] NCBI Description

Seq. No. 308340

uC-zmflmo17127g01b1 Seq. ID

BLASTN Method

```
g257040
NCBI GI
BLAST score
                   76
                   1.0e-34
E value
                   96
Match length
                   96
% identity
                  hydroxyproline-rich glycoprotein [maize, Genomic, 1703 nt]
NCBI Description
                   308341
Seq. No.
                   uC-zmflmo17127g04b1
Seq. ID
                   BLASTX
Method
                   q4521190
NCBI GI
BLAST score
                   326
                   4.0e-30
E value
                   157
Match length
                   45
% identity
```

(AB013448) Pib [Oryza sativa] >gi_4521192_dbj_BAA76282.1_ NCBI Description

(AB013449) Pib [Oryza sativa]

308342 Seq. No. uC-zmflmo17127g07b1 Seq. ID BLASTX Method q4220514 NCBI GI 180 BLAST score 4.0e-13 E value 53 Match length 66 % identity

(AL035356) putative protein [Arabidopsis thaliana] NCBI Description

308343 Seq. No. Seq. ID uC-zmflmo17128a05b1 BLASTX Method g3426064 NCBI GI BLAST score 160 9.0e-11

E value 64 Match length % identity

(AJ007588) monooxygenase [Arabidopsis thaliana] NCBI Description

>gi 4467141_emb_CAB37510_ (AL035540) monooxygenase 2 (MO2)

[Arabidopsis thaliana]

308344 Seq. No.

uC-zmflmo17128a06b1 Seq. ID

Method BLASTN NCBI GI g257040 BLAST score 335 0.0e+00E value 355 Match length 29 % identity

NCBI Description hydroxyproline-rich glycoprotein [maize, Genomic, 1703 nt]

308345 Seq. No.

uC-zmflmo17128c08b1 Seq. ID

Method BLASTX g1850968 NCBI GI BLAST score 423 1.0e-41 E value Match length 157



% identity

NCBI Description

```
% identity
                  (U79733) Hs1pro-1 [Beta procumbens]
NCBI Description
                  308346
Seq. No.
Seq. ID
                  uC-zmflmo17128e09b1
Method
                  BLASTX
                  q1731367
NCBI GI
BLAST score
                  279
                  1.0e-24
E value
                  111
Match length
% identity
                  52
                  HYPOTHETICAL PROTEIN ZAP3 >gi_887378 (L40403) ORF; putative
NCBI Description
                  [Homo sapiens]
                  308347
Seq. No.
Seq. ID
                  uC-zmflmo17128h02b1
Method
                  BLASTX
NCBI GI
                  q82040
BLAST score
                  542
                  1.0e-55
E value
                  120
Match length
% identity
                  ubiquitin precursor - flax (fragment) >gi_168304 (M57895)
NCBI Description
                  ubiquitin [Linum usitatissimum]
                  308348
Seq. No.
Seq. ID
                  uC-zmflmo17129c04b1
                  BLASTX
Method
                   q3757521
NCBI GI
BLAST score
                   356
E value
                   8.0e - 34
Match length
                   119
% identity
                   58
                  (AC005167) unknown protein [Arabidopsis thaliana]
NCBI Description
                   308349
Seq. No.
Seq. ID
                   uC-zmflmo17129d02a1
Method
                   BLASTX
                   g1169540
NCBI GI
BLAST score
                   161
E value
                   3.0e-11
Match length
                   72
% identity
                   42
                   EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE SUBSTRATE 15
NCBI Description
                   (PROTEIN EPS15) (AF-1P PROTEIN) >gi_466260 (U07707)
                   epidermal growth factor receptor substrate [Homo sapiens]
                   308350
Seq. No.
                   uC-zmflmo17129d04b1
Seq. ID
                   BLASTN
Method
                   g3015620
NCBI GI
BLAST score
                   234
                   1.0e-129
E value
                   250
Match length
```

Zea mays low molecular weight heat shock protein precursor

(hsp22) mRNA, nuclear gene encoding mitochondrial protein,

% identity

58



complete cds

```
Seq. No.
                  308351
                  uC-zmflmo17129d06b1
Seq. ID
                  BLASTN
Method
                  g22332
NCBI GI
                  305
BLAST score
                  1.0e-171
E value
                  375
Match length
% identity
                  95
NCBI Description
                  Z.mays HRGP gene
                  308352
Seq. No.
                  uC-zmflmo17129e09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1943751
BLAST score
                  496
                  2.0e-52
E value
Match length
                  156
% identity
                  69
                   (U93845) Arabidopsis thaliana ER-type calcium pump
NCBI Description
                  protein, complete sequence >gi 2078292 (U96455) ER-type
                  Ca2+-pumping ATPase; ECA1p [Arabidopsis thaliana]
                  308353
Seq. No.
Seq. ID
                  uC-zmflmo17129f07b1
                                                                                  .
                  BLASTX
Method
NCBI GI
                   q118104
BLAST score
                   544
                  8.0e-56
E value
                  123
Match length
% identity
                  85
                  PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE)
NCBI Description
                   (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN)
                  >gi_68408_pir__CSZM peptidylprolyl isomerase (EC 5.2.1.8) -
                  maize >gi 168461 (M55021) cyclophilin [Zea mays]
                  >gi_829148_emb_CAA48638_ (X68678) cyclophilin [Zea mays]
Seq. No.
                   308354
                  uC-zmflmo17129f10b1
Seq. ID
Method
                  BLASTX
                   g4490756
NCBI GI
BLAST score
                  156
E value
                  1.0e-10
                   88
Match length
                   44
% identity
                  (AL035708) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   308355
Seq. No.
Seq. ID
                   uC-zmflmo17130a04b1
Method
                  BLASTX
NCBI GI
                   q3335333
                   183
BLAST score
                  1.0e-13
E value
Match length
                   66
```

43828

NCBI Description (AC004512) Similar to chloroplast membrane-associated 30KD



protein precursor (IM30) gb_M73744 from Pisum sativum. ESTs gb N37557, gb W43887 and gb_AA042479 come from this gene. [Arabidopsis thaliana]

Seq. No. Seq. ID 308356 uC-zmflmo17130a05b1 Method BLASTX NCBI GI g3335333 BLAST score 211 E value 5.0e-1778 Match length

% identity 58

NCBI Description

(AC004512) Similar to chloroplast membrane-associated 30KD protein precursor (IM30) gb M73744 from Pisum sativum. ESTs qb N37557, gb W43887 and gb AA042479 come from this

gene. [Arabidopsis thaliana]

308357 Seq. No.

Seq. ID uC-zmflmo17130c04b1

Method BLASTX NCBI GI g902586 BLAST score 312 E value 3.0e-29 70 Match length % identity 18

(U29162) ubiquitin [Zea mays] NCBI Description

308358 Seq. No.

uC-zmflmo17130e10b1 Seq. ID

Method BLASTN NCBI GI g506138 BLAST score 36 9.0e-11 E value Match length 44 % identity 95

Zea mays Ec metallothionein class II protein mRNA, complete NCBI Description cds. >gi 987122 emb Z34469 ZMMETALLT Z.mays mRNA for class

II metallothionein

Seq. No. 308359

uC-zmflmo17130f01b1 Seq. ID

BLASTX Method g464843 NCBI GI BLAST score 235 E value 4.0e-20 Match length 44 % identity 98

[Segment 1 of 2] TUBULIN ALPHA-4 CHAIN NCBI Description

>gi 22152 emb CAA44864 (X63179) alpha-tubulin #4 [Zea

mays]

308360 Seq. No.

Seq. ID uC-zmflmo17131a08b1

Method BLASTN NCBI GI g22324 BLAST score 145 7.0e-76 E value



```
Match length 280 % identity 88
```

NCBI Description Z.mays mRNA for H2B histone (clone cH2B221)

Seq. No. 308361

Seq. ID uC-zmflmo17131d10b1

Method BLASTX
NCBI GI g3859602
BLAST score 163
E value 2.0e-11
Match length 46
% identity 54

NCBI Description (AF104919) contains similarity to human

DHHC-domain-containing cysteine-rich protein (GB:U90653) and several S. cerevisiae probable membrane proteins (GB:U20865, Z48758, U43491) [Arabidopsis thaliana]

Seq. No. 308362

Seq. ID uC-zmflmo17132a06b1

Method BLASTX
NCBI GI g1352078
BLAST score 194
E value 3.0e-15
Match length 40
% identity 90

NCBI Description BETA-GALACTOSIDASE PRECURSOR (LACTASE)

(EXO-(1-->4)-BETA-D-GALACTANASE) >gi_507278 (L29451)

b-galactosidase-related protein; putative [Malus domestica]

Seq. No. 308363

Seq. ID uC-zmflmo17132c06a1

Method BLASTX
NCBI GI g975888
BLAST score 172
E value 2.0e-12
Match length 43
% identity 77

NCBI Description (U32511) myo-inositol-1-phosphate synthase

[Mesembryanthemum crystallinum]

Seq. No. 308364

Seq. ID uC-zmflmo17132d12b1

Method BLASTX
NCBI GI g2842496
BLAST score 171
E value 2.0e-12
Match length 65
% identity 60

NCBI Description (AL021749) NAM / CUC2 -like protein [Arabidopsis thaliana]

Seq. No. 308365

Seq. ID uC-zmflmo17132e07a1

Method BLASTX
NCBI GI g3894385
BLAST score 285
E value 2.0e-25
Match length 146



```
% identity
NCBI Description (AF053994) Hcr2-0A [Lycopersicon esculentum]
                  308366
Seq. No.
                  uC-zmflmo17132g02b1
Seq. ID
                  BLASTX
Method
                  g3024577
NCBI GI
                  210
BLAST score
                  2.0e-17
E value
                  40
Match length
                  100
% identity
                  HOMEOBOX PROTEIN ROUGH SHEATH 1 >gi 1008879 (L44133) RS1
NCBI Description
                  gene product [Zea mays]
                  308367
Seq. No.
                  uC-zmflmo17132g04a1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3193286
                  186
BLAST score
                  7.0e-14
E value
                  40
Match length
                  78
% identity
                  (AF069298) T14P8.22 gene product [Arabidopsis thaliana]
NCBI Description
                  308368
Seq. No.
                  uC-zmflmo17133a10a1
Seq. ID
                  BLASTX
Method
                  g3335376
NCBI GI
BLAST score
                  163
                  2.0e-11
E value
Match length
                  46
                  54
% identity
                  (AC003028) putative ammonium transporter [Arabidopsis
NCBI Description
                  thaliana]
                  308369
Seq. No.
                  uC-zmflmo17133a12b1
Seq. ID
                  BLASTN
Method
                  g1498596
NCBI GI
                  108
BLAST score
                  7.0e-54
E value
Match length
                  133
% identity
                   96
NCBI Description Zea mays phospholipid transfer protein mRNA, complete cds
                   308370
Seq. No.
Seq. ID
                  uC-zmflmo17133d05b1
                  BLASTN
Method
NCBI GI
                  q168434
BLAST score
                   51
                   3.0e-20
E value
                   87
Match length
% identity
NCBI Description Z.mays catalase isozyme 3 (CAT-3) mRNA, complete cds
```

43831

 α

308371

uC-zmflmo17133d11a1

Seq. No. Seq. ID

÷**.



```
BLASTX
Method
NCBI GI
                  g3641839
                  177
BLAST score
                  1.0e-15
E value
Match length
                  73
% identity
                  55
                  (AL023094) isoflavone reductase - like protein [Arabidopsis
NCBI Description
                  thaliana]
                  308372
Seq. No.
                  uC-zmflmo17133h03a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3142294
BLAST score
                  137
E value
                  9.0e-09
Match length
                  27
% identity
                  85
                  (AC002411) Strong similarity to initiation factor eIF-2,
NCBI Description
                  gb U37354 from S. pombe. ESTs gb T41979, gb N37284 and
                  gb_N37529 come from this gene. [Arabidopsis thaliana]
                  308373
Seq. No.
Seq. ID
                  uC-zmflmo17134a07b1
                  BLASTX
Method
                  q4490341
NCBI GI
BLAST score
                  156
                  7.0e-11
E value
Match length
                  51
% identity
                  (AL035656) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  308374
Seq. ID
                  uC-zmflmo17134a10b1
                  BLASTX
Method
                  q100489
NCBI GI
BLAST score
                  146
                  1.0e-09
E value
Match length
                  86
% identity
NCBI Description
                  transposase Tam3 - garden snapdragon transposon Tam3
                  >gi 16064 emb CAA38906 (X55078) Tam3-transposase
                  [Antirrhinum majus] >gi_3219237_dbj_BAA28817.1_ (AB013982)
                  transposase [Antirrhinum majus] >gi 3219239_dbj_BAA28818.1_
                  (AB013983) transposase [Antirrhinum majus]
                  >qi 3219241 dbj BAA28819.1 (AB013984) transposase
                  [Antirrhinum majus] >qi 3219244 dbj BAA28820.1 (AB013986)
                  transposase [Antirrhinum majus] >qi 3219249 db; BAA28821.1
                  (AB013990) transposase [Antirrhinum majus]
                  >gi 3219251 dbj BAA28822.1 (AB013991) transposase
                  [Antirrhinum majus] >gi 3219256 dbj BAA28823.1 (AB013995)
                  transposase [Antirrhinum majus] >gi_3219259_dbj_BAA28824.1_
                  (AB013997) transposase [Antirrhinum majus]
```

Seq. No. 308375

Seq. ID uC-zmflmo17134c03b1

Method BLASTX NCBI GI g4376158



```
BLAST score
E value
                  3.0e-12
                  39
Match length
                  79
% identity
                  (X98873) aspartate kinase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  308376
Seq. ID
                  uC-zmflmo17134c12b1
Method
                  BLASTX
NCBI GI
                  g231495
                  233
BLAST score
                  9.0e-20
E value
Match length
                  60
% identity
                  82
                  ACTIN 1 >gi 100021 pir S25488 actin - garden pea
NCBI Description
                  >gi 20637 emb CAA47899 (X67666) actin [Pisum sativum]
                  308377
Seq. No.
                  uC-zmflmo17134e03a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3367536
BLAST score
                  143
                  6.0e-09
E value
Match length
                  29
% identity
                  86
                  (AC004392) Contains similarity to symbiosis-related like
NCBI Description
                  protein F1N20.80 gi_2961343 from A. thaliana BAC
                  gb AL022140. EST gb_T04695 comes from this gene.
                   [Arabidopsis thaliana]
Seq. No.
                  308378
Seq. ID
                  uC-zmflmo17134h08b1
Method
                  BLASTN
NCBI GI
                  g507770
BLAST score
                  36
                  1.0e-10
E value
Match length
                  92
                  85
% identity
                  Zea mays D3L H(+)-transporting ATPase (Mha1) gene, complete
NCBI Description
                  308379
Seq. No.
Seq. ID
                  uC-zmflmo17135d11a1
Method
                  BLASTN
                  g168617
NCBI GI
BLAST score
                  59
                  1.0e-24
E value
Match length
                  199
% identity
                  82
NCBI Description Maize putative protein kinase mRNA, 3' end
```

Seq. No. 308380

Seq. ID uC-zmflmo17136a06b1

Method BLASTX NCBI GI q553125 BLAST score 140 E value 4.0e-09



Match length 48 % identity 58

NCBI Description (L13975) dihydroxyacid dehydratase [Saccharomyces

cerevisiae]

Seq. No. 308381

Seq. ID uC-zmflmo17136a09b1

Method BLASTN
NCBI GI g4336204
BLAST score 42
E value 2.0e-14

Match length 82 % identity 88

NCBI Description Zea mays cytochrome b5 reductase (NFR) mRNA, complete cds

Seq. No. 308382

Seq. ID uC-zmflmo17136d03b1

Method BLASTX
NCBI GI g4185310
BLAST score 149
E value 6.0e-16
Match length 84
% identity 57

NCBI Description (AF090446) gag protein [Zea mays]

Seq. No. 308383

Seq. ID uC-zmflmo17136d04b1

Method BLASTX
NCBI GI g1052960
BLAST score 293
E value 5.0e-27
Match length 59
% identity 93

NCBI Description (U37437) PNIL34 [Ipomoea nil]

Seq. No. 308384

Seq. ID uC-zmflmo17136g05b1

Method BLASTN
NCBI GI g5016094
BLAST score 128
E value 4.0e-66
Match length 148
% identity 97

NCBI Description Zea mays lysine-ketoglutarate reductase/saccharopine dehydrogenase bifunctional enzyme mRNA, complete cds

Seq. No. 308385

Seq. ID uC-zmflmo17137e03b1

Method BLASTX
NCBI GI g2191187
BLAST score 152
E value 2.0e-10
Match length 59
% identity 47

NCBI Description (AF007271) contains similarity to a DNAJ-like domain

[Arabidopsis thaliana]



```
308386
Seq. No.
Seq. ID
                  uC-zmflmo17137e11b1
                  BLASTX
Method
NCBI GI
                  g1666234
BLAST score
                  156
                  5.0e-11
E value
Match length
                  34
% identity
                  88
                  (U76193) actin [Pisum sativum] >gi_1724143 (U81049) actin
NCBI Description
                  [Pisum sativum]
                  308387
Seq. No.
                  uC-zmflmo17137f05b1
Seq. ID
                  BLASTX
Method
                  g548770
NCBI GI
BLAST score
                  261
                  3.0e-23
E value
Match length
                  73
                  71
% identity
                  60S RIBOSOMAL PROTEIN L3 >gi_481228_pir_ S38359 ribosomal
NCBI Description
                  protein L3 - rice >gi_303853_dbj_BAA02155_ (D12630)
                  ribosomal protein L3 [Oryza sativa]
Seq. No.
                  308388
                  uC-zmflmo17137g04b1
Seq. ID
                  BLASTX
Method
                  g3377803
NCBI GI
BLAST score
                  188
E value
                   1.0e-14
                  56
Match length
                   68
% identity
                   (AF075597) Similar to (p)ppGpp synthetase; T2H3.9
NCBI Description
                   [Arabidopsis thaliana]
                   308389
Seq. No.
                   uC-zmflmo17137h09b1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g556557
                   39
BLAST score
                   7.0e-13
E value
Match length
                   47
                   96
% identity
NCBI Description
                  Rice mRNA for homologue of Tat binding protein, complete
                   308390
Seq. No.
Seq. ID
                   uC-zmflmo17138a04b1
                   BLASTX
Method
NCBI GI
                   g3047318
BLAST score
                   261
                   7.0e-23
E value
                   88
Match length
% identity
NCBI Description
                  (AF056625) poly-ubiquitin [Magnaporthe grisea]
```

43835

308391

uC-zmflmo17138a05b1

Seq. No.

Seq. ID



```
Method
                  BLASTX
NCBI GI
                  g2262195
BLAST score
                  159
                  8.0e-11
E value
                  59
Match length
                  44
% identity
NCBI Description (U64820) josephin MJD1 [Homo sapiens]
                  308392
Seq. No.
Seq. ID
                  uC-zmflmo17138b08b1
                  BLASTX
Method
                  g3445208
NCBI GI
                  143
BLAST score
                  1.0e-11
E value
                  69
Match length
                  59
% identity
                  (AC004786) putative amino-acid acetyltransferase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  308393
                  uC-zmflmo17138b09b1
Seq. ID
                  BLASTN
Method
                  g4007864
NCBI GI
BLAST score
                  223
                  1.0e-122
E value
                  317
Match length
                  96
% identity
NCBI Description Zea mays HRGP gene, AC1503 line
                  308394
Seq. No.
                  uC-zmflmo17138d08b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q584706
BLAST score
                   414
                   1.0e-40
E value
                   93
Match length
% identity
                  ASPARTATE AMINOTRANSFERASE, CYTOPLASMIC (TRANSAMINASE A)
NCBI Description
                   >gi 2130066 pir JC5124 aspartate transaminase (EC
                   2.6.1.1), cytoplasmic - rice >gi_287298_dbj_BAA03504_
                   (D14673) aspartate aminotransferase [Oryza sativa]
Seq. No.
                   308395
Seq. ID
                   uC-zmflmo17138e12b1
Method
                   BLASTX
NCBI GI
                   g2662310
BLAST score
                   315
E value
                   4.0e-29
Match length
                   100
% identity
                   62
                  (AB009307) bpw1 [Hordeum vulgare]
NCBI Description
Seq. No.
                   308396
                   uC-zmflmo17138f10b1
Seq. ID
```

BLASTN Method g1532072 NCBI GI BLAST score 37

```
1.0e-11
 E value
Match length
                    41
                    98
 % identity
                    Z.mays mRNA for S-adenosylmethionine decarboxylase
 NCBI Description
                    308397
 Seq. No.
 Seq. ID
                    uC-zmflmo17138h03b1
 Method
                    BLASTX
 NCBI GI
                    g1076678
 BLAST score
                    321
                    9.0e-30
 E value
                    71
 Match length
                    93
 % identity
                   ubiquitin / ribosomal protein S27a - potato (fragment)
 NCBI Description
                    308398
 Seq. No.
                    uC-zmflmo17138h07b1
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g112972
 BLAST score
                    166
 E value
                    5.0e-12
 Match length
                    73
                    48
 % identity
                    ASPARTATE AMINOTRANSFERASE, CYTOPLASMIC (TRANSAMINASE A)
 NCBI Description
                    >gi_167546 (M92660) aspartate aminotransferase [Daucus
                    carota] >gi 445587 prf 1909339A Asp aminotransferase
                    [Daucus carota]
 Seq. No.
                    308399
                    uC-zmflmo17139b10b1
 Seq. ID
 Method
                    BLASTX
                    g1724100
 NCBI GI
 BLAST score
                    261
                    1.0e-22
 E value
                    98
 Match length
                    53
 % identity
 NCBI Description (U79765) porin [Mesembryanthemum crystallinum]
 Seq. No.
                    308400
                    uC-zmflmo17139c01b1
 Seq. ID
 Method
                    BLASTN
 NCBI GI
                    g4240032
 BLAST score
                    62
 E value
                    6.0e-27
 Match length
                    86
                    93
 % identity
 NCBI Description Zea mays ZmGRla mRNA, complete cds
 Seq. No.
                    308401
 Seq. ID
                    uC-zmflmo17139c10b1
 Method
                    BLASTN
 NCBI GI
                    q902200
 BLAST score
                    121
 E value
                    1.0e-61
 Match length
                    221
                    89
 % identity
 NCBI Description Z.mays complete chloroplast genome
```

```
308402
Seq. No.
                   uC-zmflmo17139d01b1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g22483
BLAST score
                   53
                   4.0e-21
E value
Match length
                   180
% identity
                   91
                   Z.mays RNA for superoxide dismutase Sod4
NCBI Description
                   308403
Seq. No.
                   uC-zmflmo17139d03b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g112994
BLAST score
                   164
E value
                   9.0e-12
                   51
Match length
% identity
                   75
                   GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN
NCBI Description
                   >gi_82685_pir__S04536 embryonic abundant protein,
glycine-rich - maize >gi_22313_emb_CAA31077_ (X12564)
                   ABA-inducible gene protein [Zea mays]
                   >qi 226091 prf 1410284A abscisic acid inducible gene [Zea
                   mays]
                   308404
Seq. No.
Seq. ID
                   uC-zmflmo17139d05b1
Method
                   BLASTX
NCBI GI
                   g541849
                   151
BLAST score
                   4.0e-10
E value
Match length
                   40
                   70
% identity
                   anthranilate synthase (EC 4.1.3.27) beta chain -
NCBI Description
                   Arabidopsis thaliana >gi 403434 (L22585) anthranilate
                   synthase beta subunit [Arabidopsis thaliana]
                   308405
Seq. No.
Seq. ID
                   uC-zmflmo17139g02a1
                   BLASTX
Method
NCBI GI
                   g2244792
BLAST score
                   146
                   3.0e-09
E value
Match length
                   71
% identity
                   (Z97336) ankyrin homolog [Arabidopsis thaliana]
NCBI Description
                   308406
Seq. No.
                   uC-zmflmo17139g08b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3249064
                   197
BLAST score
E value
                   2.0e-15
Match length
                   92
% identity
                   (AC004473) Strong similarity to trehalose-6-phosphate
NCBI Description
```

synthase homolog gb 2245136 from A. thaliana chromosome 4 contig gb Z97344. [Arabidopsis thaliana]

308407 Seq. No.

Seq. ID uC-zmflmo17139h05b1

Method BLASTN NCBI GI g1906603 BLAST score 153 1.0e-80 E value 277 Match length

89 % identity

Zea mays ACCase gene, intron containing colonist1 and NCBI Description

colonist2 retrotransposons and reverse transcriptase

pseudogene, complete sequence

308408 Seq. No.

Seq. ID uC-zmflmo17139h10b1

BLASTN Method NCBI GI g257040 BLAST score 149 2.0e-78 E value 243 Match length 29 % identity

NCBI Description hydroxyproline-rich glycoprotein [maize, Genomic, 1703 nt]

308409 Seq. No.

Seq. ID uC-zmflmo17140a10a1

Method BLASTN NCBI GI g1244652 BLAST score 205 E value 1.0e-111 Match length 327

% identity 46

Zea mays copia-type retroelement PREM-2 gag gene, complete NCBI Description

308410 Seq. No.

Seq. ID uC-zmflmo17140g03a1

Method BLASTX NCBI GI g4417289 BLAST score 203 E value 8.0e-16 Match length 107 % identity 45

NCBI Description (AC007019) unknown protein [Arabidopsis thaliana]

Seq. No. 308411

Seq. ID uC-zmflmo17141b05a1

Method BLASTX NCBI GI g3152576 BLAST score 170 4.0e-12 E value Match length 48 % identity 65

(AC002986) Similar to liver-specific transport protein NCBI Description

qb L27651 from Rattus norviegicus. [Arabidopsis thaliana]



```
Seq. No.
                  uC-zmflmo17141d11a1
Seq. ID
                  BLASTX
Method
                  g3023275
NCBI GI
                  540
BLAST score
                  2.0e-55
E value
Match length
                  132
                   79
% identity
                  ALPHA-GLUCOSIDASE PRECURSOR (MALTASE)
NCBI Description
                  >gi_2130027_pir__S65057 alpha-glucosidase (EC 3.2.1.20) -
                  barley >gi 944901 (U22450) alpha-glucosidase [Hordeum
                   vulgare]
                   308413
Seq. No.
                   uC-zmflmo17141e03a1
Seq. ID
                   BLASTN
Method
                   g1546918
NCBI GI
                   66
BLAST score
                   3.0e-29
E value
                   82
Match length
                   95
% identity
                   Z.mays mRNA for translation initiation factor 5A
NCBI Description
                   308414
Seq. No.
                   uC-zmflmo17150a02b1
Seq. ID
                   BLASTX
Method
                   g4455359
NCBI GI
                   334
BLAST score
                   4.0e-31
E value
                   124
Match length
                   49
% identity
                   (AL035524) putative protein [Arabidopsis thaliana]
NCBI Description
                   308415
Seq. No.
                   uC-zmflmo17150b05b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4587549
BLAST score
                   264
                   6.0e-23
E value
                   69
Match length
% identity
                   (AC006577) Similar to gb U55861 RNA binding protein
NCBI Description
                   nucleolysin (TIAR) from \overline{	ext{M}}us musculus and contains several
                   PF 00076 RNA recognition motif domains. ESTs gb_T21032 and
                   gb T44127 come from this gene. [Arabidopsis t
                   308416
Seq. No.
Seq. ID
                   uC-zmflmo17150c02b1
Method
                   BLASTN
                   q3821780
NCBI GI
BLAST score
                   36
                   1.0e-10
E value
                   48
Match length
```

% identity 67

Xenopus laevis cDNA clone 27A6-1 NCBI Description

308417 Seq. No.



```
uC\text{-}zmflmo17150d04b1\\
Seq. ID
                  BLASTX
Method
NCBI GI
                  ~g3868859
                  273
BLAST score
                  5.0e-24
E value
Match length
                  67
% identity
                  78
NCBI Description (AB013887) RAV2 [Arabidopsis thaliana]
                  308418
Seq. No.
                  uC-zmflmo17150d05b1
Seq. ID
Method
                  BLASTX
                  g3395431
NCBI GI
BLAST score
                  173
E value
                   3.0e-12
Match length
                   64
% identity
                   50
NCBI Description (AC004683) unknown protein [Arabidopsis thaliana]
Seq. No.
                   308419
                   uC-zmflmo17150e03b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2500725
BLAST score
                   657
E value
                   5.0e-69
Match length
                   154
                   81
% identity
NCBI Description PREPROTEIN TRANSLOCASE SECA SUBUNIT PRECURSOR
                   >gi 939976_emb_CAA88933_ (Z49124) SecA [Spinacia oleracea]
Seq. No. Seq. ID
                   308420
                   uC-zmflmo17150e06b1
                   BLASTX
Method
                   g4210332
NCBI GI
BLAST score
                   314
                   6.0e-40
E value
                   171
Match length
                   57
% identity
                  (AJ223803) 2-oxoglutarate dehydrogenase E2 subunit
NCBI Description
                   [Arabidopsis thaliana]
                   308421
Seq. No.
                   uC-zmflmo17150e09a1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g2984708
BLAST score
                   137
                   4.0e-71
E value
                   227
Match length
                   97
% identity
NCBI Description Zea mays DnaJ-related protein ZMDJ1 (mdJ1) gene, complete
                   308422
Seq. No.
                   uC-zmflmo17150e09b1
```

Seq. ID

Method BLASTX NCBI GI q2984709 BLAST score 532



```
2.0e-54
E value
Match length
                  101
                  99
% identity
                  (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]
NCBI Description
                  308423
Seq. No.
                  uC-zmflmo17150e12b1
Seq. ID
Method
                  BLASTX
                  g2244866
NCBI GI
BLAST score
                  152
                  8.0e-10
E value
                  157
Match length
                  24
% identity
                  (Z97337) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  308424
Seq. No.
                  uC-zmflmo17150f09b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4415919
                  170
BLAST score
                  7.0e-12
E value
Match length
                  46
                   67
% identity
                  (AC006282) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  308425
Seq. No.
                  uC-zmflmo17150f12b1
Seq. ID
                  BLASTX
Method
NCBI GI
                   g3935170
                   357
BLAST score
                   5.0e-34
E value
                  104
Match length
% identity
                   63
                  (AC004557) F17L21.13 [Arabidopsis thaliana]
NCBI Description
                   308426
Seq. No.
                   uC-zmflmo17150g01a1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g1698669
                   96
BLAST score
                   1.0e-46
E value
                   262
Match length
                   86
% identity
NCBI Description Zea mays S-like RNase (kin1) mRNA, complete cds
                   308427
Seq. No.
                   uC-zmflmo17150g02a1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g1276930
                   95
BLAST score
                   2.0e-46
E value
                   147
Match length
% identity
```

NCBI Description Zea luxurians Doebley M018 from ITS1, 5.8S ribosomal RNA, ITS2

Seq. No.

Seq. ID uC-zmflmo17151a09a1 BLASTX Method g2149640 NCBI GI 313 BLAST score 9.0e-29 E value 79 Match length % identity (U91995) Argonaute protein [Arabidopsis thaliana] NCBI Description 308429 Seq. No. uC-zmflmo17151c09b1 Seq. ID Method BLASTX NCBI GI g115511 BLAST score 224 5.0e-29 E value 95 Match length % identity CALMODULIN >gi 231682_sp_P29612_CALM_ORYSA CALMODULIN NCBI Description >gi 71682 pir MCBH calmodulin - barley

>gi 100666 pir S24952 calmodulin 1 (clone lambda DASH) rice >gi_20188_emb_CAA78287_ (Z12827) calmodulin [Oryza sativa] >gi 167008 (M27303) calmodulin [Hordeum vulgare] >gi 170072 (L01431) calmodulin [Glycine max] >gi_310315 (L18913) calmodulin [Oryza sativa] $>gi_506850$ (L $\overline{2}0691$) calmodulin [Vigna radiata] >gi 1478370 bbs 176852 (S81594) auxin-regulated calmodulin, arCaM [Vigna radiata=mung bean, Wilczek, seedling, Peptide, 149 aa] [Vigna radiata] >gi 1742989_emb_CAA70982_ (Y09853) CaM protein [Cicer arietinum] $\overline{}$ gi $\overline{}$ 754991 ($\overline{}$ 48242) calmodulin TaCaM1-1 [Triticum aestivum] >gi_1754993 (U48688) calmodulin TaCaM1-2 [Triticum aest \overline{i} vum] >gi_1754995 (U48689) calmodulin TaCaM1-3 [Triticum aestivum] >gi 1755003 (U48693) calmodulin TaCaM3-1 [Triticum aestīvum] >gi 1755005 (U49103) calmodulin TaCaM3-2 [Triticum aestivum] >gi_1755007 (U49104) calmodulin TaCaM3-3 [Triticum aestivum] >gi 1755009 (U49105) calmodulin TaCaM4-1 [Triticum aestīvum] >gi 3617842 (AF042840) calmodulin [Oryza sativa] >gi_226769_prf 1604476A calmodulin [Hordeum vulgare var. distichum] >qi 1583768 prf 2121384B calmodulin [Glycine max]

-__

Seq. No. 308430

Seq. ID uC-zmflmo17151d08b1

Method BLASTN q22332 NCBI GI BLAST score 288 1.0e-161 E value 461 Match length % identity 91

NCBI Description Z.mays HRGP gene

Seq. No. 308431

Seq. ID uC-zmflmo17151e06b1

Method BLASTX g2500522 NCBI GI 190 BLAST score 1.0e-14 E value

```
81
Match length
                  53
% identity
NCBI Description EUKARYOTIC INITIATION FACTOR 4A (EIF-4A) >gi_603190
                  (U17979) translation initiation factor eIF-4A [Zea mays]
                  308432
Seq. No.
                  uC-zmflmo17151e08b1
Seq. ID
                  BLASTX
Method
                  g1076746
NCBI GI
                  696
BLAST score
                  2.0e-73
E value
                  144
Match length
                   94
% identity
                  heat shock protein 70 - rice (fragment)
NCBI Description
                  >gi_763160_emb_CAA47948_ (X67711) heat shock protein 70
                   [Oryza sativa]
                   308433
Seq. No.
                  uC-zmflmo17151f06b1
Seq. ID
                  BLASTX
Method
                   g4468979
NCBI GI
                   157
BLAST score
                   1.0e-10
E value
                   37
Match length
                   76
% identity
                  (AL035605) putative protein [Arabidopsis thaliana]
NCBI_Description
                   308434
Seq. No.
                   uC-zmflmo17151f12b1
Seq. ID
                   BLASTX
Method
                   g1524383
NCBI GI
                   644
BLAST score
                   1.0e-67
E value
Match length
                   145
                   90
% identity
                   (X63374) 3-phosphoshikimate 1-carboxyvinyltransferase [Zea
NCBI Description
                   mays]
                   308435
Seq. No.
                   uC-zmflmo17151h06a1
Seq. ID
                   BLASTN
Method
                   g22243
NCBI GI
BLAST score
                   42
                   1.0e-14
E value
                   78
Match length
                   88
 % identity
NCBI Description Zea mays Cin1 repeat from Cin1 middle repetitive family
 Seq. No.
                   308436
                   uC-zmflmo17152a02b1
 Seq. ID
                   BLASTX
 Method
                   g2781355
 NCBI GI
 BLAST score
                   306
 E value
                   6.0e-28
 Match length
                   80
                   65
 % identity
                   (AC003113) F2401.11 [Arabidopsis thaliana]
 NCBI Description
```

43844

. . . .

% identity

NCBI Description

35

```
308437
Seq. No.
                  uC-zmflmo17152a06b1
Seq. ID
                  BLASTX
Method
                  g4455213
NCBI GI
BLAST score
                  172
E value
                  1.0e-17
                  78
Match length
                   62
% identity
                  (AL035440) glutamine amidotransferase/cyclase [Arabidopsis
NCBI Description
                  thaliana]
                  308438
Seq. No.
                  uC-zmflmo17152b05b1
Seq. ID
                  BLASTN
Method
                  g1657765
NCBI GI
BLAST score
                  103
E value
                   1.0e-50
                  187
Match length
% identity
                   89
                  Zea mays retrotransposon Milt 5' LTR and primer binding
NCBI Description
                   site DNA sequence
                   308439
Seq. No.
                  uC-zmflmo17152d04b1
Seq. ID
                  BLASTX
Method
NCBI GI
                   g1173225
BLAST score
                   195
                   7.0e-15
E value
Match length
                   133
                   37
% identity
                   30S RIBOSOMAL PROTEIN S1 >gi 1075612 pir S51485 rps1
NCBI Description
                   homolog protein 307 - Synechococcus sp
                   >gi 666973 dbj BAA05946_ (D28752) ribosomal protein S1
                   [Synechococcus sp.]
                   308440
Seq. No.
Seq. ID
                   uC-zmflmo17152d05b1
                   BLASTX
Method
NCBI GI
                   g1345588
                   420
BLAST score
E value
                   2.0e-41
Match length
                   98
% identity
                   88
                   14-3-3-LIKE PROTEIN GF14-12 >qi 998432 bbs 164524
NCBI Description
                   GF14-12=GRF2 product/14-3-3 protein homolog [Zea mays,
                   XL80, Peptide, 261 aa]
Seq. No.
                   308441
Seq. ID
                   uC-zmflmo17152d07a1
Method
                   BLASTX
NCBI GI
                   g2262116
BLAST score
                   157
E value
                   2.0e-10
Match length
                   124
```

(AC002343) cellulose synthase isolog [Arabidopsis thaliana]

Seq. No.

Seq. ID

308447

uC-zmflmo17153c06b1

```
308442
   Seq. No.
   Seq. ID
                     uC-zmflmo17152e04b1
  Method
                     BLASTX
  NCBI GI
                     g3043415
  BLAST score
                     156
  E value
                     5.0e-17
                     92
  Match length
                     59
   % identity
  NCBI Description (Y17053) At-hsc70-3 [Arabidopsis thaliana]
                     308443
   Seq. No.
   Seq. ID
                     uC-zmflmo17152e12b1
                     BLASTX
  Method
  NCBI GI
                     g2827160
                     151
  BLAST score
  E value
                     1.0e-09
                     88
  Match length
                     36
   % identity
  NCBI Description (AF032667) rexo70 [Rattus norvegicus]
                     308444
  Seq. No.
  Seq. ID
                     uC-zmflmo17152f05b1
  Method
                     BLASTN
  NCBI GI
                     g11957
  BLAST score
                     39
  E value
                     2.0e-12
  Match length
                     103
   % identity
                     86
  NCBI Description Rice complete chloroplast genome
                     308445
  Seq. No.
   Seq. ID
                     uC-zmflmo17152h10b1
  Method
                     BLASTN
  NCBI GI
                     g1906603
  BLAST score
                     39
🛬 E value
                     2.0e-12
  Match length
                     99
   % identity
                     85
  NCBI Description
                     Zea mays ACCase gene, intron containing colonist1 and
                     colonist2 retrotransposons and reverse transcriptase
                     pseudogene, complete sequence
   Seq. No.
                     308446
   Seq. ID
                     uC-zmflmo17153a03b1
  Method
                     BLASTX
  NCBI GI
                     g3128231
  BLAST score
                     197
                     5.0e-15
  E value
  Match length
                     160
   % identity
                     11
  NCBI Description
                     (AC004077) hypothetical protein [Arabidopsis thaliana]
                     >gi_3337370 (AC004481) hypothetical protein [Arabidopsis
                     thaliana]
```



```
Method
                  BLASTX
NCBI GI
                  g2465923
BLAST score
                  557
                  3.0e-57
E value
                  162
Match length
                  65
% identity
NCBI Description
                  (AF024648) receptor-like serine/threonine kinase
                  [Arabidopsis thaliana]
                  308448
Seq. No.
Seq. ID
                  uC-zmflmo17153d04a1
Method
                  BLASTN
NCBI GI
                  g159369
BLAST score
                  34
                  7.0e-10
E value
Match length
                  42
                  95
% identity
                  Leishmania enriettii multidrug resistant protein (mdr1)
NCBI Description
                  gene, complete cds
Seq. No.
                  308449
Seq. ID
                  uC-zmflmo17153g08b1
Method
                  BLASTX
NCBI GI
                  g2921304
BLAST score
                  496
                  3.0e-50
E value
Match length
                  115
                  90
% identity
NCBI Description
                  (AF033496) herbicide safener binding protein [Zea mays]
                  308450
Seq. No.
Seq. ID
                  uC-zmflmo17154b04b1
Method
                  BLASTN
NCBI GI
                  g473185
BLAST score
                  65
E value
                  5.0e-28
Match length
                  209
                  83
% identity
NCBI Description Z.mays U3snRNA pseudogene
Seq. No.
                  308451
Seq. ID
                  uC-zmflmo17154d02b1
Method
                  BLASTX
NCBI GI
                  g3738306
BLAST score
                  149
                  2.0e-09
E value
Match length
                  55
% identity
                  64
                  (AC005309) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  308452
Seq. ID
                  uC-zmflmo17154d07b1
Method
                  BLASTX
```

NCBI GI g1706885
BLAST score 241
E value 3.0e-20
Match length 155

% identity

```
% identity
                  FOLYLPOLYGLUTAMATE SYNTHASE, MITOCHONDRIAL PRECURSOR
NCBI Description
                  (FOLYLPOLY-GAMMA-GLUTAMATE SYNTHETASE) (FPGS) >gi_1345106
                  (U33557) folylpolyglutamate synthetase precursor [Mus
                  musculus]
                  308453
Seq. No.
Seq. ID
                  uC-zmflmo17154e11a1
Method
                  BLASTN
NCBI GI
                  g1532072
BLAST score
                  208
E value
                  1.0e-113
Match length
                  311
% identity
                  92
NCBI Description Z.mays mRNA for S-adenosylmethionine decarboxylase
Seq. No.
                  308454
                  uC-zmflmo17154g03b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g710626
BLAST score
                  158
E value
                  6.0e-11
Match length
                  52
% identity
NCBI Description
                  (D30719) ERD15 protein [Arabidopsis thaliana] >gi 3241941
                   (AC004625) dehydration-induced protein ERD15 [Arabidopsis
                  thaliana] >gi_3894181 (AC005662) ERD15 protein [Arabidopsis
                  thaliana]
Seq. No.
                  308455
                  uC-zmflmo17154g12a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3281853
BLAST score
                  203
                  6.0e-16
E value
                  79
Match length
% identity
NCBI Description (AL031004) putative protein [Arabidopsis thaliana]
                  308456
Seq. No.
Seq. ID
                  uC-zmflmo17154h04b1
                  BLASTX
Method
                  g2618702
NCBI GI
BLAST score
                  263
E value
                  3.0e-29
                  87
Match length
% identity
NCBI Description (AC002510) unknown protein [Arabidopsis thaliana]
                   308457
Seq. No.
                  uC-zmflmo17155a06b1
Seq. ID
                  BLASTX
Method
                  q2586082
NCBI GI
BLAST score
                  155
                   1.0e-18
E value
Match length
                   95
```



```
(U72725) retrofit [Oryza longistaminata]
NCBI Description
                  308458
Seq. No.
Seq. ID
                  uC-zmflmo17155a12b1
Method
                  BLASTN
NCBI GI
                  q4185305
BLAST score
                  52
                  2.0e-20
E value
                  184
Match length
                  84
% identity
                  Zea mays cosmid IV.1E1 22-kDa alpha zein protein 21
NCBI Description
                  (sz22-21) gene, complete cds; retrotransposon Opie-2 gag
                  protein, polyprotein, and copia protein genes, complete
                  cds; and unknown genes
                  308459
Seq. No.
Seq. ID
                  uC-zmflmo17155b02b1
                  BLASTN
Method
NCBI GI
                  q473185
BLAST score
                  81
                  2.0e-37
E value
                  188
Match length
% identity
                  86
                  Z.mays U3snRNA pseudogene
NCBI Description
                  308460
Seq. No.
Seq. ID
                  uC-zmflmo17155b06b1
Method
                  BLASTX
NCBI GI
                  g2668742
BLAST score
                  332
                  6.0e-31
E value
Match length
                  67
% identity
                  (AF034945) glycine-rich RNA binding protein [Zea mays]
NCBI Description
                  308461
Seq. No.
Seq. ID
                  uC-zmflmo17155e06b1
Method
                  BLASTX
                  q4538939
NCBI GI
BLAST score
                  260
                  1.0e-22
E value
Match length
                  121
% identity
                   (AL049483) Col-O casein kinase I-like protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                   308462
Seq. ID
                  uC-zmflmo17155f09b1
Method
                  BLASTN
NCBI GI
                  g639721
```

Method BLASTN
NCBI GI g639721
BLAST score 35
E value 3.0e-10

Match length 39 % identity 97

NCBI Description Zea mays calcium-dependent protein kinase (CDPK) gene,

exons 1-7 and partial cds



308463 Seq. No. uC-zmflmo17155g10b1 Seq. ID Method BLASTN NCBI GI g257040 159 BLAST score 2.0e-84 E value 223 Match length % identity 93 NCBI Description hydroxyproline-rich glycoprotein [maize, Genomic, 1703 nt] 308464 Seq. No. uC-zmflmo17156b07b1 Seq. ID BLASTX Method NCBI GI g2500345 287 BLAST score 1.0e-25 E value 74 Match length 74 % identity NHP2/RS6 FAMILY PROTEIN YEL026W HOMOLOG (HIGH MOBILITY NCBI Description GROUP-LIKE NUCLEAR PROTEIN 2 HOMOLOG) >gi_2618578_dbj_BAA23363_ (D50420) OTK27 [Homo sapiens] $\overline{3859990}$ (AF $\overline{0}$ 91076) OTK27 [Homo sapiens] >gi 1589072 prf 2210268A nuclear protein-NHP2-like protein [Homo sapiens] 308465 Seq. No. uC-zmflmo17156g03b1Seq. ID BLASTX Method NCBI GI g4416302 453 BLAST score 4.0e-45 E value Match length 144 58 % identity (AF105716) copia-type pol polyprotein [Zea mays] NCBI Description 308466 Seq. No. Seq. ID uC-zmflmo17156g07b1 BLASTX Method NCBI GI g2911052 BLAST score 430 2.0e-42 E value 133 Match length 62 % identity. NCBI Description (AL021961) putative protein [Arabidopsis thaliana] 308467 Seq. No.

Seq. ID uC-zmflmo17156h09b1

Method BLASTN
NCBI GI g257040
BLAST score 235
E value 1.0e-129
Match length 280
% identity 18

NCBI Description hydroxyproline-rich glycoprotein [maize, Genomic, 1703 nt]

Seq. No. 308468

Seq. ID uC-zmflmo17157b06a1

Seq. No.

Seq. ID Method

308473

BLASTX

uC-zmflmo17159a06b1



```
BLASTX
Method
                  g3915039
NCBI GI
                  174
BLAST score
                  1.0e-12
E value
                  55
Match length
                  60
% identity
                  SUGAR CARRIER PROTEIN C >gi 169718 (L08196) sugar carrier
NCBI Description
                  protein [Ricinus communis]
                  308469
Seq. No.
                  uC-zmflmo17157d03a1
Seq. ID
                  BLASTN
Method
                  q3511235
NCBI GI
BLAST score
                  170
                  9.0e-91
E value
                  231
Match length
                  94
% identity
                  Zea mays starch branching enzyme IIb (ae) gene, complete
NCBI Description
                  308470
Seq. No.
Seq. ID
                  uC-zmflmo17157f03a1
                  BLASTX
Method
                  q4581181
NCBI GI
BLAST score
                  167
                   1.0e-11
E value
                  73
Match length
                   40
% identity
                  (AC006220) unknown protein [Arabidopsis thaliana]
NCBI Description
                   308471
Seq. No.
                   uC-zmflmo17158d03b1
Seq. ID
                  BLASTX
Method
NCBI GI
                   g3335347
                   316
BLAST score
                   4.0e-29
E value
Match length
                   93
                   69
% identity
                   (AC004512) Contains similarity to ARI, RING finger protein
NCBI Description
                   gb X98309 from Drosophila melanogaster. ESTs gb_T44383,
                   gb W43120, gb N65868, gb H36013, gb AA042241, gb T76869 and
                   gb AA042359 come from this gene. [Arabidopsis thaliana]
                   308472
Seq. No.
Seq. ID
                   uC-zmflmo17158f01a1
Method
                   BLASTX
                   q4454471
NCBI GI
BLAST score
                   146
E value
                   1.0e-09
Match length
                   53
% identity
                   (AC006234) putative G protein coupled receptor [Arabidopsis
NCBI Description
                   thaliana]
```



```
NCBI GI
                  g4455169
BLAST score
                  175
E value
                  1.0e-12
                  59
Match length
% identity
                  51
                  (AL035521) putative aldehyde dehydrogenase [Arabidopsis
NCBI Description
                  thaliana]
                  308474
Seq. No.
Seq. ID
                  uC-zmflmo17159a08b1
Method
                  BLASTX
NCBI GI
                  g3687237
BLAST score
                  144
                  7.0e-09
E value
Match length
                  54
                  54
% identity
                   (AC005169) putative Cys3His zinc-finger protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  308475
Seq. ID
                  uC-zmflmo17159b08b1
Method
                  BLASTX
NCBI GI
                  g3355477
BLAST score
                  251
E value
                  1.0e-21
Match length
                  109
% identity
                  48
                  (AC004218) putative P-glycoprotein, pgp1 [Arabidopsis
NCBI Description
                  thaliana]
                  308476
Seq. No.
Seq. ID
                  uC-zmflmo17159b10a1
Method
                  BLASTX
NCBI GI
                  g4512651
BLAST score
                  219
E value
                  8.0e-18
Match length
                  72
                  51
% identity
NCBI Description
                  (AC007048) putative tyrosine transaminase [Arabidopsis
                  thaliana]
                  308477
Seq. No.
Seq. ID
                  uC-zmflmo17159e08b1
Method
                  BLASTX
NCBI GI
                  g1078080
BLAST score
                  145
E value
                  6.0e-09
Match length
                  69
% identity
                  41
NCBI Description
                  hypothetical protein YLR316c - yeast (Saccharomyces
                  cerevisiae)
```

Seq. No. 308478

Seq. ID uC-zmflmo17159f04a1

Method BLASTN NCBI GI g4140643 BLAST score 37



```
E value
                  2.0e-11
Match length
                  77
                  87
% identity
NCBI Description
                  Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster,
                  complete sequence
Seq. No.
                  308479
Seq. ID
                  uC-zmflmo17159f12b1
Method
                  BLASTX
NCBI GI
                  q282994
BLAST score
                  420
E value
                  2.0e-51
Match length
                  124
                  80
% identity
                  Sip1 protein - barley >gi_167100 (M77475) seed imbibition
NCBI Description
                  protein [Hordeum vulgare]
                  308480
Seq. No.
Seq. ID
                  uC-zmflmo17160a02a1
Method
                  BLASTN
NCBI GI
                  g2257755
BLAST score
                  39
E value
                  9.0e-13
Match length
                  47
                  96
% identity
                  Zea mays nucleolar histone deacetylase HD2-p39 mRNA,
NCBI Description
                  complete cds
Seq. No.
                  308481
Seq. ID
                  uC-zmflmo17160b05b1
Method
                  BLASTN
NCBI GI
                  g303852
BLAST score
                  38
E value
                  7.0e-12
Match length
                  86
% identity
                  86
NCBI Description Rice mRNA for ribosomal protein L3, complete cds
Seq. No.
                  308482
Seq. ID
                  uC-zmflmo17160b12b1
Method
                  BLASTX
NCBI GI
                  q4091080
BLAST score
                  184
E value
                  1.0e-13
Match length
                  86
% identity
                  47
NCBI Description
                  (AF045571) nucleic acid binding protein [Oryza sativa]
Seq. No.
                  308483
Seq. ID
                  uC-zmflmo17160c10b1
```

Method BLASTX NCBI GI g2894607 BLAST score 234 E value 2.0e-19 Match length 90 % identity 54

NCBI Description (AL021889) NAM (no apical meristem) - like protein



[Arabidopsis thaliana]

```
308484
Seq. No.
Seq. ID
                  uC-zmflmo17160f05b1
                  BLASTX
Method
NCBI GI
                  g1684913
BLAST score
                  159
E value
                  1.0e-10
Match length
                  106
% identity
                   43
                  (U77888) receptor-like protein kinase [Ipomoea nil]
NCBI Description
                  308485
Seq. No.
                  uC-zmflmo17160g02b1
Seq. ID
Method
                  BLASTN
NCBI GI
                   g257040
BLAST score
                   74
                   2.0e-33
E value
Match length
                   186
% identity
                   68
NCBI Description hydroxyproline-rich glycoprotein [maize, Genomic, 1703 nt]
Seq. No.
                   308486
                   uC-zmflmo17161a02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2618688
BLAST score
                   175
E value
                   2.0e-13
Match length
                   74
% identity
                   59
                  (AC002510) putative esterase D [Arabidopsis thaliana]
NCBI Description
                   308487
Seq. No.
Seq. ID
                   uC-zmflmo17161f01b1
Method
                   BLASTX
NCBI GI
                   g3860263
BLAST score
                   398
                   1.0e-38
E value
Match length
                   142
                   58
% identity
                   (AC005824) putative cytochrome p450 protein [Arabidopsis
NCBI Description
                   thaliana]
                   308488
Seq. No.
Seq. ID
                   uC-zmflmo17161f06b1
Method
                   BLASTX
NCBI GI
                   q4415931
BLAST score
                   341
E value
                   6.0e-32
Match length
                   165
% identity
                   44
                   (AC006418) unknown protein [Arabidopsis thaliana]
NCBI Description
                   >qi 4559393 gb AAD23053.1 AC006526 18 (AC006526) unknown
                   protein [Arabidopsis thaliana]
```

43854

308489

uC-zmflmo17163a06b1

Seq. No. Seq. ID

NCBI GI

BLAST score

q169843

65



```
Method
                  BLASTX
NCBI GI
                  g2984709
BLAST score
                  323
                  5.0e-30
E value
                  67
Match length
                  93
% identity
NCBI Description (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]
                  308490
Seq. No.
Seq. ID
                  uC-zmflmo17163a09b1
                  BLASTX
Method
NCBI GI
                  g3292826
BLAST score
                  619
                  2.0e-64
E value
                  129
Match length
                  78
% identity
                  (AL031018) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  308491
Seq. ID
                  uC-zmflmo17163b12b1
                  BLASTN
Method
NCBI GI
                  g4185305
BLAST score
                  53
E value
                  2.0e-21
                  86
Match length
                  88
% identity
                  Zea mays cosmid IV.1E1 22-kDa alpha zein protein 21
NCBI Description
                  (sz22-21) gene, complete cds; retrotransposon Opie-2 gag
                  protein, polyprotein, and copia protein genes, complete
                  cds; and unknown genes
                  308492
Seq. No.
                  uC-zmflmo17163c10b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4467148
BLAST score
                  378
E value
                  3.0e-36
                  173
Match length
% identity
                  50
                  (AL035540) putative protein [Arabidopsis thaliana]
NCBI Description
                  308493
Seq. No.
Seq. ID
                  uC-zmflmo17163d02b1
Method
                  BLASTN
NCBI GI
                  g1244652
BLAST score
                  51
                  9.0e-20
E value
Match length
                  63
% identity
                  48
                  Zea mays copia-type retroelement PREM-2 gag gene, complete
NCBI Description
Seq. No.
                  308494
Seq. ID
                  uC-zmflmo17163e05b1
Method
                  BLASTN
```

% identity



```
6.0e-28
E value
Match length
                  133
% identity
                  87
                  Saccharum sp. phosphoenolpyruvate carboxylase (SCPEPCD1)
NCBI Description
                  gene, complete cds
Seq. No.
                  308495
Seq. ID
                  uC-zmflmo17163g11b1
                  BLASTN
Method
NCBI GI
                  g22258
BLAST score
                  41
                  1.0e-13
E value
                  53
Match length
                  94
% identity
NCBI Description Maize DNA for Ds103 controlling element (Ds1-related)
                  308496
Seq. No.
Seq. ID
                  uC-zmflmo17163h07b1
                  BLASTX
Method
NCBI GI
                  g3169170
                  198
BLAST score
                  2.0e-15
E value
Match length
                  117
% identity
                  44
                  (AC004401) putative chloroplast envelope Ca2+-ATPase, 5'
NCBI Description
                  partial [Arabidopsis thaliana]
                  308497
Seq. No.
                  uC-zmflmo17164a02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2760345
BLAST score
                  614
                  5.0e-64
E value
Match length
                  141
% identity
                  26
                  (U84967) ubiquitin [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  308498
                  uC-zmflmo17164c08b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g22332
BLAST score
                  274
E value
                  1.0e-153
Match length
                  361
                   94
% identity
NCBI Description Z.mays HRGP gene
                  308499
Seq. No.
Seq. ID
                  uC-zmflmo17164e07b1
Method
                  BLASTX
NCBI GI
                  g2323410
BLAST score
                  186
E value
                  8.0e-14
Match length
                  124
```

NCBI Description (AF015913) Skb1Hs [Homo sapiens]



```
Seq. No.
                  308500
Seq. ID
                  uC-zmflmo17164e12b1
Method
                  BLASTN
NCBI GI
                  g22332
BLAST score
                  220
E value
                  1.0e-120
Match length
                  394
                  89
% identity
NCBI Description
                  Z.mays HRGP gene
Seq. No.
                  308501
Seq. ID
                  uC-zmflmo17164g03b1
Method
                  BLASTN
NCBI GI
                  g4582786
BLAST score
                  47
E value
                  2.0e-17
Match length
                  47
                  100
% identity
NCBI Description Zea mays mRNA for adenosine kinase, putative
                  308502
Seq. No.
Seq. ID
                  uC-zmflmo17165a04b1
Method
                  BLASTX
NCBI GI
                  g416641
BLAST score
                  179
E value
                  3.0e-13
Match length
                  68
% identity
                  49
NCBI Description
                  INDOLE-3-ACETIC ACID INDUCED PROTEIN ARG4
                  >gi_287568_dbj_BAA03309_ (D14413) ORF [Vigna radiata]
                  308503
Seq. No.
Seq. ID
                  uC-zmflmo17165a07b1
Method
                  BLASTX
NCBI GI
                  g4510406
BLAST score
                  236
E value
                  1.0e-19
Match length
                  131
% identity
                  44
NCBI Description (AC006587) putative protein kinase [Arabidopsis thaliana]
                  308504
Seq. No.
Seq. ID
                  uC-zmflmo17165b08b1
Method
                  BLASTX
NCBI GI
                  g118104
BLAST score
                  437
E value
                  2.0e-43
Match length
                  98
% identity
                  85
```

NCBI Description PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE)

(CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN)

>gi_68408_pir__CSZM peptidylprolyl isomerase (EC 5.2.1.8) -

maize >gi_168461 (M55021) cyclophilin [Zea mays]

>gi_829148_emb_CAA48638_ (X68678) cyclophilin [Zea mays]

Seq. No. 308505

Seq. ID uC-zmflmo17165b11b1

NCBI GI

E value

BLAST score

g2191168

1.0e-25

286



```
Method
NCBI GI
                  g4539383
                  142
BLAST score
                  5.0e-09
E value
Match length
                  62
% identity
                  53
NCBI Description
                  (AL035526) putative protein (fragment) [Arabidopsis
                  thaliana]
                  308506
Seq. No.
Seq. ID
                  uC-zmflmo17165c11b1
Method
                  BLASTX
NCBI GI
                  g1155261
BLAST score
                  160
                  3.0e-14
E value
Match length
                  98
                  56
% identity
NCBI Description
                  (U40217) eukaryotic release factor 1 homolog [Arabidopsis
                  thaliana]
                  308507
Seq. No.
Seq. ID
                  uC-zmflmo17165d09b1
Method
                  BLASTX
                  g4115377
NCBI GI
BLAST -score
                  170
E value
                  2.0e-15
Match length
                  136
% identity
                  43
NCBI Description (AC005967) unknown protein [Arabidopsis thaliana]
Seq. No.
                  308508
Seq. ID
                  uC-zmflmo17165e11b1
Method
                  BLASTN
NCBI GI
                  q4007864
BLAST score
                  49
                  9.0e-19
E value
                  93
Match length
% identity
                  88
NCBI Description Zea mays HRGP gene, AC1503 line
                  308509
Seq. No.
Seq. ID
                  uC-zmflmo17165e12b1
Method
                  BLASTN
NCBI GI
                  g22312
BLAST score
                  45
E value
                  3.0e-16
Match length
                  69
                  91
% identity
NCBI Description
                  Maize ABA-inducible gene for glycine-rich protein ( ABA =
                  abscisic acid)
Seq. No.
                  308510
Seq. ID
                  uC-zmflmo17165f10b1
Method
                  BLASTX
```



Match length 130 % identity 45

NCBI Description (AF007270) contains similarity to myosin heavy chain

[Arabidopsis thaliana]

Seq. No. 308511

Seq. ID uC-zmflmo17165h03b1

Method BLASTX
NCBI GI g4033421
BLAST score 252
E value 1.0e-21
Match length 80
% identity 65

NCBI Description SOLUBLE INORGANIC PYROPHOSPHATASE (PYROPHOSPHATE

PHOSPHO-HYDROLASE) (PPASE) >gi_2570501 (AF022733) inorganic

pyrophosphatase [Oryza sativa]

Seq. No. 308512

Seq. ID uC-zmflmo17165h12b1

Method BLASTX
NCBI GI g1709000
BLAST score 156
E value 1.0e-10
Match length 47
% identity 68

NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE

ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)

>gi_960357_dbj_BAA09895_ (D63835) S-adenosylmethionine

synthetase [Hordeum vulgare]

Seq. No. 308513

Seq. ID uC-zmflmo17166a05b1

Method BLASTN
NCBI GI g497239
BLAST score 38
E value 7.0e-12
Match length 38
% identity 100

NCBI Description Zea mays W22 plasma-membrane H+ ATPase (Zmpma1) mRNA,

partial cds

Seq. No. 308514

Seq. ID uC-zmflmo17166a08b1

Method BLASTX
NCBI GI g2668742
BLAST score 162
E value 3.0e-11
Match length 49
% identity 69

NCBI Description (AF034945) glycine-rich RNA binding protein [Zea mays]

Seq. No. 308515

Seq. ID uC-zmflmo17166b03b1

Method BLASTX
NCBI GI g2224911
BLAST score 605
E value 6.0e-63

NCBI GI

E value

BLAST score

Match length

% identity

g312178

1.0e-19

51

55

98

```
Match length
% identity
                  (U93048) somatic embryogenesis receptor-like kinase [Daucus
NCBI Description
                  carota]
Seq. No.
                  308516
                  uC-zmflmo17166f08b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1171966
BLAST score
                  146
E value
                  4.0e-09
Match length
                  50
                  68
% identity
                  PHOSPHATIDYLINOSITOL 3-KINASE, NODULE ISOFORM (PI3-KINASE)
NCBI Description
                  (PTDINS-3-KINASE) (PI3K) (SPI3K-1) >gi_736337 (L29770)
                  phosphatidylinositol 3-kinase [Glycine max]
                  308517
Seq. No.
Seq. ID
                  uC-zmflmo17166h10b1
                  BLASTX
Method
NCBI GI
                  g2464915
BLAST score
                  246
                  7.0e-21
E value
                  125
Match length
                  47
% identity
                  (Z99708) transcription initiation factor like protein
NCBI Description
                  [Arabidopsis thaliana]
                  308518
Seq. No.
Seq. ID
                  uC-zmflmo17168a11b1
Method
                  BLASTX
NCBI GI
                  q3643611
BLAST score
                  313
                  9.0e-29
E value
Match length
                  61
                  87
% identity
NCBI Description (AC005395) putative casein kinase [Arabidopsis thaliana]
                  308519
Seq. No.
                  uC-zmflmo17168c09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2244871
BLAST score
                  339
E value
                  1.0e-31
Match length
                  70
% identity
                  (Z97338) phosphocholine cytidylyltransferase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  308520
Seg. ID
                  uC-zmflmo17168d01a1
Method
                  BLASTN
```



```
NCBI Description Z.mays GapC2 gene
                  308521
Seq. No.
                  uC-zmflmo17168d04a1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g22468
BLAST score
                   44
E value
                  5.0e-16
                  44
Match length
                  100
% identity
                  Z.mays mRNA for root-origin phosphoenolpyruvate carboxylase
NCBI Description
                   (PEPC)
                   308522
Seq. No.
Seq. ID
                  uC-zmflmo17168d05b1
Method
                  BLASTX
NCBI GI
                  g3617837
BLAST score
                  151
                   1.0e-09
E value
Match length
                   48
% identity
                   73
                  (AF035820) gibberellin action negative regulator SPY
NCBI Description
                   [Hordeum vulgare]
                   308523
Seq. No.
Seq. ID
                   uC-zmflmo17168f04b1
Method
                  BLASTX
NCBI GI
                   g3482974
BLAST score
                   458
                   1.0e-45
E value
Match length
                   134
                   67
% identity
                   (AL031369) ATP-dependent Clp proteinase-like protein
NCBI Description
                   [Arabidopsis thaliana]
                   308524
Seq. No.
Seq. ID
                   uC-zmflmo17168h04b1
Method
                   BLASTX
NCBI GI
                   g3445397
BLAST score
                   227
                   9.0e-19
E value
Match length
                   125
% identity
                   39
NCBI Description
                  (AJ010166) S-domain receptor-like protein kinase [Zea mays]
                   308525
Seq. No.
Seq. ID
                   uC-zmflmo17169a01b1
Method
                   BLASTX
NCBI GI
                   g1076515
BLAST score
                   169
E value
                   3.0e-12
Match length
                   55
% identity
                   64
NCBI Description
                  pectinesterase precursor - kidney bean
                   >gi 732913 emb CAA59482 (X85216) pectinesterase [Phaseolus
```

vulgaris]



```
Seq. No.
                  308526
Seq. ID
                  uC-zmflmo17169a04a1
Method
                  BLASTX
NCBI GI
                  g2695711
BLAST score
                  263
E value
                  1.0e-42
Match length
                  100
% identity
                  85
                  (AJ001370) cytochome b5 [Olea europaea]
NCBI Description
                  308527
Seq. No.
Seq. ID
                  uC-zmflmo17169a05a1
Method
                  BLASTX
NCBI GI
                  q3928142
BLAST score
                  641
E value
                  3.0e-67
Match length
                  134
% identity
                  50
NCBI Description (AJ131045) protein phosphatase [Cicer arietinum]
Seq. No.
                  308528
Seq. ID
                  uC-zmflmo17169a07a1
Method
                  BLASTX
NCBI GI
                  q3912917
BLAST score
                  587
E value
                  5.0e-61
Match length
                  116
% identity
                  94
NCBI Description
                  (AF001308) putative NAK-like ser/thr protein kinase
                  [Arabidopsis thaliana]
Seq. No.
                  308529
Seq. ID
                  uC-zmflmo17169a07b1
Method
                  BLASTX
NCBI GI
                  g3912917
BLAST score
                  238
E value
                  6.0e-20
Match length
                  90
% identity
                  61
NCBI Description
                  (AF001308) putative NAK-like ser/thr protein kinase
                  [Arabidopsis thaliana]
                  308530
Seq. ID
                  uC-zmflmo17169a08a1
Method
                  BLASTX
```

Seq. No.

NCBI GI g3915847 BLAST score 308 E value 3.0e-28 Match length 70 % identity 83

40S RIBOSOMAL PROTEIN S2 >gi 2335095 (AC002339) putative NCBI Description

40S ribosomal protein S2 [Arabidopsis thaliana]

Seq. No. 308531

Seq. ID uC-zmflmo17169a08b1

Method BLASTX NCBI GI g3915847



```
BLAST score 439
E value 2.0e-43
Match length 88
% identity 94
NCBI Description 40S RIBOSOMAL PROTEIN S2 >gi_2335095 (AC002339) putative 40S ribosomal protein S2 [Arabidopsis thaliana]

Seq. No. 308532
```

Seq. ID uC-zmflmo17169a09a1

Method BLASTX
NCBI GI g1421741
BLAST score 475
E value 9.0e-48
Match length 144
% identity 65

NCBI Description (U54770) cytochrome P450 homolog [Lycopersicon esculentum]

Seq. No. 308533

Seq. ID uC-zmflmo17169a09b1

Method BLASTX
NCBI GI g1421741
BLAST score 197
E value 2.0e-29
Match length 125
% identity 37

NCBI Description (U54770) cytochrome P450 homolog [Lycopersicon esculentum]

Seq. No. 308534

Seq. ID uC-zmflmo17169a12a1

Method BLASTX
NCBI GI g1778370
BLAST score 588
E value 3.0e-61
Match length 108
% identity 100

NCBI Description (U77678) asparagine synthetase 2 [Glycine max]

Seq. No. 308535

Seq. ID uC-zmflmo17169a12b1

Method BLASTX
NCBI GI g1778370
BLAST score 393
E value 4.0e-38
Match length 79
% identity 96

NCBI Description (U77678) asparagine synthetase 2 [Glycine max]

Seq. No. 308536

Seq. ID uC-zmflmo17169b04a1

Method BLASTX
NCBI GI g4262226
BLAST score 240
E value 4.0e-20
Match length 159
% identity 45

NCBI Description (AC006200) putative protein kinase [Arabidopsis thaliana]



Seq. No. 308537

Seq. ID uC-zmflmo17169b05a1

Method BLASTX
NCBI GI g1871192
BLAST score 174
E value 2.0e-23
Match length 95
% identity 72

NCBI Description (U90439) Cys3His zinc finger protein isolog [Arabidopsis

thaliana]

Seq. No. 308538

Seq. ID uC-zmflmo17169b06a1

Method BLASTX
NCBI GI g3023839
BLAST score 699
E value 5.0e-74
Match length 147
% identity 87

NCBI Description GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT 2

>gi_1835163_emb_CAB06619_ (Z84821) G protein beta subunit

[Nicotiana tabacum]

Seq. No. 308539

Seq. ID uC-zmflmo17169b08a1

Method BLASTX
NCBI GI g1710840
BLAST score 576
E value 1.0e-59
Match length 122
% identity 87

NCBI Description ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE

HYDROLASE) (ADOHCYASE) (CYTOKININ BINDING PROTEIN CBP57)
>gi_441217_dbj_BAA03709_ (D16138) S-adenosyl-L-homocystein
hydrolase [Nicotiana sylvestris] >gi_1857024_dbj_BAA08142_
(D45204) S-adenosyl-L-homocysteine hydrolase [Nicotiana

tabacum] >gi_2588781_dbj_BAA23164_ (D49804)

S-adenosyl-L-homocysteine hydrolase [Nicotiana tabacum]

Seq. No. 308540

Seq. ID uC-zmflmo17169b08b1

Method BLASTN
NCBI GI g535583
BLAST score 61
E value 1.0e-25
Match length 136
% identity 87

NCBI Description Medicago sativa adenosylhomocysteinase mRNA, complete cds

Seq. No. 308541

Seq. ID uC-zmflmo17169b09a1

Method BLASTX
NCBI GI g1076515
BLAST score 444
E value 7.0e-50
Match length 161
% identity 68



```
NCBI Description
                  pectinesterase precursor - kidney bean
                  >gi 732913 emb CAA59482 (X85216) pectinesterase [Phaseolus
                  vulgaris]
                  308542
Seq. No.
Seq. ID
                  uC-zmflmo17169b09b1
Method
                  BLASTX
NCBI GI
                  g1076515
BLAST score
                  506
E value
                  2.0e-51
Match length
                  116
% identity
                  81
                  pectinesterase precursor - kidney bean
NCBI Description
                  >gi 732913 emb CAA59482 (X85216) pectinesterase [Phaseolus
                  vulgaris]
Seq. No.
                  308543
Seq. ID
                  uC-zmflmo17169b10a1
Method
                  BLASTX
NCBI GI
                  g2344889
BLAST score
                  274
E value
                  4.0e-24
Match length
                  73
                  60
% identity
NCBI Description
                 (AC002388) unknown protein [Arabidopsis thaliana]
Seq. No.
                  308544
Seq. ID
                  uC-zmflmo17169b11a1
Method
                  BLASTX
NCBI GI
                  g4262174
BLAST score
                  549
E value
                  1.0e-56
Match length
                  116
                  85
% identity
NCBI Description (AC005508) 9058 [Arabidopsis thaliana]
                  308545
Seq. No.
Seq. ID
                  uC-zmflmo17169b12b1
Method
                  BLASTX
NCBI GI
                  g2695711
BLAST score
                  236
E value
                  2.0e-21
Match length
                  71
                  77
% identity
NCBI Description
                 (AJ001370) cytochome b5 [Olea europaea]
Seq. No.
                  308546
Seq. ID
                  uC-zmflmo17169c03a1
Method
                  BLASTX
NCBI GI
                  g2388580
BLAST score
                  501
```

E value 8.0e-51 Match length 95 % identity 92

NCBI Description (AC000098) Similar to Sequence 10 from patent 5477002

(gb_1253956). [Arabidopsis thaliana]

1.00



```
Seq. No.
                  308547
                  uC-zmflmo17169c04a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2959781
BLAST score
                  515
E value
                  1.0e-52
Match length
                  122
% identity
                  80
                  (AJ223508) Zwille protein [Arabidopsis thaliana]
NCBI Description
                  308548
Seq. No.
Seq. ID
                  uC-zmflmo17169c05a1
Method
                  BLASTX
NCBI GI
                  q4589062
BLAST score
                  189
E value
                  6.0e-25
Match length
                  96
% identity
                  68
NCBI Description
                  (AF120146) myo-inositol 1-phosphate synthase [Triticum
                  aestivum] >gi 4589064 gb AAD26331.1 AF120147 1 (AF120147)
                  myo-inositol 1-phosphate synthase [Triticum aestivum]
                  >gi_4589066 gb_AAD26332.1_AF120148_1 (AF120148)
                  myo-inositol 1-phosphate synthase [Triticum aestivum]
                  308549
Seq. No.
Seq. ID
                  uC-zmflmo17169c06a1
Method
                  BLASTX
NCBI GI
                  g1351974
BLAST score
                  369
                  4.0e-44
E value
Match length
                  95
% identity
                  99
NCBI Description
                  ADP-RIBOSYLATION FACTOR >gi 1076788 pir S49325
                  ADP-ribosylation factor - maize >gi 1076789 pir S53486
                  ADP-ribosylation factor - maize >gi 556686 emb CAA56351
                  (X80042) ADP-ribosylation factor [Zea mays]
Seq. No.
                  308550
Seq. ID
                  uC-zmflmo17169c07a1
Method
                  BLASTX
NCBI GI
                  g2244986
BLAST score
                  209
E value
                  2.0e-16
Match length
                  97
% identity
NCBI Description
                  (Z97340) FCA gamma [Arabidopsis thaliana]
```

Seq. No. 308551 Seq. ID uC-zmflmo17169c08b1

Method BLASTX NCBI GI g4588001 BLAST score 308 E value 4.0e-28 Match length 135 % identity 47

NCBI Description (AF085279) hypothetical Ser-Thr protein kinase [Arabidopsis

thaliana]



```
Seq. No.
                  308552
Seq. ID
                  uC-zmflmo17169c09a1
Method
                  BLASTX
NCBI GI
                  g1370180
BLAST score
                  663
                  9.0e-70
E value
Match length
                  137
                  94
% identity
NCBI Description (Z73939) RAB5B [Lotus japonicus]
Seq. No.
                  308553
Seq. ID
                  uC-zmflmo17169c09b1
Method
                  BLASTX
NCBI GI
                  g1370180
BLAST score
                  191
E value
                  4.0e-23
Match length
                  65
% identity
NCBI Description (273939) RAB5B [Lotus japonicus]
Seq. No.
                  308554
                  uC-zmflmo17169c10a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q542179
BLAST score
                  456
E value
                  1.0e-45
Match length
                  89
% identity
NCBI Description
                  alpha tubulin - maize >gi_629837_pir_ S39998 tubulin alpha
                  chain - maize (fragment) >gi 393401 emb CAA52158 (X73980)
                  alpha tubulin [Zea mays]
Seq. No.
                  308555
Seq. ID
                  uC-zmflmo17169c10b1
Method
                  BLASTX
NCBI GI
                  g320960
BLAST score
                  238
E value
                  5.0e-20
Match length
                  59
% identity
                  83
                  tubulin alpha-II chain - Plasmodium falciparum >gi_160108
NCBI Description
                  (M34390) alpha-tubulin II [Plasmodium falciparum]
Seq. No.
                  308556
Seq. ID
                  uC-zmflmo17169d03a1
Method
                  BLASTX
                  g4105772
                  699
                  6.0e-74
                  157
```

NCBI GI BLAST score E value Match length % identity 52

NCBI Description (AF049917) PGP9B [Petunia x hybrida]

Seq. No. 308557

Seq. ID uC-zmflmo17169d04a1

Method BLASTX



NCBI GI g1170568
BLAST score 322
E value 4.0e-40
Match length 118
% identity 73

NCBI Description MYO-INOSITOL-1-PHOSPHATE SYNTHASE (IPS)

>gi 2147316 pir S60302 D-myo-inositol-3-phosphate synthase

(EC 5.5.1.4) - Spirodela polyrrhiza >qi 558648 emb CAA77751 (Z11693)

D-myo-inositol-3-phosphate synthase [Spirodela polyrrhiza]

Seq. No. 308558

Seq. ID uC-zmflmo17169d08b1

Method BLASTX
NCBI GI g2827700
BLAST score 148
E value 5.0e-10
Match length 52
% identity 58

NCBI Description (ALO21684) DEAD box ATP dependent helicase protein

[Arabidopsis thaliana]

Seq. No. 308559

Seq. ID uC-zmflmo17169d10a1

Method BLASTX
NCBI GI g2407790
BLAST score 565
E value 7.0e-67
Match length 139
% identity 96

NCBI Description (AF019910) grr1 [Glycine max]

Seq. No. 308560

Seq. ID uC-zmflmo17169d10b1

Method BLASTN
NCBI GI g2407789
BLAST score 274
E value 1.0e-153
Match length 338
% identity 94

NCBI Description Glycine max grr1 (grr1) mRNA, complete cds

Seq. No. 308561

Seq. ID uC-zmflmo17169d11a1

Method BLASTX
NCBI GI g3953603
BLAST score 220
E value 3.0e-24
Match length 91
% identity 74

NCBI Description (AB008490) response regulator 7 [Arabidopsis thaliana]

Seq. No. 308562

Seq. ID uC-zmflmo17169e03a1

Method BLASTX
NCBI GI g3243234
BLAST score 646

- 5



```
E value
                  8.0e-68
Match length
                  148
% identity
NCBI Description
                  (AF071477) isoflavone reductase related protein [Pyrus
                  communis]
Seq. No.
                  308563
Seq. ID
                  uC-zmflmo17169e03b1
                  {\tt BLASTX}
Method
NCBI GI
                  g3243234
BLAST score
                  477
E value
                  7.0e-48
Match length
                  111
                  83
% identity
NCBI Description
                  (AF071477) isoflavone reductase related protein [Pyrus
                  communis]
Seq. No.
                  308564
Seq. ID
                  uC-zmflmo17169e08a1
Method
                  BLASTX
NCBI GI
                  g3834307
BLAST score
                  639
E value
                  6.0e-67
Match length
                  159
% identity
                  74
NCBI Description
                  (AC005679) Strong similarity to gene T10I14.120 gi 2832679
                  putative protein from Arabidopsis thaliana BAC qb AL021712.
                  ESTs gb N65887 and gb N65627 come from this gene.
                  [Arabidopsis thaliana]
Seq. No.
                  308565
Seq. ID
                  uC-zmflmo17169e12a1
Method
                  BLASTX
NCBI GI
                  g3023271
BLAST score
                  385
E value
                  2.0e-37
Match length
                  86
% identity
                  GLUTATHIONE-DEPENDENT FORMALDEHYDE DEHYDROGENASE (FDH)
NCBI Description
                   (FALDH) (GSH-FDH) >gi_1675394 (U77637) class III ADH enzyme
                  [Oryza sativa]
Seq. No.
                  308566
Seq. ID
                  uC-zmflmo17169f02a1
Method
                  BLASTX
NCBI GI
                  q4204294
BLAST score
                  393
E value
                  4.0e-38
Match length
                  106
% identity
```

NCBI Description (AC003027) lcl prt seq No definition line found

[Arabidopsis thaliana]

Seq. No. 308567

Seq. ID uC-zmflmo17169f02b1

Method BLASTX NCBI GI g4204294

```
BLAST score
E value
                  8.0e-18
Match length
                  69
% identity
NCBI Description
                  (AC003027) lcl_prt_seq No definition line found
                  [Arabidopsis thaliana]
                  308568
Seq. No.
Seq. ID
                  uC-zmflmo17169f03a1
Method
                  BLASTX
NCBI GI
                  g3024502
BLAST score
                  216
                  3.0e-17
E value
Match length
                  51
                  82
% identity
NCBI Description
                  RAS-RELATED PROTEIN RAB11D >gi_1370148_emb_CAA98180_
                  (Z73952) RAB11D [Lotus japonicus]
Seq. No.
                  308569
Seq. ID
                  uC-zmflmo17169f07a1
Method
                  BLASTX
NCBI GI
                  g1468977
BLAST score
                  600
E value
                  2.0e-62
Match length
                  163
                  67
% identity
NCBI Description (U62550) AT-PHH1 [Arabidopsis thaliana]
                  308570
Seq. No.
Seq. ID
                  uC-zmflmo17169f08a1
Method
                  BLASTX
NCBI GI
                  g4006895
BLAST score
                  567
E value
                  2.0e-58
Match length
                  161
% identity
                  68
NCBI Description (Z99708) putative protein [Arabidopsis thaliana]
Seq. No.
                  308571
Seq. ID
                  uC-zmflmo17169g02a1
Method
                  BLASTX
NCBI GI
                  g2911042
BLAST score
                  380
E value
                  2.0e-36
Match length
                  146
% identity
NCBI Description
                  (AL021961) Phosphoglycerate dehydrogenase - like protein
                  [Arabidopsis thaliana]
Seq. No.
                  308572
Seq. ID
                  uC-zmflmo17169g02b1
```

Method BLASTX NCBI GI g2911042 BLAST score 194 E value 7.0e-38 Match length 106 % identity 82



```
(AL021961) Phosphoglycerate dehydrogenase - like protein
NCBI Description
                   [Arabidopsis thaliana]
                   308573
Seq. No.
Seq. ID
                   uC-zmflmo17169g03a1
Method
                   BLASTN
NCBI GI
                   g256142
BLAST score
                   76
                   4.0e-35
E value
                   88
Match length
                   97
% identity
                   cytosolic glutamine synthetase [Glycine max=soybeans, var
NCBI Description
                   Prize, mRNA, 1450 nt]
                   308574
Seq. No.
Seq. ID
                   uC-zmflmo17169g04a1
Method
                   BLASTX
NCBI GI
                   g129590
BLAST score
                   590
E value
                   1.0e-62
Match length
                   129
                   96
% identity
                   PHENYLALANINE AMMONIA-LYASE >gi 99990 pir S17444
NCBI Description
                   phenylalanine ammonia-lyase (EC 4.3.1.5) 1 - alfalfa
                   >gi_19650_emb_CAA41169_ (X58180) phenylalanine ammonia-lyase [Medicago sativa]
Seq. No.
                   308575
Seq. ID
                   uC-zmflmo17169g04b1
Method
                   BLASTX
NCBI GI
                   q81807
BLAST score
                   146
E value
                   4.0e-09
Match length
                   46
                   70
% identity
NCBI Description
                   phenylalanine ammonia-lyase (EC 4.3.1.5) - soybean
                   (fragment)
Seq. No.
                   308576
Seq. ID
                   uC-zmflmo17169g08a1
Method
                   BLASTX
NCBI GI
                   g1326161
BLAST score
                   290
E value
                   6.0e-26
Match length
                   148
% identity
                  (U54703) dehydrin [Phaseolus vulgaris]
NCBI Description
Seq. No.
                   308577
                   uC-zmflmo17169g08b1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g1326160
```

5.0e-31 E value Match length 134

70

% identity 95

BLAST score

NCBI Description Phaseolus vulgaris dehydrin mRNA, complete cds



```
308578
Seq. No.
Seq. ID
                  uC-zmflmo17169g09a1
Method
                  BLASTX
NCBI GI
                  g4506223
BLAST score
                  227
E value
                  1.0e-18
Match length
                  156
% identity
                  33
NCBI Description proteasome (prosome, macropain) 26S subunit, non-ATPase, 13
                  >gi 3618343 dbj BAA33214 (AB009398) 26S proteasome subunit
                  p40.5 [Homo sapiens]
Seq. No.
                  308579
Seq. ID
                  uC-zmflmo17169g10a1
Method
                  BLASTX
NCBI GI
                  q4467095
BLAST score
                  167
                  1.0e-15
E value
Match length
                  93
% identity
NCBI Description
                  (AL035538) putative protein [Arabidopsis thaliana]
Seq. No.
                  308580
Seq. ID
                  uC-zmflmo17169g10b1
Method
                  BLASTX
NCBI GI
                  q4467095
BLAST score
                  265
E value
                  4.0e-23
Match length
                  106
% identity
NCBI Description
                  (AL035538) putative protein [Arabidopsis thaliana]
Seq. No.
                  308581
Seq. ID
                  uC-zmflmo17169g12a1
Method
                  BLASTN
NCBI GI
                  g304108
BLAST score
                  34
E value
                  1.0e-09
Match length
                  46
% identity
                  93
NCBI Description
                  Arabidopsis thaliana poly(A)-binding protein mRNA, complete
                  cds
Seq. No.
                  308582
Seq. ID
                  uC-zmflmo17169g12b1
Method
                  BLASTX
NCBI GI
                  g2213871
BLAST score
                  279
```

E value 9.0e-25 Match length 71 % identity 86

NCBI Description (AF003126) poly(A)-binding protein [Mesembryanthemum

crystallinum]

Seq. No. 308583

uC-zmflmo17169h03a1 Seq. ID



Method BLASTX
NCBI GI g4587525
BLAST score 224
E value 5.0e-31
Match length 158
% identity 47

NCBI Description (AC007060) Contains the PF 00650 CRAL/TRIO

phosphatidyl-inositol-transfer protein domain. ESTs gb_T76582, gb_N06574 and gb_Z25700 come from this gene.

[Arabidopsis thaliana]

Seq. No. 308584

Seq. ID uC-zmflmo17169h06a1

Method BLASTX
NCBI GI g2055230
BLAST score 635
E value 2.0e-68
Match length 150
% identity 86

NCBI Description (AB000130) SRC2 [Glycine max]

Seq. No. 308585

Seq. ID uC-zmflmo17169h06b1

Method BLASTN
NCBI GI g2055229
BLAST score 172
E value 7.0e-92
Match length 347
% identity 93

NCBI Description Soybean mRNA for SRC2, complete cds

Seq. No. 308586

Seq. ID uC-zmflmo17169h08a1

Method BLASTN
NCBI GI g6598550
BLAST score 39
E value 1.0e-12
Match length 75
% identity 88

NCBI Description Arabidopsis thaliana chromosome II BAC T1B3 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 308587

Seq. ID uC-zmflmo17169h10a1

Method BLASTX
NCBI GI g135406
BLAST score 634
E value 2.0e-66
Match length 151
% identity 85

NCBI Description TUBULIN ALPHA-3/ALPHA-5 CHAIN >gi_99768_pir_ A32712 tubulin

alpha-5 chain - Arabidopsis thaliana >gi 166912 (M17189) alpha-tubulin [Arabidopsis thaliana] >gi 166918 (M84698)

alpha-5 tubulin [Arabidopsis thaliana]

Seq. No. 308588

Seq. ID uC-zmflmo17169h11a1

Match length

% identity

74



```
Method
                   BLASTX
NCBI GI
                   g479386
BLAST score
                   640
E value
                   2.0e-67
Match length
                   145
% identity
                   94
NCBI Description isocitrate dehydrogenase - soybean
Seq. No.
                   308589
Seq. ID
                   uC-zmflmo17169h11b1
Method
                   BLASTN
NCBI GI
                   g169988
BLAST score
                   371
E value
                   0.0e + 00
Match length
                   430
% identity
                   97
                   Glycine max NADP-specific isocitrate dehydrogenase (idh1)
NCBI Description
                   mRNA, 3' end
Seq. No.
                   308590
Seq. ID
                   uC-zmflmo17169h12b1
Method
                   BLASTX
NCBI GI
                   g479386
BLAST score
                   248
                   4.0e-21
E value
Match length
                   59
% identity
                   85
NCBI Description isocitrate dehydrogenase - soybean
Seq. No.
                   308591
Seq. ID
                   uC-zmflmo17171a11b1
Method
                   BLASTX
NCBI GI
                   q3688173
BLAST score
                   374
E value
                   6.0e-36
Match length
                   124
% identity
                   56
NCBI Description
                  (AL031804) putative protein [Arabidopsis thaliana]
Seq. No.
                   308592
Seq. ID
                   uC-zmflmo17171b06b1
Method
                   BLASTX
NCBI GI
                   g939785
BLAST score
                   277
E value
                   1.0e-24
Match length
                   62
% identity
                   89
NCBI Description
                  (L46400) MADS box protein [Zea mays]
                   308593
Seq. No.
Seq. ID
                  uC-zmflmo17171b07a1
Method
                  BLASTX
NCBI GI
                  g4539348
BLAST score
                  259
E value
                  1.0e-22
```

```
(AL035539) putative pollen allergen [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  308594
Seq. ID
                  uC-zmflmo17171b07b1
Method
                  BLASTN
NCBI GI
                  q3821780
BLAST score
                  34
E value
                  1.0e-09
                                                     No.
Match length
                  34
% identity
                  100
NCBI Description
                  Xenopus laevis cDNA clone 27A6-1
Seq. No.
                  308595
Seq. ID
                  uC-zmflmo17171d06b1
Method
                  BLASTN
NCBI GI
                  q4206305
                                 ٠.
BLAST score
                  97
E value
                  4.0e-47
Match length
                  213
% identity
                  87
NCBI Description
                 Zea mays retrotransposon Cinful-1, complete sequence
Seq. No.
                  308596
Seq. ID
                  uC-zmflmo17171g05b1
Method
                  BLASTX
NCBI GI
                  q4539452
BLAST score
                  180
E value
                  2.0e-13
Match length
                  84
% identity
NCBI Description
                  (AL049500) putative phosphoribosylanthranilate transferase
                  [Arabidopsis thaliana]
```

Seq. No. 308597

Seq. ID uC-zmflmo17171g06b1

Method BLASTN
NCBI GI g4185305
BLAST score 61
E value 1.0e-25
Match length 156

Match length 156 % identity 43

NCBI Description Zea mays cosmid IV.1E1 22-kDa alpha zein protein 21 (sz22-21) gene, complete cds; retrotransposon Opie-2 ga

(sz22-21) gene, complete cds; retrotransposon Opie-2 gag protein, polyprotein, and copia protein genes, complete

cds; and unknown genes

Seq. No. 308598

Seq. ID uC-zmflmo17171g07b1

Method BLASTX
NCBI GI g4406784
BLAST score 252
E value 1.0e-21
Match length 116
% identity 36

NCBI Description (AC006532) putative oligopeptide transport protein

[Arabidopsis thaliana]

```
308599
Seq. No.
Seq. ID
                  uC-zmflmo17171g11b1
Method
                  BLASTX
NCBI GI
                  g3063447
BLAST score
                  321
                  1.0e-29
E value
                  153
Match length
% identity
NCBI Description (AC003981) F22013.9 [Arabidopsis thaliana]
Seq. No.
                  308600
Seq. ID
                  uC-zmflmo17171h09b1
Method
                  BLASTX
NCBI GI
                  g2984709
BLAST score
                  417
E value
                  6.0e-41
Match length
                  90
% identity
                  92
NCBI Description (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]
                  308601
Seq. No.
Seq. ID
                  uC-zmflmo17172a12a1
Method
                  BLASTN
NCBI GI
                  g485376
BLAST score
                  37
                  2.0e-11
E value
Match length
                  73
% identity
                  88
NCBI Description Zea mays alpha-3-tubulin gene, complete cds
                  308602
Seq. No.
Seq. ID
                  uC-zmflmo17172d03a1
Method
                  BLASTX
NCBI GI
                  q2425066
BLAST score
                  139
E value
                  6.0e-09
Match length
                  36
% identity
NCBI Description (AF019147) cysteine proteinase Mir3 [Zea mays]
Seq. No.
                  308603
                  uC-zmflmo17172e04a1
                  BLASTN
                  g1181330
                  78
                  4.0e-36
```

Seq. ID Method NCBI GI BLAST score E value

Match length 125 % identity 93

NCBI Description Z.mays CNX mRNA

Seq. No. 308604

uC-zmflmo17173b11b1 Seq. ID

Method BLASTX NCBI GI g2605617 BLAST score 330 E value 3.0e-31 Match length 64



```
% identity
NCBI Description
                  (D88617) OSMYB1 [Oryza sativa]
Seq. No.
                  308605
Seq. ID
                  uC-zmflmo17173c12b1
                  BLASTX
Method
NCBI GI
                  g2232254
BLAST score
                  230
                                                                   -3,
E value
                  5.0e-24
Match length
                  73
% identity
                  67
NCBI Description
                  (AF005237) old-yellow-enzyme homolog [Catharanthus roseus]
Seq. No.
                  308606
Seq. ID
                  uC-zmflmo17173d05b1
Method
                  BLASTN
NCBI GI
                  q22292
BLAST score
                  89
E value
                  2.0e-42
Match length
                  280
% identity
                  85
NCBI Description Z.mays mRNA for glycine-rich protein
                  308607
Seq. No.
Seq. ID
                  uC-zmflmo17173d11b1
Method
                  BLASTX
NCBI GI
                  g902584
BLAST score
                  294
E value
                  6.0e-37
Match length
                  136
% identity
                  9
NCBI Description
                  (U29159) polyubiquitin containing 7 ubiquitin monomers [Zea
                  mays]
                  308608
Seq. No.
Seq. ID
                  uC-zmflmo17174a04b1
Method
                  BLASTN
NCBI GI
                  g3821780
BLAST score
                  36
E value
                  1.0e-10
Match length
                  36
% identity
                  100
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                  308609
Seq. ID
                  uC-zmflmo17174b07b1
Method
                  BLASTN
NCBI GI
                  g22646
BLAST score
                  45
E value
                  3.0e-16
Match length
                  68
% identity
                  94
```

Seq. No. 308610

Seq. ID uC-zmflmo17174c06b1

NCBI Description Z.mays MFS18 mRNA

Method BLASTN

```
NCBI GI
                   g2286152
BLAST score
                   218
E value
                   1.0e-119
Match length
                   289
% identity
                   94
```

Zea mays cytoplasmic malate dehydrogenase mRNA, complete NCBI Description

cds

Seq. No. 308611

Seq. ID uC-zmflmo17174c11b1

Method BLASTN NCBI GI g3821780 BLAST score 36 E value 1.0e-10 Match length 48 % identity 67

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 308612

Seq. ID uC-zmflmo17174d09b1

Method BLASTX NCBI GI g4580398 BLAST score 245 E value 6.0e-21 Match length 71 % identity 63

NCBI Description (AC007171) putative protein kinase APK1A [Arabidopsis

thaliana]

Seq. No. 308613

Seq. ID uC-zmflmo17174g01a1

Method BLASTN NCBI GI q4140643 BLAST score 140 E value 7.0e-73 Match length 244 % identity 90

Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster, NCBI Description

complete sequence

Seq. No. 308614

Seq. ID uC-zmflmo17174g09b1

Method BLASTX NCBI GI g4007490 BLAST score 163 5.0e-11 E value Match length 64 47 % identity

NCBI Description (AF094763) SNF4/AMP-activated protein kinase gamma subunit;

SNF4A; noncatalytic subunit of the SNF/AMPK complex

[Drosophila melanogaster]

Seq. No. 308615

Seq. ID uC-zmflmo17175a02b1

Method BLASTN NCBI GI g2062691 BLAST score 34



E value 2.0e-09
Match length 34
% identity 100
NCRI Description Human s

NCBI Description Human sodium phosphate transporter (NPT4) mRNA, complete

cds

Seq. No. 308616

Seq. ID uC-zmflmo17175h10b1

Method BLASTX
NCBI GI g567890
BLAST score 150
E value 8.0e-10
Match length 69
% identity 45

NCBI Description (L37352) beta-galactosidase-complementation protein

[Cloning vector]

Seq. No. 308617

Seq. ID uC-zmflmo17176a01b1

Method BLASTX
NCBI GI g82306
BLAST score 328
E value 2.0e-30
Match length 73
% identity 78

NCBI Description myb protein 305 - garden snapdragon

Seq. No. 308618

Seq. ID uC-zmflmo17176b12b1

Method BLASTX
NCBI GI g2239083
BLAST score 164
E value 4.0e-11
Match length 148
% identity 32

NCBI Description (Z84383) anthranilate N-hydroxycinnamoyl/benzoyltransferase

[Dianthus caryophyllus] >gi_2239087_emb_CAB06429_ (Z84385)

anthranilate N-hydroxycinnamoyl/benzoyltransferase

[Dianthus caryophyllus]

Seq. No. 308619

Seq. ID uC-zmflmo17176c06b1

Method BLASTX
NCBI GI g3927831
BLAST score 248
E value 4.0e-21
Match length 124
% identity 41

NCBI Description (AC005727) similar to mouse ankyrin 3 [Arabidopsis

thaliana]

Seq. No. 308620

Seq. ID uC-zmflmo17176c11b1

Method BLASTX
NCBI GI g1717957
BLAST score 197
E value 2.0e-29



Match length 76 88 % identity

NCBI Description UBIQUINOL-CYTOCHROME C REDUCTASE IRON-SULFUR SUBUNIT

PRECURSOR (RIESKE IRON-SULFUR PROTEIN) (RISP)

>gi 100923 pir A41607 ubiquinol--cytochrome-c reductase (EC 1.10.2.2) iron-sulfur protein precursor - maize >gi_168607 (M77224) Rieske Fe-S protein [Zea mays]

Seq. No. 308621

uC-zmflmo17176d03b1 Seq. ID

Method BLASTX NCBI GI g3236259 BLAST score 235 E value 1.0e-19 Match length 110 % identity 78

NCBI Description (AC004684) putative alcohol dehydrogenase [Arabidopsis

thaliana

Seq. No.

308622 Seq. ID uC-zmflmo17176d04b1

Method BLASTX NCBI GI g2130082 BLAST score 181 E value 2.0e-13 Match length 91

% identity 41

NCBI Description protein kinase Xa21 (EC 2.7.1.-) - rice >qi 1122443

(U37133) receptor kinase-like protein [Oryza sativa] >gi 2586085 (U72723) receptor kinase-like protein [Oryza

longistaminata] >gi_1586408 prf 2203451A receptor

kinase-like protein [Oryza sativa]

Seq. No. 308623

Seq. ID uC-zmflmo17176g07b1

Method BLASTX NCBI GI g4587533 BLAST score 150 E value 1.0e-09 Match length 55 % identity 55

(AC007060) EST gb AA721821 comes from this gene. NCBI Description

[Arabidopsis thaliana]

Seq. No. 308624

Seq. ID uC-zmflmo17176h01b1

Method BLASTX NCBI GI g2262103 BLAST score 311 E value 2.0e-28 Match length 113 % identity 57

NCBI Description (AC002343) unknown protein [Arabidopsis thaliana]

Seq. No. 308625

Seq. ID uC-zmflmo17176h05b1

Method BLASTX



NCBI GI g3142300 BLAST score 299 E value 6.0e-27 Match length 117 % identity 47

NCBI Description (AC002411) Contains similarity to pre-mRNA processing

protein PRP39 gb_L29224 from S. cerevisiae. ESTs gb_R64908 and gb_T88158, gb_N38703 and gb_AA651043 come from this

gene. [Arabidopsis thaliana]

Seq. No. 308626

Seq. ID uC-zmflmo17176h10b1

Method BLASTX
NCBI GI g4582787
BLAST score 619
E value 1.0e-64
Match length 141
% identity 84

NCBI Description (AJ012281) adenosine kinase [Zea mays]

Seq. No. 308627

Seq. ID uC-zmflmo17177a10a1

Method BLASTN
NCBI GI g1906603
BLAST score 54
E value 1.0e-21
Match length 179
% identity 82

NCBI Description Zea mays ACCase gene, intron containing colonist1 and

colonist2 retrotransposons and reverse transcriptase

pseudogene, complete sequence

Seq. No. 308628

Seq. ID uC-zmflmo17177b02a1

Method BLASTX
NCBI GI g1906804
BLAST score 336
E value 2.0e-31
Match length 146
% identity 45

NCBI Description (D87750) farnesyl cysteine carboxyl methyltransferase

[Xenopus laevis]

Seq. No. 308629

Seq. ID uC-zmflmo17177f01a1

Method BLASTX
NCBI GI g3334761
BLAST score 256
E value 4.0e-22
Match length 99
% identity 51

NCBI Description (Z97029) ribonuclease HI large subunit [Homo sapiens]

Seq. No. 308630

Seq. ID uC-zmflmo17179c03b1

Method BLASTX NCBI GI g2352492

BLAST score 257 E value 4.0e-22 Match length 80 % identity 59

NCBI Description (AF005047) transport inhibitor response 1 [Arabidopsis

thaliana] >gi 2352494 (AF005048) transport inhibitor

response 1 [Arabidopsis thaliana]

Seq. No. 308631

Seq. ID uC-zmflmo17179d05b1

Method BLASTX
NCBI GI g3297824
BLAST score 208
E value 3.0e-16
Match length 108
% identity 51

NCBI Description (ALO31032) bZIP transcription factor-like protein

[Arabidopsis thaliana]

Seq. No. 308632

Seq. ID uC-zmflmo17179d07a1

Method BLASTX
NCBI GI g2088650
BLAST score 148
E value 2.0e-09
Match length 38
% identity 76

NCBI Description (AF002109) peroxisomal ATP/ADP carrier protein isolog

[Arabidopsis thaliana]

Seq. No. 308633

Seq. ID uC-zmflmo17179d09b1

Method BLASTN
NCBI GI g22646
BLAST score 44
E value 1.0e-15
Match length 76
% identity 89

NCBI Description Z.mays MFS18 mRNA

Seq. No. 308634

Seq. ID uC-zmflmo17179e01b1

Method BLASTX
NCBI GI g3121837
BLAST score 205
E value 5.0e-16
Match length 80
% identity 55

NCBI Description PHOSPHATIDATE CYTIDYLYLTRANSFERASE (CDP-DIGLYCERIDE

SYNTHETASE) (CDP-DIGLYCERIDE PYROPHOSPHORYLASE)

(CDP-DIACYLGLYCEROL SYNTHASE) (CDS) (CTP:PHOSPHATIDATE

CYTIDYLYLTRANSFERASE) (CDP-DAG SYNTHASE)

>gi_2182104_emb_CAA63004_ (X91909) CDP-diacylglycerol

synthetase [Solanum tuberosum]

Seq. No. 308635

Seq. ID uC-zmflmo17179e10b1



```
Method
                  BLASTX
NCBI GI
                  g2880051
BLAST score
                  157
                   9.0e-17
E value
                  79
Match length
                  58
% identity
                  (AC002340) putative protein kinase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  308636
                  uC-zmflmo17179f08a1
Seq. ID
                  BLASTX
Method
                   g4538896
NCBI GI
BLAST score
                   216
E value
                  2.0e-17
Match length
                  86
% identity
                   53
                  (AL049482) putative protein [Arabidopsis thaliana]
NCBI Description
                   308637
Seq. No.
                   uC-zmflmo17179g07b1
Seq. ID
Method
                   BLASTN
NCBI GI
                   q22332
BLAST score
                   456
E value
                   0.0e + 00
Match length
                   594
% identity
                   60
NCBI Description Z.mays HRGP gene
Seq. No.
                   308638
                   uC-zmflmo17179h12b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q2088650
BLAST score
                   198
                   4.0e-15
E value
Match length
                   90
% identity
                   48
                  (AF002109) peroxisomal ATP/ADP carrier protein isolog
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   308639
                   uC-zmflmo17180a08b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3360289
BLAST score
                   138
E value
                   1.0e-08
Match length
                   76
% identity
                   42
                   (AF023164) leucine-rich repeat transmembrane protein kinase
NCBI Description
                   1 [Zea mays]
Seq. No. Seq. ID
                   308640
                   uC-zmflmo17180b07b1
Method
                   BLASTN
NCBI GI
                   g257040
```

Match length 271

1.0e-109

200

BLAST score

E value

```
% identity
  NCBI Description hydroxyproline-rich glycoprotein [maize, Genomic, 1703 nt]
  Seq. No.
                     308641
  Seq. ID
                     uC-zmflmo17180c06b1
  Method
                     BLASTX
  NCBI GI
                     g1658313
  BLAST score
                    <sub>2</sub>, 432
  E value
                     8.0e-43
  Match length
                     103
  % identity
                     41
  NCBI Description (Y08987) osr40g2 [Oryza sativa]
                     308642
  Seq. No.
  Seq. ID
                     uC-zmflmo17180d10a1
  Method
                     BLASTN
  NCBI GI
                     g1532072
  BLAST score
                     50
  E value
                     1.0e-19
  Match length
                     113
% identity 87
NCBI Description Z.mays mRNA for S-adenosylmethionine decarboxylase
  Seq. No.
                     308643
  Seq. ID
                     uC-zmflmo17180d10b1
  Method
                     BLASTX
  NCBI GI
                     g2129921
  BLAST score
                     179
  E value
                     5.0e-13
  Match length
                     50
                     72
  % identity
  NCBI Description
                    hypothetical protein 1 - Madagascar periwinkle >gi 758694
                     (U12573) putative [Catharanthus roseus]
                     308644
  Seq. No.
  Seq. ID
                     uC-zmflmo17180h05b1
  Method
                     BLASTX
  NCBI GI
```

Method BLASTX
NCBI GI g1362008
BLAST score 257
E value 3.0e-22
Match length 68
% identity 15

NCBI Description ubiquitin-like protein 12 - Arabidopsis thaliana

Seq. No. 308645

Seq. ID uC-zmflmo17181a03b1

Method BLASTN
NCBI GI g2668743
BLAST score 96
E value 1.0e-46
Match length 289
% identity 90

NCBI Description Zea mays ubiquitin conjugating enzyme (UBC) mRNA, complete

cds

Seq. No. 308646

Seq. ID uC-zmflmo17181b04b1

```
BLASTN
Method
NCBI GI
                  g3135542
BLAST score
                  122
E value
                  2.0e-62
                  194
Match length
                  91
% identity
NCBI Description Oryza sativa aquaporin (PIP2a) mRNA, complete cds
                  308647
Seq. No.
Seq. ID
                  uC-zmflmo17181c01b1
                  BLASTX
Method
NCBI GI
                  g2760839
BLAST score
                  198
E value
                  2.0e-15
Match length
                  102
% identity
                  47
                  (AC003105) putative receptor kinase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  308648
                  uC-zmflmo17181c05b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2347189
BLAST score
                  191
E value
                  9.0e-15
Match length
                  81
% identity
                  49
                  (AC002338) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  >gi 3150399 (AC004165) hypothetical protein [Arabidopsis
                  thaliana]
Seq. No.
                  308649
                  uC-zmflmo17181e03b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1706256
BLAST score
                  145
                  4.0e-09
E value
Match length
                  46
                  59
% identity
                  PEPTIDYL-PROLYL CIS-TRANS ISOMERASE 10 (PPIASE) (ROTAMASE)
NCBI Description
                   (CYCLOPHILIN-10) >gi 733577 (U23453) similar to
                  peptidyl-prolyl cis-trans isomerase (PPIASE) (CYCLOPHILIN)
                   [Caenorhabditis elegans] >gi 1155225 (U34954) cyclophilin
                  isoform 10 [Caenorhabditis elegans]
Seq. No.
                  308650
Seq. ID
                  uC-zmflmo17181e11b1
Method
                  BLASTX
                  g4337191
NCBI GI
```

Method BLASTX
NCBI GI g433719:
BLAST score 401
E value 3.0e-39
Match length 120
% identity 61

NCBI Description (AC006403) hypothetical protein [Arabidopsis thaliana]

Seq. No. 308651

Seq. ID uC-zmflmo17183h07a1

Method BLASTN



```
NCBI GI
                    g4416300
BLAST score
                    49
E value
                    1.0e-18
Match length
                    112
% identity
                    43
NCBI Description
                    Zea mays chromosome 4 22 kDa zein-associated intercluster
                    region, complete sequence
Seq. No.
                    308652
Seq. ID
                    uC-zmflmo17184b02b1
Method
                    BLASTX
NCBI GI
                    q626042
BLAST score
                    782
                    1.0e-83
E value
Match length
                    154
% identity
                    92
                   beta-glucosidase, root meristem (EC 3.2.1.-) precursor - maize >gi_435313_emb_CAA52293_ (X74217) beta-glucosidase
NCBI Description
                    [Zea mays]
Seq. No.
                    308653
Seq. ID
                   uC-zmflmo17184e12b1
Method
                   BLASTX
                   g1173630
NCBI GI
BLAST score
                    468
E value
                   8.0e-47
Match length
                   166
% identity
                    58
NCBI Description
                   (U34747) cysteine proteinase [Phalaenopsis sp. 'hybrid
                   308654
Seq. No.
Seq. ID
                   uC-zmflmo17184f02b1
Method
                   BLASTX
NCBI GI
                   g4185310
BLAST score
                   496
E value
                   4.0e-50
Match length
                   148
% identity
                   66
NCBI Description
                   (AF090446) gag protein [Zea mays]
Seq. No.
                   308655
Seq. ID
                   uC-zmflmo17184q02b1
Method
                   BLASTX
NCBI GI
                   g4204232
BLAST score
                   177
E value
                   3.0e-13
Match length
                   39
% identity
                   92
NCBI Description
                   (AF035378) MADS-box protein 1 [Lolium temulentum]
Seq. No.
                   308656
Seq. ID
                   uC-zmflmo17184h01b1
Method
                   BLASTX
```

Method BLASTX
NCBI GI g100484
BLAST score 232
E value 3.0e-19



Match length 64 % identity

NCBI Description hypothetical protein - garden snapdragon

Seq. No.

308657

uC-zmflmo17184h03b1 Seq. ID

Method BLASTN NCBI GI q22332 BLAST score 117 E value 4.0e-59 Match length 251 % identity 93

NCBI Description Z.mays HRGP gene

Seq. No.

308658

Seq. ID uC-zmflmo17185b10b1

BLASTX Method NCBI GI q3746069 BLAST score 189 E value 4.0e-16 Match length 139 % identity

NCBI Description (AC005311) putative reverse transcriptase [Arabidopsis

thaliana]

Seq. No.

308659

Seq. ID uC-zmflmo17185g01b1

Method BLASTX NCBI GI g4263707 BLAST score 541 E value 2.0e-55 Match length 162 % identity 65

NCBI Description (AC006223) putative 70kD heat shock protein [Arabidopsis

thaliana]

Seq. No. 308660

Seq. ID uC-zmflmo17185g09b1

Method BLASTN NCBI GI g4185305 BLAST score 88 E value 9.0e-42 Match length 168 % identity 89

NCBI Description Zea mays cosmid IV.1E1 22-kDa alpha zein protein 21

(sz22-21) gene, complete cds; retrotransposon Opie-2 gag protein, polyprotein, and copia protein genes, complete

cds; and unknown genes

Seq. No. 308661

Seq. ID uC-zmflmo17185h03b1

Method BLASTX NCBI GI g2984709 BLAST score 462 E value 3.0e-46 Match length 99 % identity 91

```
NCBI Description
                  (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]
Seq. No.
                  308662
Seq. ID
                  uC-zmflmo17186a02b1
Method
                  BLASTN
NCBI GI
                  g22332
BLAST score
                  222
E value
                  1.0e-122
Match length
                  297
% identity
                  94
NCBI Description
                  Z.mays HRGP gene
Seq. No.
                  308663
Seq. ID
                  uC-zmflmo17186a06b1
Method
                  BLASTX
NCBI GI
                  q135449
BLAST score
                  634 ..
E value
                  2.0e-66
Match length
                  144
% identity
                  83
NCBI Description
                  TUBULIN BETA-1 CHAIN >qi 100932 pir S14701 tubulin beta-1
                  chain - maize >gi_295851_emb_CAA37060_ (X52878) beta 1
                  tubulin [Zea mays]
Seq. No.
                  308664
Seq. ID
                  uC-zmflmo17186a09b1
Method
                  BLASTN
NCBI GI
                  g257040
BLAST score
                  48
E value
                  2.0e-18
Match length
                  48
% identity
                  100
NCBI Description hydroxyproline-rich glycoprotein [maize, Genomic, 1703 nt]
                  308665
Seq. No.
Seq. ID
                  uC-zmflmo17186a11b1
Method
                  BLASTN
NCBI GI
                  g2062705
BLAST score
                  36
E value
                  1.0e-10
Match length
                  36
% identity
                  100
NCBI Description
                  Human butyrophilin (BTF5) mRNA, complete cds
                  308666
Seq. No.
Seq. ID
                  uC-zmflmo17186b05b1
Method
                  BLASTX
NCBI GI
                  g4432863
BLAST score
                  143
E value
                  4.0e-09
Match length
                  48
% identity
                  56
NCBI Description
                  (AC006300) putative phosphate/phosphoenolpyruvate
```

Seq. No. 308667

Seq. ID uC-zmflmo17186b08b1

43888

translocator protein [Arabidopsis thaliana]



```
Method
                  BLASTX
NCBI GI
                  g112994
BLAST score
                  406
E value
                  9.0e-40
Match length
                  86
% identity
                  94
                  GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN
NCBI Description
                  >qi 82685 pir S04536 embryonic abundant protein,
                  glycine-rich - maize >gi 22313 emb CAA31077 (X12564)
                  ABA-inducible gene protein [Zea mays]
                  >gi 226091 prf 1410284A abscisic acid inducible gene [Zea
                  mays]
                  308668
Seq. No.
Seq. ID
                  uC-zmflmo17186b09b1
Method
                  BLASTX
                  q1370196
NCBI GI
BLAST score
                  375
E value
                  5.0e-36
Match length
                  103
% identity
                  73
NCBI Description
                  (Z73947) RAB8D [Lotus japonicus]
Seq. No.
                  308669
Seq. ID
                  uC-zmflmo17186b12b1
Method
                  BLASTN
NCBI GI
                  g2429617
BLAST score
                  65
E value
                  6.0e-28
Match length
                  166
% identity
                  86
NCBI Description
                  Oryza sativa mRNA for ferrochelatase, partial cds
                  308670
Seq. No.
                  uC-zmflmo17186c08b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q113460
BLAST score
                  503
E value
                  5.0e-51
Match length
                  102
% identity
                  94
NCBI Description
                  ADP, ATP CARRIER PROTEIN 2 PRECURSOR (ADP/ATP TRANSLOCASE 2)
                  (ADENINE NUCLEOTIDE TRANSLOCATOR 2) (ANT 2)
                  >gi 100851 pir S16568 ADP, ATP carrier protein precursor -
                  maize >gi 22164 emb CAA41812 (X59086) adenine nucleotide
                  translocator [Zea mays]
Seq. No.
                  308671
Seq. ID
                  uC-zmflmo17186d01b1
Method
                  BLASTN
NCBI GI
                  g1657766
BLAST score
                  41
```

E value 8.0e-14 Match length 57 93 % identity

NCBI Description Zea mays retrotransposon Opie-2 5' LTR, primer binding site, gag gene, pol gene, complete cds, polypurine tract



and 3' LTR

```
308672
Seq. No.
Seq. ID
                  uC-zmflmo17186d05b1
Method
                  BLASTX
NCBI GI
                  q4469124
BLAST score
                  150
E value
                  1.0e-17
                  69
Match length
                  72
% identity
NCBI Description
                  (AJ236870) methionin synthase-like enzyme [Arabidopsis
                  thaliana]
                  308673
Seq. No.
                  uC-zmflmo17186h06b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1203832
BLAST score
                  198
E value
                  2.0e-15
Match length
                  116
                  43
% identity
NCBI Description
                  (U46003) beta-D-glucan exohydrolase, isoenzyme ExoII
                  [Hordeum vulgare] >qi 1588407 prf 2208395A beta-D-glucan
                  exohydrolase [Hordeum vulgare]
                  308674
Seq. No.
Seq. ID
                  uC-zmflmo17186h07b1
Method
                  BLASTX
NCBI GI
                  g1203832
BLAST score
                  252
                  1.0e-21
E value
Match length
                  106
% identity
                  53
                  (U46003) beta-D-glucan exohydrolase, isoenzyme ExoII
NCBI Description
                  [Hordeum vulgare] >gi 1588407 prf 2208395A beta-D-glucan
                  exohydrolase [Hordeum vulgare]
Seq. No.
                  308675
Seq. ID
                  uC-zmflmo17187a03b1
Method
                  BLASTX
NCBI GI
                  q1076812
BLAST score
                  179
E value
                  7.0e-13
Match length
                  133
% identity
                  40
                  initiator-binding protein - maize >gi 483490 emb CAA55691
NCBI Description
                   (X79085) initiator binding protein [Zea mays]
                  308676
Seq. No.
                  uC-zmflmo17187a07b1
Seq. ID
Method
                  BLASTX
                  g2498329
NCBI GI
BLAST score
                  521
E value
                  3.0e-53
                  138
Match length
% identity
                  68
NCBI Description PATTERN FORMATION PROTEIN EMB30 >gi 2129665 pir_S65571
```



pattern-formation protein GNOM - Arabidopsis thaliana >gi_1209633 (U36433) GNOM gene product [Arabidopsis thaliana] >gi_1335997 (U56140) similar to the Saccharomyces cerevisiae Sec7 protein, GenBank Accession Number J03918 [Arabidopsis thaliana] >gi_1335999 (U56141) similar to the Saccharomyces cerevisiae Sec7 protein, GenBank Accession Number J03918 [Arabidopsis thaliana]

Seq. No. 308677

Seq. ID uC-zmflmo17187b04b1

Method BLASTX
NCBI GI g2618698
BLAST score 340
E value 6.0e-32
Match length 135
% identity 56

NCBI Description (AC002510) unknown protein [Arabidopsis thaliana]

Seq. No. 308678

Seq. ID uC-zmflmo17187e06b1

Method BLASTX
NCBI GI g4432846
BLAST score 582
E value 3.0e-60
Match length 164
% identity 70

NCBI Description (AC006283) unknown protein [Arabidopsis thaliana]

Seq. No. 308679

Seq. ID uC-zmflmo17187e09b1

Method BLASTX
NCBI GI g115771
BLAST score 742
E value 5.0e-79
Match length 140
% identity 99

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-1) (LHCP) >gi 82682 pir S04453 chlorophyll

a/b-binding protein precursor - maize

>gi 22224 emb CAA32900 (X14794) chlorophyll a/b-binding

preprotein (AA 1 - 262) [Zea mays]

Seq. No. 308680

Seq. ID uC-zmflmo17187f05b1

Method BLASTX
NCBI GI g2576411
BLAST score 234
E value 2.0e-26
Match length 172
% identity 48

NCBI Description (AF012833) similar to dynamin-like protein encoded by

GenBank Accession Number X99669 [Arabidopsis thaliana]

Seq. No. 308681

Seq. ID uC-zmflmo17187g04b1

Method BLASTX NCBI GI g2984709

```
BLAST score
E value
                  7.0e-53
Match length
                   99
                   99
% identity
NCBI Description
                  (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]
                  308682
Seq. No.
```

Seq. ID uC-zmflmo17187h03b1

BLASTN Method NCBI GI g22332 BLAST score 323 0.0e+00 E value 477 Match length % identity 92

NCBI Description Z.mays HRGP gene

Seq. No. 308683

uC-zmflmo17190a05b1 Seq. ID

Method BLASTX NCBI GI g112994 236 BLAST score 1.0e-26 E value 77 Match length % identity 87

GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN NCBI Description

>gi 82685 pir S04536 embryonic abundant protein,

glycine-rich - maize >gi 22313 emb CAA31077 (X12564)

ABA-inducible gene protein [Zea mays]

>gi_226091_prf__1410284A abscisic acid inducible gene [Zea

ź

mays]

308684 Seq. No.

Seq. ID uC-zmflmo17190a07b1

BLASTX Method q2921304 NCBI GI BLAST score 228 E value 7.0e-19 Match length 118 % identity

NCBI Description (AF033496) herbicide safener binding protein [Zea mays]

Seq. No. 308685

Seq. ID uC-zmflmo17190b11b1

Method BLASTX NCBI GI q2979559 BLAST score 165 E value 2.0e-11 Match length 64 % identity

(AC003680) putative DNA binding protein [Arabidopsis NCBI Description

thaliana]

Seq. No. 308686

Seq. ID uC-zmflmo17190f12b1

Method BLASTN g4007864 NCBI GI BLAST score 56



```
5.0e-23
E value
Match length
                  80
% identity
                  93
NCBI Description
                  Zea mays HRGP gene, AC1503 line
Seq. No.
                  308687
Seq. ID
                  uC-zmflmo17192c07b1
Method
                  BLASTN
NCBI GI
                  q2832242
BLAST score
                  60
E value
                  3.0e-25
Match length
                  196
                  82
% identity
NCBI Description Zea mays 22-kDa alpha zein gene cluster, complete sequence
Seq. No.
                  308688
Seq. ID
                  uC-zmflmo17192d08b1
Method
                  BLASTN
NCBI GI
                  g22149
BLAST score
                  34
                  4.0e-10
E value
Match length
                  58
                  90
% identity
NCBI Description Z.mays mRNA for alpha-tubulin
                  3086895
Seq. No.
Seq. ID
                  uC-zmflmo17192f03a1
                  BLASTN
Method
                  g940445
NCBI GI
BLAST score
                   35
E value
                  2.0e-10
Match length
                   47
% identity
                  94
NCBI Description A.thaliana mRNA for cytochrome P450
Seq. No.
                   308690
Seq. ID
                   uC-zmflmo17193c12b1
Method
                  BLASTX
NCBI GI
                   g3281853
BLAST score
                   186
E value
                   2.0e-14
Match length
                   48
% identity
                   77
                  (AL031004) putative protein [Arabidopsis thaliana]
NCBI Description
                   308691
Seq. No.
                   uC-zmflmo17193h10b1
Seq. ID
Method
                  BLASTX
                   g1076678
NCBI GI
BLAST score
                   291
                   2.0e-26
E value
Match length
                  71
% identity
                   86
```

4

Seq. No. 308692

NCBI Description

Seq. ID uC-zmflmo17195b07b1

43893

ubiquitin / ribosomal protein S27a - potato (fragment)

```
BLASTN
Method
                  g3821780
NCBI GI
BLAST score
                  36
E value
                  7.0e-11
Match length
                  36
% identity
                  100
NCBI Description
                  Xenopus laevis cDNA clone 27A6-1
Seq. No.
                  308693
Seq. ID
                  uC-zmflmo17195e10b1
Method
                  BLASTN
NCBI GI
                  g899607
BLAST score
                  65
E value
                  1.0e-28
                  93
Match length
% identity
                  58
NCBI Description
                  Zea mays polyubiquitin (MubC5) mRNA, complete cds
                  308694
Seq. No.
Seq. ID
                  uC-zmflmo17195h11b1
Method
                  BLASTX
NCBI GI
                  q3548816
BLAST score
                  266
E value
                  3.0e-23
Match length
                  144
% identity
                  40
NCBI Description
                  (AC005313) LEA-like protein [Arabidopsis thaliana]
                  308695
Seq. No.
Seq. ID
                  uC-zmflmo17197d01b1
Method
                  BLASTX
NCBI GI
                  g1805669
BLAST score
                  157
E value
                  2.0e-10
Match length
                  130
% identity
                  33
NCBI Description
                  (Z34883) peptide synthetase ORF4 [Bacillus subtilis]
                  >gi_2634214_emb_CAB13714_ (Z99113) peptide synthetase
                   [Bacillus subtilis]
                  308696
Seq. No.
Seq. ID
                  uC-zmflmo17197d03b1
Method
                  BLASTX
NCBI GI
                  g2746086
BLAST score
                  276
                  9.0e-32
E value
Match length
                  140
% identity
                  61
                  (AF025292) putative high-affinity potassium transporter
NCBI Description
                   [Hordeum vulgare]
Seq. No.
                  308697
Seq. ID
                  uC-zmflmo17197d08b1
Method
                  BLASTN
NCBI GI
```

g22136

1.0e-64

126

BLAST score

E value



Match length 242 % identity 88 NCBI Description Mai

Maize Adh2-N mRNA for alcohol dehydrogenase

Seq. No. Seq. ID 308698 uC-zmflmo17197d09a1

Method BLASTN
NCBI GI g4468793
BLAST score 94
E value 1.0e-45
Match length 150
% identity 91

NCBI Description Zea mays mRNA for glutathione transferase III(b)

Seq. No. 308699

Seq. ID uC-zmflmo17197g01b1

Method BLASTX
NCBI GI g4056428
BLAST score 381
E value 4.0e-37
Match length 90
% identity 78

NCBI Description (AC005322) Similar to gb_U43629 integral membrane protein

from Beta vulgaris and a member of sugar transporter family

PF_00083. [Arabidopsis thaliana]

Seq. No. 308700

Seq. ID uC-zmflmo17197g07b1

Method BLASTX
NCBI GI g82696
BLAST score 265
E value 2.0e-23
Match length 68
% identity 78

NCBI Description glycine-rich protein - maize >gi 22293 emb CAA43431

(X61121) glycine-rich protein [Zea mays]

Seq. No. 308701

Seq. ID uC-zmflmo17197h11b1

Method BLASTX
NCBI GI g3201541
BLAST score 291
E value 2.0e-26
Match length 108
% identity 56

NCBI Description (AJ005077) TCTR2 protein [Lycopersicon esculentum]

Seq. No. 308702

Seq. ID uC-zmflmo17198b01b1

Method BLASTN
NCBI GI g940880
BLAST score 115
E value 5.0e-58
Match length 169
% identity 93

NCBI Description Z.mays zag2 gene

```
308703
Seq. No.
                  uC-zmflmo17198d02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2252843
BLAST score
                  237
E value
                  1.0e-19
Match length
                  167
                  35
% identity
                  (AF013293) No definition line found [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  308704
                  uC-zmflmo17198f01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4006886
BLAST score
                  163
E value
                  3.0e-11
Match length
                  125
% identity
                  37
                  (Z99708) putative protein [Arabidopsis thaliana]
NCBI Description
                  308705
Seq. No.
Seq. ID
                  uC-zmflmo17198f11b1
                  BLASTX
Method
NCBI GI
                  g4406781
BLAST score
                  267
E value
                  2.0e-23
Match length
                  127
% identity
                  (AC006532) putative Na+/H+ antiporter [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  308706
                  uC-zmflmo17198g01b1
Seq. ID
Method
                  BLASTX
                  g115786
NCBI GI
BLAST score
                   678
E value
                  2.0e-71
Match length
                  145
% identity
                   90
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                   (CAB) (LHCP) >gi 82680 pir A29119 chlorophyll a/b-binding
                  protein - maize >gi_22357_emb_CAA68451_ (Y00379) LHCP [Zea
                  mays]
                   308707
Seq. No.
                  uC-zmflmo17198g03b1
Seq. ID
Method
                  BLASTX
                   g135060
NCBI GI
BLAST score
                   179
                   2.0e-13
E value
Match length
                  71
                   63
% identity
                  SUCROSE SYNTHASE 1 (SUCROSE-UDP GLUCOSYLTRANSFERASE 1)
NCBI Description
```

43896

sucrose synthase [Zea mays]

(SHRUNKEN-1) >gi_66570_pir__YUZMS sucrose synthase (EC 2.4.1.13) - maize >gi_22486_emb_CAA26247_ (X02400) sucrose

synthase [Zea mays] >gi_22488_emb_CAA26229_ (X02382)

```
308708
Seq. No.
Seq. ID
                  uC-zmflmo17198h05b1
                  BLASTX
Method
NCBI GI
                  g3355468
BLAST score
                  151
                  1.0e-12
E value
                  75
Match length
% identity
                  (ACO04218) putative ribosomal protein L35 [Arabidopsis
NCBI Description
                  thaliana]
                  308709
Seq. No.
                  uC-zmflmo17199a04b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2980765
BLAST score
                  149
                  2.0e-09
E value
Match length
                  94
                   43
% identity
                  (AL022198) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  308710
Seq. No.
                  uC-zmflmo17199c05b1
Seq. ID
Method
                  BLASTX
                   q2791834
NCBI GI
BLAST score
                   282
E value
                   5.0e-33
                  123
Match length
                   65
% identity
NCBI Description (AF041463) elongation factor 1-alpha [Manihot esculenta]
Seq. No.
                   308711
                   uC-zmflmo17199d05b1
Seq. ID
                   BLASTX
Method
                   q4539404
NCBI GI
BLAST score
                   408
E value
                   5.0e-40
Match length
                   124
% identity
                  (AL049524) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   308712
                   uC-zmflmo17199d09b1
Seq. ID
Method
                   BLASTN
NCBI GI
                   q507770
BLAST score
                   76
E value
                   2.0e-34
Match length
                   195
% identity
                   86
                   Zea mays D3L H(+)-transporting ATPase (Mha1) gene, complete
NCBI Description
                   308713
Seq. No.
                   uC-zmflmo17199f09b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1076746
```



BLAST score 351 E value 3.0e-33 Match length 104 % identity 65

NCBI Description heat shock protein 70 - rice (fragment)

>gi 763160 emb CAA47948 (X67711) heat shock protein 70

[Oryza sativa]

Seq. No. 308714

Seq. ID uC-zmflmo17199g02b1

Method BLASTX
NCBI GI g1718097
BLAST score 256
E value 3.0e-22
Match length 97
% identity 52

NCBI Description VACUOLAR ATP SYNTHASE SUBUNIT AC39 (V-ATPASE AC39 SUBUNIT)

(41 KD ACCESSORY PROTEIN) (DVA41) >gi_626048_pir__A55016

lysosomal membrane protein DVA41 - slime mold

(Dictyostelium discoideum) >gi_532733 (U13150) vacuolar

ATPase subunit DVA41 [Dictyostelium discoideum]

Seq. No. 308715

Seq. ID uC-zmflmo17199g04b1

Method BLASTX
NCBI GI g1699023
BLAST score 198
E value 4.0e-15
Match length 105
% identity 43

NCBI Description (U78866) putative arginine-aspartate-rich RNA binding protein [Arabidopsis thaliana] >gi 1699051 (U78867)

protein [Arabidopsis thaliana] >gi_1699051 (0/886/) putative aspartate-arginine-rich mRNA binding protein

[Arabidopsis thaliana]

Seq. No. 308716

Seq. ID uC-zmflmo17199g09b1

Method BLASTX
NCBI GI g2443881
BLAST score 318
E value 3.0e-29
Match length 76
% identity 78

NCBI Description (AC002294) contains beta-transducin motif [Arabidopsis

thaliana]

Seq. No. 308717

Seq. ID uC-zmflmo17199h04b1

Method BLASTX
NCBI GI g1707642
BLAST score 217
E value 2.0e-17
Match length 92
% identity 52

NCBI Description (Y07748) TMK [Oryza sativa]

Seq. No. 308718

```
uC-zmflmo17199h07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g401115
BLAST score
                  436
E value
                   4.0e-43
Match length
                  130
% identity
                   63
                  SUCROSE-PHOSPHATE SYNTHASE (UDP-GLUCOSE-FRUCTOSE-PHOSPHATE
NCBI Description
                  GLUCOSYLTRANSFERASE) >gi 539007 pir JQ2277
                   sucrose-phosphate synthase (EC \overline{2.4.1.14}) - spinach
                  >gi 170147 (L04803) sucrose phosphate synthase [Spinacia
                  oleracea]
Seq. No.
                   308719
                  uC-zmflmo17199h09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g283045
BLAST score
                  192
E value
                  1.0e-14
Match length
                  81
                   48
% identity
NCBI Description
                  hydroxyproline-rich glycoprotein - maize
                  >gi 22333 emb CAA44844 (X63134) hydroxyproline-rich
                   glycoprotein [Zea mays] >gi 228936 prf 1814452A Hyp-rich
                   glycoprotein [Zea mays]
Seq. No.
                   308720
Seq. ID
                  uC-zmflmo17201c04b1
Method
                  BLASTX
NCBI GI
                   q3885334
BLAST score
                   275
                   2.0e-24
E value
Match length
                   127
                   47
% identity
NCBI Description
                   (AC005623) putative argonaute protein [Arabidopsis
                   thaliana]
Seq. No.
                   308721
Seq. ID
                   uC-zmflmo17201c12b1
Method
                  BLASTX
NCBI GI
                   q2894600
BLAST score
                   185
E value
                   1.0e-13
Match length
                   67
% identity
NCBI Description
                  (AL021889) putative protein [Arabidopsis thaliana]
```

Seq. No. 308722

Seq. ID uC-zmflmo17201h03b1

Method BLASTX NCBI GI g3668089 BLAST score 259 E value 8.0e-23 Match length 77 % identity 62

(AC004667) unknown protein [Arabidopsis thaliana] NCBI Description

E value

Match length % identity

NCBI Description

8.0e-14 86

44



```
308723
Seq. No.
Seq. ID
                   uC-zmflmo17201h06b1
Method
                   BLASTN
NCBI GI
                   g2984708
BLAST score
                   160
E value
                   1.0e-84
Match length
                   192
                   96
% identity
                   Zea mays DnaJ-related protein ZMDJ1 (mdJ1) gene, complete
NCBI Description
                   308724
Seq. No.
                   uC-zmflmo17201h08b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g123620
BLAST score
                   222
E value
                   4.0e-18
                   136
Match length
% identity
                   43
                   HEAT SHOCK COGNATE 70 KD PROTEIN 2 >gi 100224 pir S14950
NCBI Description
                   heat shock cognate protein 70 - tomato
                   >gi 19258 emb CAA37971 (X54030) heat shock protein cognate
                   70 [Lycopersicon esculentum]
Seq. No.
                   308725
Seq. ID
                   uC-zmflmo17201h10a1
                   BLASTN
Method
NCBI GI
                   g600115
BLAST score
                   77
                   1.0e-35
E value
Match length
                   150
% identity
                   88
                   Z.mays apx gene encoding cytosolic ascorbate peroxidase
NCBI Description
                   308726
Seq. No.
                   uC-zmflmo17201h10b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q1076800
BLAST score
                   167
E value
                   1.0e-11
Match length
                   50
% identity
                   70
NCBI Description
                   L-ascorbate peroxidase (EC 1.11.1.11), cytosolic isozyme -
                   maize >qi 600116 emb CAA84406 (Z34934) cytosolic ascorbate
                   peroxidase [Zea mays] >gi 1096503 prf 2111423A ascorbate
                   peroxidase [Zea mays]
Seq. No.
                   308727
                   uC-zmflmo17201h12b1
Seq. ID
Method
                   BLASTX
                   g3135254
NCBI GI
BLAST score
                   186
```

(AC003058) hypothetical protein [Arabidopsis thaliana]



```
Seq. No.
Seq. ID
                  uC-zmflmo17202a04b1
Method
                  BLASTN
NCBI GI
                  g2182028
BLAST score
                  34
E value
                  1.0e-09
Match length
                  58
                  90
% identity
NCBI Description Oryza sativa mRNA for shaggy-like kinase etha
                  308729
Seq. No.
                  uC-zmflmo17202b08b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4235644
BLAST score
                  453
                  6.0e-45
E value
Match length
                  179
                  47
% identity
NCBI Description (AF119040) polyprotein [Lycopersicon esculentum]
                  308730
Seq. No.
                  uC-zmflmo17202b09b1
Seq. ID
Method
                  BLASTX
                  g2828284
NCBI GI
                  191
BLAST score
                  3.0e-14
E value
                  62
Match length
                  58
% identity
                  (AL021687) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  >gi 2832637 emb CAA16766 (AL021711) hypothetical protein
                   [Arabidopsis thaliana]
Seq. No.
                  308731
Seq. ID
                  uC-zmflmo17202b12a1
Method
                  BLASTX
NCBI GI
                  q3219149
BLAST score
                  167
E value
                  2.0e-15
Match length
                  109
% identity
NCBI Description
                  (AB015180) cdc2 related [Mesembryanthemum crystallinum]
Seq. No.
                  308732
                  uC-zmflmo17202q04b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q22332
BLAST score
                  413
E value
                  0.0e+00
Match length
                  580
% identity
                  49
NCBI Description
                  Z.mays HRGP gene
```

Seq. ID uC-zmflmo17202h01b1

308733

Method BLASTX NCBI GI g4467100 BLAST score 307

Seq. No.



```
4.0e-29
E value
Match length
                  90
% identity
                  (AL035538) MADS-box protein AGL17-like protein [Arabidopsis
NCBI Description
                  thaliana]
                  308734
Seq. No.
                  uC-zmflmo17203b02a1
Seq. ID
                  BLASTN
Method
                  q596022
NCBI GI
BLAST score
                  34
                  8.0e-10
E value
                  58
Match length
                  90
% identity
                  Zea mays glucose-6 phosphate isomerase (phi1) mRNA,
NCBI Description
                  complete cds
                   308735
Seq. No.
                  uC-zmflmo17203c04a1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2160172
BLAST score
                   157
                   2.0e-10
E value
                   72
Match length
% identity
                   (AC000132) No definition line found [Arabidopsis thaliana]
NCBI Description
                   308736
Seq. No.
Seq. ID
                   uC-zmflmo17203g05a1
Method
                   BLASTX
NCBI GI
                   q4559366
BLAST score
                   182
E value
                   3.0e-13
                   91
Match length
% identity
                   (AC006585) putative tyrosine transaminase [Arabidopsis
NCBI Description
                   thaliana]
                   308737
Seq. No.
                   uC-zmflmo17204b10b1
Seq. ID
Method
                   BLASTX
                   g112994
NCBI GI
BLAST score
                   437
                   3.0e-43
E value
                   86
Match length
                   100
% identity
                   GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN
NCBI Description
                   >gi_82685_pir__S04536 embryonic abundant protein,
                   glycine-rich - maize >gi_22313_emb_CAA31077_ (X12564)
                   ABA-inducible gene protein [Zea mays]
                   >gi 226091 prf 1410284A abscisic acid inducible gene [Zea
                   mays]
```

ű.

Seq. No. 308738

Seq. ID uC-zmflmo17204c06a1

Method BLASTN NCBI GI g602605

```
BLAST score
                   2.0e-28
E value
                   157
Match length
                   85
% identity
NCBI Description Zea mays tandem genes for alphal-tubulin and alpha2-tubulin
                   308739
Seq. No.
                   uC-zmflmo17204d02b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2429543
BLAST score
                   274
                   3.0e-24
E value
                   109
Match length
                   49
% identity
                   (AF025472) contains similarity to S. cerevisiae
NCBI Description
                   mitochondrial DNA repair and recombination protein PIF1
                   (NID:g5771350 [Caenorhabditis elegans]
Seq. No.
                   308740
                   uC-zmflmo17204e10a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3608133
BLAST score
                   142
                   8.0e-09
E value
                   39
Match length
                   64
% identity
NCBI Description (AC005314) hypothetical protein [Arabidopsis thaliana]
                   308741
Seq. No.
Seq. ID
                   uC-zmflmo17204g08a1
Method
                   BLASTN
NCBI GI
                   g602605
BLAST score
                   122
E value
                   3.0e-62
Match length
                   298
                   85
% identity
NCBI Description
                   Zea mays tandem genes for alpha1-tubulin and alpha2-tubulin
Seq. No.
                   308742
                   uC-zmflmo17204h03b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4416302
BLAST score
                   767
                   6.0e-82
E value
Match length
                   159
% identity
                   89
                   (AF105716) copia-type pol polyprotein [Zea mays]
NCBI Description
                   308743
Seq. No.
                   uC-zmflmo17205c05a1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2760321
BLAST score
                   256
                   2.0e-22
E value
Match length
                   101
```

(AC002130) F1N21.6 [Arabidopsis thaliana]

52

% identity

NCBI Description

Match length

NCBI Description

% identity

153

88

```
308744
Seq. No.
Seq. ID
                  uC-zmflmo17205c12a1
Method
                  BLASTX
NCBI GI
                  g4314362
BLAST score
                  264
                  3.0e-23
E value
Match length
                  105
% identity
                  49
                  (AC006340) putative D-amino acid dehydrogenase [Arabidopsis
NCBI Description
                  thaliana]
                  308745
Seq. No.
                  uC-zmflmo17206e04a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g22091
BLAST score
                  47
E value
                  2.0e-17
Match length
                  188
% identity
                  82
NCBI Description
                  Z.diploperennis gene for hydroxyproline-rich glycoprotein
Seq. No.
                  308746
                  uC-zmflmo17206f05a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g136632
BLAST score
                  180
E value
                  2.0e-13
Match length
                  44
                  80
% identity
                  UBIQUITIN-ACTIVATING ENZYME E1 1 >gi_100841_pir__A38373
NCBI Description
                  ubiquitin--protein ligase (EC 6.3.2.19) E1 - wheat
                  >gi 285451 pir A42873 ubiquitin-activating enzyme E1, UBA1
                   - Wheat >gi 170780 (M55604) ubiquitin-activating enzyme E1
                   [Triticum aestivum]
                  308747
Seq. No.
                  uC-zmflmo17206h04a1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g4416300
BLAST score
                  229
                  1.0e-126
E value
Match length
                  325
                  93
% identity
                  Zea mays chromosome 4 22 kDa zein-associated intercluster
NCBI Description
                  region, complete sequence
                   308748
Seq. No.
                  uC-zmflmo17206h10a1
Seq. ID
                  BLASTN
Method
NCBI GI
                  q1498596
                   39
BLAST score
                   6.0e-13
E value
```

Zea mays phospholipid transfer protein mRNA, complete cds

Method

NCBI GI

BLASTX

g3559814

```
308749
Seq. No.
                  uC-zmflmo17209a08a1
Seq. ID
                  BLASTN
Method
                  g416146
NCBI GI
                  39
BLAST score
                  4.0e-13
E value
Match length
                  119
                  83
% identity
NCBI Description Zea mays beta-6 tubulin (tub6) gene and mRNA, complete cds
                  308750
Seq. No.
Seq. ID
                  uC-zmflmo17209b10a1
Method
                  BLASTX
NCBI GI
                  g4204695
BLAST score
                  168
                  6.0e-12
E value
                - 51
Match length
                  63
% identity
NCBI Description (AF117062) putative inositol polyphosphate 5-phosphatase
                  At5P1 [Arabidopsis thaliana]
                  308751
Seq. No.
Seq. ID
                  uC-zmflmo17209h03a1
Method
                  BLASTX
                  g283004
NCBI GI
BLAST score
                  166
E value
                  1.0e-11
                  57
Match length
                   65
% identity
                  DNA-binding protein Gt-2 - rice >gi 20249_emb_CAA48328_
NCBI Description
                   (X68261) gt-2 [Oryza sativa]
                   308752
Seq. No.
                  uC-zmflmo17209h05a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g22461
                  222
BLAST score
E value
                   1.0e-122
Match length
                   274
                   96
% identity
NCBI Description Maize RAB-17 gene
Seq. No.
                   308753
Seq. ID
                   uC-zmflmo17209h09a1
Method
                   BLASTX
NCBI GI
                   g4415917
BLAST score
                   149
                   2.0e-09
E value
Match length
                   95
% identity
                  (AC006282) putative protein containing zinc finger domain
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   308754
                   uC-zmflmo17210b02a1
Seq. ID
```

```
BLAST score
                  1.0e-10
E value
                  34
Match length
                  88
% identity
                  (Y15781) transketolase 1 [Capsicum annuum]
NCBI Description
Seq. No.
                  308755
                  uC-zmflmo17210b09a1
Seq. ID
                  BLASTX
Method
                  g135406
NCBI GI
                  254
BLAST score
                   5.0e-28
E value
Match length
                   64
                   96
% identity
                  TUBULIN ALPHA-3/ALPHA-5 CHAIN >gi_99768_pir__A32712 tubulin
NCBI Description
                   alpha-5 chain - Arabidopsis thaliana >gi 166912 (M17189)
                   alpha-tubulin [Arabidopsis thaliana] >gi_166918 (M84698)
                   alpha-5 tubulin [Arabidopsis thaliana]
                   308756
Seq. No.
                   uC-zmflmo17210e05a1
Seq. ID
                  BLASTN
Method
                   g168406
NCBI GI
BLAST score
                   77
                   3.0e - 35
E value
                   186
Match length
                   85
% identity
                   Z.mays alcohol dehydrogenase (ADH-1 C-m allele) gene,
NCBI Description
                   complete cds
                   308757
Seq. No.
                   uC-zmflmo17211c11a1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g2109456
BLAST score
                   44
                   1.0e-15
E value
Match length
                   96.
% identity
                   86
NCBI Description Oryza sativa clone MIRCH38 chitinase mRNA, partial cds
                   308758
Seq. No.
                   uC-zmflmo17212e08a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1297187
                   181
BLAST score
                   2.0e-13
E value
                   86
Match length
```

% identity 49

(U53501) similar to protein encoded by GenBank Accession NCBI Description

Number U41815, nucleoporin 98 [Arabidopsis thaliana]

308759 Seq. No.

uC-zmflmo17212e12a1 Seq. ID

Method BLASTX NCBI GI q416664 BLAST score 161 5.0e-11 E value

```
Match length
                  85
                  42
% identity
                  PLASMA MEMBRANE ATPASE 4 (PROTON PUMP)
NCBI Description
                  >gi_485504_pir__S33548 H+-transporting ATPase (EC 3.6.1.35)
                  type 4, plasma membrane - curled-leaved tobacco
                  >qi 19704 emb CAA47275 (X66737) plasma membrane H+-ATPase
                   [Nicotiana plumbaginifolia]
                  308760
Seq. No.
                  uC-zmflmo17212f08a1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q111159
                  236
BLAST score
                   9.0e-20
E value
                   67
Match length
                   60
% identity
                  TPA-induced protein 11B - mouse
NCBI Description
                   308761
Seq. No.
Seq. ID
                  uC-zmflmo17215b01b1
Method
                  BLASTX
NCBI GI
                   g119355
BLAST score
                   585
                   2.0e-60
E value
                   133
Match length
                   89
% identity
                  ENOLASE 1 (2-PHOSPHOGLYCERATE DEHYDRATASE 1)
NCBI Description
                   (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE 1)
                   >gi 100869_pir__S16257 phosphopyruvate hydratase (EC
                   4.2.1.11) - maize >gi_22273_emb_CAA39454_ (X55981) enolase
                   [Zea mays]
                   308762
Seq. No.
                   uC-zmflmo17215b03b1
Seq. ID
                   BLASTX
Method
                   q3927830
NCBI GI
BLAST score
                   201
E value
                   9.0e-16
                   93
Match length
% identity
                   (AC005727) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   308763
Seq. ID
                   uC-zmflmo17215d09b1
                   BLASTX
Method
NCBI GI
                   q3355465
BLAST score
                   541
E value
                   2.0e-55
Match length
                   144
% identity
                   68
```

NCBI Description (AC004218) putative Ser/Thr protein kinase [Arabidopsis

thaliana]

Seq. No. 308764

Seq. ID uC-zmflmo17215f11b1

Method BLASTN NCBI GI g3821780

E value

Match length

NCBI Description

% identity

1.0e-16

77 69

```
BLAST score
                  2.0e-09
E value
                  34
Match length
                  100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                  308765
Seq. No.
                  uC-zmflmo17215h09b1
Seq. ID
                  BLASTX
Method
                   g3327196
NCBI GI
BLAST score
                   210
                   6.0e-17
E value
                   54
Match length
                   70
% identity
                  (AB014591) KIAA0691 protein [Homo sapiens]
NCBI Description
                   308766
Seq. No.
                   uC-zmflmo17217a09b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4572674
                   173
BLAST score
                   2.0e-12
E value
                   76
Match length
                   46
% identity
NCBI Description (AC006954) unknown protein [Arabidopsis thaliana]
                   308767
Seq. No.
                   uC-zmflmo17217b02b1
Seq. ID
                   BLASTX
Method
                   g2253583
NCBI GI
                   176
BLAST score
                   1.0e-12
E value
                   75
Match length
% identity
                   (U78721) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   308768
Seq. No.
                   uC-zmflmo17217b06b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2660669
                   316
BLAST score
                   4.0e-29
E value
Match length
                   110
% identity
                   (AC002342) human Mi-2 autoantigen-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   308769
Seq. No.
                   uC-zmflmo17217c02b1
Seq. ID
                   BLASTX
Method
                   g3004950
NCBI GI
                   198
BLAST score
```

43908

(AF037061) tonoplast intrinsic protein; ZmTIP1 [Zea mays]

Seq. No.

308775

```
Seq. No.
                  uC-zmflmo17217g12b1
Seq. ID
                  BLASTN
Method
                  g3821780
NCBI GI
BLAST score
                  36
E value
                  1.0e-10
Match length
                  48
                  67 :
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                  308771
Seq. No.
                  uC-zmflmo17217h08b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2501491
BLAST score
                  313
                   8.0e-29
E value
Match length
                  137
                   48
% identity
                  FLAVONOL 3-O-GLUCOSYLTRANSFERASE 1 (UDP-GLUCOSE FLAVONOID
NCBI Description
                   3-O-GLUCOSYLTRANSFERASE 1) >gi 542014 pir S41950
                  UTP-glucose glucosyltransferase - cassava
                  >qi 453246 emb CAA54609 (X77459) UTP-glucose
                   glucosyltransferase [Manihot esculenta]
                   308772
Seq. No.
                  uC-zmflmo17219c09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3875410
BLAST score
                   203
                   1.0e-15
E value
                   107
Match length
% identity
                   41
                   (Z81052) Similarity to Yeast ABC1P protein (SW:ABC1_YEAST);
NCBI Description
                   cDNA EST yk229g8.3 comes from this gene; cDNA EST yk229g8.5
                   comes from this gene [Caenorhabditis elegans]
                   308773
Seq. No.
Seq. ID
                   uC-zmflmo17219d06b1
Method
                   BLASTX
NCBI GI
                   g4220480
BLAST score
                   190
E value
                   2.0e-14
Match length
                   98
% identity
                   (AC006069) unknown protein [Arabidopsis thaliana]
NCBI Description
                   308774
Seq. No.
Seq. ID
                   uC-zmflmo17219e08b1
Method
                   BLASTX
NCBI GI
                   g1091678
BLAST score
                   155
                   4.0e-10
E value
Match length
                   84
% identity
                   38
                   activator-like transposable element [Pennisetum glaucum]
NCBI Description
```

```
uC-zmflmo17219e10b1
Seq. ID
                  BLASTN
Method
                  g22332
NCBI GI
                  318
BLAST score
                  1.0e-179
E value
                  457
Match length
                  93
% identity
NCBI Description
                  Z.mays HRGP gene
                  308776
Seq. No.
                  uC-zmflmo17219h08b1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g257040
                  182
BLAST score
                   8.0e-98
E value
Match length
                   469
                   49
% identity
                  hydroxyproline-rich glycoprotein [maize, Genomic, 1703 nt]
NCBI Description
                   308777
Seq. No.
                   uC-zmflmo17220a04b1
Seq. ID
                   BLASTX
Method
                   g120507
NCBI GI
BLAST score
                   326
                   1.0e-30
E value
                   96
Match length
                  71
% identity
NCBI Description FERRITIN 1 PRECURSOR >gi_82687_pir__S22498 ferritin
                   precursor (clone FM1) - maize (fragment)
                   >gi_22276_emb_CAA43663_ (X61391) ferritin [Zea mays]
                   308778
Seq. No.
                   uC-zmflmo17220b03b1
Seq. ID
                   BLASTN
Method
                   g257040
NCBI GI
                   83
BLAST score
                   7.0e-39
E value
                   111
Match length
% identity
                  hydroxyproline-rich glycoprotein [maize, Genomic, 1703 nt]
NCBI Description
                   308779
Seq. No.
Seq. ID
                   uC-zmflmo17220b07b1
Method
                   BLASTX
                   q1777312
NCBI GI
                   227
BLAST score
                   9.0e-19
E value
                   120
Match length
% identity
                   (D30622) novel serine/threonine protein kinase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   308780
                   uC-zmflmo17220d04b1
Seq. ID
```

BLASTX

317

g2852447

Method

NCBI GI BLAST score

```
2.0e-40
E value
                  127
Match length
                  66
% identity
                  (D88206) protein kinase [Arabidopsis thaliana]
NCBI Description
                  308781
Seq. No.
                  uC-zmflmo17220d06b1
Seq. ID
                  BLASTX
Method
                  g3108220
NCBI GI
                  348
BLAST score
                   9.0e-33
E value
                   159
Match length
                   46
% identity
                   (AF048986) MutS homolog 5 [Homo sapiens]
NCBI Description
                   308782
Seq. No.
                   uC-zmflmo17220g03a1
Seq. ID
                   {\tt BLASTN}
Method
                   g2984708
NCBI GI
BLAST score
                   88
                   6.0e-42
E value
Match length
                   144
                   90
% identity
                   Zea mays DnaJ-related protein ZMDJ1 (mdJ1) gene, complete
NCBI Description
                   cds
                   308783
Seq. No.
                   uC-zmflmo17220h02b1
Seq. ID
                   BLASTX
Method
                   g3894214
NCBI GI
                   157
BLAST score
                   9.0e-11
E value
                   58
Match length
                   62
% identity
                   (D83726) elongation factor 1 beta 2 [Oryza sativa]
NCBI Description
                   >gi_3894216_dbj_BAA34599_ (D83727) elongation factor 1 beta
                   2 [Oryza sativa]
                   308784
Seq. No.
                   uC-zmflmo17220h08a1
Seq. ID
Method
                   BLASTN
NCBI GI
                   q5091496
BLAST score
                   122
E value
                   4.0e-62
                   333
Match length
                   85
 % identity
                   Oryza sativa genomic DNA, chromosome 6, clone P0680A03,
NCBI Description
                   complete sequence
                   308785
 Seq. No.
                   uC-zmflmo17220h10b1
 Seq. ID
Method
                   BLASTX
NCBI GI
                   g4417271
 BLAST score
                   152
```

4.0e-10

33 76

E value Match length

% identity



```
(AC007019) putative cellulose synthase catalytic subunit
NCBI Description
                   [Arabidopsis thaliana]
                   308786
Seq. No.
                  uC-zmflmo17221b11b1
Seq. ID
                  BLASTN
Method
                  g4416300
NCBI GI
                  37
BLAST score
                   2.0e-11
E value
                   64
Match length
                   45
% identity
                  Zea mays chromosome 4 22 kDa zein-associated intercluster
NCBI Description
                   region, complete sequence
                   308787
Seq. No.
                   uC-zmflmo17221c01a1
Seq. ID
                   BLASTX
Method
                   g4558673
NCBI GI
                   406
BLAST score
                   1.0e-39
E value
                   131
Match length
                   53
% identity
                  (AC007063) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   308788
Seq. No.
                   uC-zmflmo17221d02b1
Seq. ID
                   BLASTN
Method
                   g22292
NCBI GI
BLAST score
                   58
                   2.0e-24
E value
                   93
Match length
                   91
% identity
                  Z.mays mRNA for glycine-rich protein
NCBI Description
                   308789
Seq. No.
                   uC-zmflmo17221e10b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3150415
                   276
BLAST score
                   2.0e-24
E value
                   67
Match length
% identity
                   (AC004165) sec13-related protein [Arabidopsis thaliana]
NCBI Description
                   >gi 3420046 (AC004680) sec13-related protein [Arabidopsis
                   thaliana]
                   308790
Seq. No.
                   uC-zmflmo17221f08a1
Seq. ID
Method
                   BLASTX
                   g3980397
NCBI GI
BLAST score
                   235
                   4.0e-20
E value
                   100
Match length
% identity
                   59
                   (AC004561) putative protein phosphatase 2C [Arabidopsis
NCBI Description
```

thaliana]



88

Match length

NCBI Description

% identity

```
308791
Seq. No.
                  uC-zmflmo17221g12a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q731777
BLAST score
                  146
                  3.0e-09
E value
                  66
Match length
% identity
                  HYPOTHETICAL 11.0 KD PROTEIN IN FAA3-MAS3 INTERGENIC REGION
NCBI Description
                  >gi_626357_pir__S48449 hypothetical protein YIL008w - yeast
                   (Saccharomyces cerevisiae) >gi_558396_emb_CAA86243
                   (Z38113) orf, len: 99, CAI=0.21 [Saccharomyces cerevisiae]
                  308792
Seq. No.
                  uC-zmflmo17221h12a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3342552
BLAST score
                   143
                   8.0e-09
E value
                   92
Match length
% identity
                   (AF076979) putative strictosidine synthase [Arabidopsis
NCBI Description
                   thaliana]
                   308793
Seq. No.
                   uC-zmflmo17222f05b1
Seq. ID
Method
                   BLASTN
                   g22332
NCBI GI
                   387
BLAST score
E value
                   0.0e + 00
                   485
Match length
                   95
% identity
NCBI Description
                   Z.mays HRGP gene
                   308794
Seq. No.
Seq. ID
                   uC-zmflmo17222g11b1
                   BLASTX
Method
NCBI GI
                   g123650
BLAST score
                   160
                   2.0e-17
E value
Match length
                   89
% identity
                   HEAT SHOCK COGNATE 70 KD PROTEIN >gi_82245_pir__S03250 heat
NCBI Description
                   shock protein 70 (clone pMON9743) - garden petunia
                   >qi 20557 emb CAA30018 (X06932) heat shock protein 70
                   [Petunia \bar{x} hybrida]
                   308795
Seq. No.
                   uC-zmflmo17222h04b1
Seq. ID
                   BLASTX
Method
                   g2984709
NCBI GI
                   261
BLAST score
                   1.0e-43
E value
```

(AF053468) DnaJ-related protein ZMDJ1 [Zea mays]

```
308796
Seq. No.
                  uC-zmflmo17222h08b1
Seq. ID
                  BLASTN
Method
                  q22268
NCBI GI
BLAST score
                  45
E value
                  2.0e-16
                  89
Match length
% identity
                  Maize (strain E41) mRNA for cell wall glycoprotein
NCBI Description
                   (partial) >gi_168458_gb_M36914_MZECWAC Z.mays cell wall
                  protein mRNA, 3' end
                  308797
Seq. No.
                  uC-zmflmo17223a06b1
Seq. ID
                  BLASTX
Method
NCBI GI
                   q1498326
BLAST score
                   209
                   1.0e-16
E value
                   68
Match length
% identity
                   (U60496) actin [Glycine max]
NCBI Description
                   308798
Seq. No.
                   uC-zmflmo17223a10b1
Seq. ID
                   BLASTX
Method
                   g1839022
NCBI GI
BLAST score
                   201
                   1.0e-15
E value
                   125
Match length
% identity
                   37
                  (Y11121) amino acid carrier [Ricinus communis]
NCBI Description
Seq. No.
                   308799
                   uC-zmflmo17223b05a1
Seq. ID
Method
                   BLASTX
                   g4539394
NCBI GI
BLAST score
                   260
                   1.0e-22
E value
Match length
                   75
                   56
% identity
                   (AL035526) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   308800
                   uC-zmflmo17223b05b1
Seq. ID
                   BLASTX
Method
                   g2827553
NCBI GI
                   317
BLAST score
                   3.0e-29
E value
                   140
Match length
                   47
% identity
                   (AL021635) predicted protein [Arabidopsis thaliana]
NCBI Description
                   308801
Seq. No.
                   uC-zmflmo17223c02b1
Seq. ID
```

BLASTX

368

g3319876

Method

NCBI GI BLAST score

```
4.0e-35
E value
                  175
Match length
                  50
% identity
NCBI Description (AJ007791) Msh3 protein [Arabidopsis thaliana]
                  308802
Seq. No.
                  uC-zmflmo17223c09b1
Seq. ID
Method
                  BLASTX
                  g2443887
NCBI GI
                  200
BLAST score
                  2.0e-15
E value
                  169
Match length
                  36
% identity
                  (AC002294) Similar to transcription factor
NCBI Description
                  gb Z46606 1658307 and others [Arabidopsis thaliana]
                  308803
Seq. No.
                  uC-zmflmo17223c10b1
Seq. ID
                  BLASTX
Method
                  g129881
NCBI GI
BLAST score
                  281
                  6.0e-25
E value
                  63
Match length
                  86
% identity
                  PYROPHOSPHATE--FRUCTOSE 6-PHOSPHATE 1-PHOSPHOTRANSFERASE
NCBI Description
                  ALPHA SUBUNIT (PFP) (6-PHOSPHOFRUCTOKINASE (PYROPHOSPHATE))
                   (PYROPHOSPHATE-DEPENDENT 6-PHOSPHOFRUCTOSE-1-KINASE)
                   (PPI-PFK) >gi_482294_pir__A36094
                   pyrophosphate--fructose-6-phosphate 1-phosphotransferase
                   (EC 2.7.1.90) alpha chain - potato (cv. Kennebec)
                   >gi 169538 (M55190) pyrophosphate-fructose 6-phosphate
                   1-phosphotransferase alpha-subunit [Solanum tuberosum]
                   308804
Seq. No.
                   uC-zmflmo17223d05b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1652057
BLAST score
                   461
                   6.0e-46
E value
                   140
Match length
% identity
                  (D90902) hypothetical protein [Synechocystis sp.]
NCBI Description
                   308805
Seq. No.
                   uC-zmflmo17223d08b1
Seq. ID
                   BLASTX
Method
                   q4033424
NCBI GI
                   260
BLAST score
E value
                   2.0e-22
                   57
Match length
                   91
% identity
                   SOLUBLE INORGANIC PYROPHOSPHATASE (PYROPHOSPHATE
NCBI Description
```

PHOSPHO-HYDROLASE) (PPASE) >gi_2668746 (AF034947) inorganic pyrophosphatase [Zea mays]

Seq. No. 308806

Seq. ID uC-zmflmo17223e02b1

Match length

% identity

55 58

```
BLASTX
Method
                  g4099090
NCBI GI
BLAST score
                  251
                  2.0e-21
E value
Match length
                  132
% identity
                   47
NCBI Description (U83178) unknown [Arabidopsis thaliana]
                  308807
Seq. No.
Seq. ID
                  uC-zmflmo17223e05b1
Method
                  BLASTX
NCBI GI
                   g2911059
BLAST score
                   319
E value
                   1.0e-29
Match length
                   104
% identity
                   68
                  (AL021961) putative protein [Arabidopsis thaliana]
NCBI Description
                   308808
Seq. No.
Seq. ID
                   uC-zmflmo17223f08b1
                   BLASTN
Method
NCBI GI
                   q3688588
                   44
BLAST score
                   1.0e-15
E value
                   84
Match length
                   88
% identity
                   Triticum aestivum TaMADS#11 mRNA for MADS box transcription
NCBI Description
                   factor, complete cds
                   308809
Seq. No.
                   uC-zmflmo17223g01b1
Seq. ID
Method
                   BLASTX
                   g2443886
NCBI GI
                   265
BLAST score
                   3.0e-23
E value
                   105
Match length
% identity
                   57
                   (AC002294) Unknown protein [Arabidopsis thaliana]
NCBI Description
                   308810
Seq. No.
                   uC-zmflmo17223g08b1
Seq. ID
                   BLASTX
Method
                   g2980806
NCBI GI
BLAST score
                   182
                   3.0e-13
E value
                   69
Match length
% identity
                   52
                   (AL022197) putative protein [Arabidopsis thaliana]
NCBI Description
                   308811
Seq. No.
                   uC-zmflmo17223h07b1
Seq. ID
Method
                   BLASTX
                   q4539003
NCBI GI
                   152
BLAST score
E value
                   8.0e-10
```



BLASTN

217

94

g1651897

1.0e-119 293

NCBI Description

Seq. No.

Seq. ID

NCBI GI

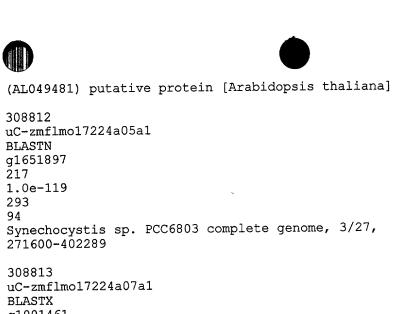
BLAST score E value

Match length

NCBI Description

% identity

Method



308813 Seq. No. uC-zmflmo17224a07a1 Seq. ID BLASTX Method g1001461 NCBI GI BLAST score 861--7.0e-93 E value 187 Match length 5

% identity (D63999) hypothetical protein [Synechocystis sp.] NCBI Description

Seq. No. 308814 uC-zmflmo17224b03a1 Seq. ID BLASTN Method q1653228 NCBI GI 473 BLAST score 0.0e+00E value 481 Match length

100 % identity Synechocystis sp. PCC6803 complete genome, 14/27, NCBI Description 1719644-1848241

308815 Seq. No. Seq. ID uC-zmflmo17224b04a1 BLASTX Method NCBI GI g1001398

BLAST score 611 1.0e-63 E value 125 Match length 100 % identity

(D63999) RNA polymerase sigma factor [Synechocystis sp.] NCBI Description

308816 Seq. No.

uC-zmflmo17224c08a1 Seq. ID

BLASTX Method q1653819 NCBI GI BLAST score 361 3.0e-34 E value 69 Match length % identity 100

(D90916) sensory transduction histidine kinase NCBI Description

[Synechocystis sp.]

308817 Seq. No.

uC-zmflmo17224c09a1 Seq. ID

```
BLASTN
Method
                  g1652956
NCBI GI
                  345
BLAST score
                  0.0e+00
E value
                  381
Match length
                  98
% identity
                  Synechocystis sp. PCC6803 complete genome, 12/27,
NCBI Description
                  1430419-1576592
                  308818
Seq. No.
                  uC-zmflmo17224e06a1
Seq. ID
                  BLASTN
Method
                  g1653083
NCBI GI
                   300
BLAST score
                   1.0e-168
E value
                   344
Match length
                   97
% identity
                   Synechocystis sp. PCC6803 complete genome, 13/27,
NCBI Description
                   1576593-1719643
                   308819
Seq. No.
                   uC-zmflmo17224f08a1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g1001200
                   447
BLAST score
                   0.0e+00
E value
                   483
Match length
                   98
% identity
                   Synechocystis sp. PCC6803 complete genome, 22/27,
NCBI Description
                   2755703-2868766
                   308820
Seq. No.
Seq. ID
                   uC-zmflmo17224f10a1
Method
                   BLASTX
                   q1653897
NCBI GI
                   770
BLAST score
                   3.0e-82
E value
Match length
                   154
% identity
                   99
                   (D90917) dihydroxyacid dehydratase [Synechocystis sp.]
NCBI Description
                   308821
Seq. No.
Seq. ID
                   uC-zmflmo17224f11a1
Method
                   BLASTX
                   q1652217
NCBI GI
BLAST score
                   654
                   9.0e-69
E value
                   121
Match length
% identity
```

NCBI Description (D90903) hypothetical protein [Synechocystis sp.]

Seq. No. 308822

Seq. ID uC-zmflmo17224g03a1

Method BLASTX
NCBI GI g1653181
BLAST score 627
E value 1.0e-65



```
Match length
% identity
                   (D90911) hydrogenase subunit [Synechocystis sp.]
NCBI Description
                  >gi_1771717_emb_CAA66209_ (X97610) hydrogenase subunit
                  [Synechocystis sp.]
                  308823
Seq. No.
                  uC-zmflmo17224g06a1
Seq. ID
                  BLASTN
Method
NCBI GI
                  q1652844
BLAST score
                  113
                   3.0e-57
E value
                  133
Match length
                   96
% identity
                  Synechocystis sp. PCC6803 complete genome, 11/27,
NCBI Description
                   1311235-1430418
                   308824
Seq. No.
                   uC-zmflmo17224g11a1
Seq. ID
Method
                   BLASTX
                   g1742348
NCBI GI
                   166
BLAST score
                   2.0e-11
E value
                   87
Match length
                   45
% identity
                   (D90783) Tyrosine aminotransferase (EC 2.6.1.5)
NCBI Description
                   (L-tyrosine: 2-oxoglutarate aminotransferase) (TAT).
                   [Escherichia coli] >gi 1742355_dbj_BAA15075_ (D90784)
                   Tyrosine aminotransferase (EC 2.6.1.5)
                   (L-tyrosine: 2-oxoglutarate aminotransferase) (TAT).
                   [Escherichia coli] >gi_1787710 (AE000241) multi modular;
                   putative transcriptional regulator; also putative
                   ATP-binding component of a transport system [Escherichia
                   coli]
                   308825
Seq. No.
Seq. ID
                   uC-zmflmo17224h01a1
                   BLASTN
Method
                   g1652225
NCBI GI
                   159
BLAST score
                   3.0e-84
E value
Match length
                   324
% identity
                   95
                   Synechocystis sp. PCC6803 complete genome, 6/27,
NCBI Description
                   630555-781448
Seq. No.
                   308826
                   uC-zmflmo17224h09a1
Seq. ID
Method
                   BLASTX
                   g1001545
NCBI GI
```

Method BLASTX
NCBI GI g1001545
BLAST score 620
E value 8.0e-65
Match length 128
% identity 96

NCBI Description (D64000) oligopeptide transport system permease protein

[Synechocystis sp.]



```
Seq. No.
                  uC-zmflmo17225a03a1
Seq. ID
                  BLASTX
Method
                  q3122315
NCBI GI
BLAST score
                  726
E value
                  4.0e-77
                  152
Match length
                   99
% identity
NCBI Description PYRUVATE KINASE 2 (PK 2) >gi_1652654_dbj_BAA17574_ (D90907)
                  pyruvate kinase [Synechocystis sp.]
                   308828
Seq. No.
                   uC-zmflmo17225a04a1
Seq. ID
                   BLASTN
Method
                   g1653348
NCBI GI
BLAST score
                   494
                   0.0e+00
E value
                   498
Match length
                   100
% identity
                   Synechocystis sp. PCC6803 complete genome, 15/27,
NCBI Description
                   1848242-1991549
                   308829
Seq. No.
Seq. ID
                   uC-zmflmo17225a05a1
                   BLASTX
Method
                   g1001316
NCBI GI
                   686
BLAST score
                   2.0e-72
E value
                   151
Match length
                   89
% identity
NCBI Description (D64006) nitrate transport 45kD protein [Synechocystis sp.]
Seq. No.
                   308830
                   uC-zmflmo17225a07a1
Seq. ID
                   BLASTN
Method
                   g1653083
NCBI GI
BLAST score
                   284
E value
                   1.0e-159
                   296
Match length
                   99
% identity
                   Synechocystis sp. PCC6803 complete genome, 13/27,
NCBI Description
                   1576593-1719643
                   308831
Seq. No.
                   uC-zmflmo17225a09a1
Seq. ID
                   BLASTN
Method
                   g1001102
NCBI GI
BLAST score
                   428
                   0.0e+00
E value
                   436
Match length
                   100
 % identity
                   Synechocystis sp. PCC6803 complete genome, 20/27,
NCBI Description
                   2539000-2644794
```

Seq. No. 308832 Seq. ID uC-zmf1

Seq. ID uC-zmflmo17225a12a1

Method BLASTN

```
q1651650
NCBI GI
BLAST score
                   400
                  0.0e + 00
E value
                   414
Match length
                   100
% identity
                  Synechocystis sp. PCC6803 complete genome, 1/27, 1-133859
NCBI Description
                   308833
Seq. No.
                  uC-zmflmo17225b01a1
Seq. ID
```

Method BLASTX
NCBI GI g2496794
BLAST score 394
E value 1.0e-38
Match length 78

% identity 100
NCBI Description HYPOTHETICAL 36.7 KD PROTEIN SLL0501

>gi 1001347 dbj BAA10834 (D64006) hypothetical protein

[Synechocystis sp.]

 Seq. No.
 308834

 Seq. ID
 uC-zmflmo17225b04a1

 Method
 BLASTN

 NCBI GI
 g1653083

 BLAST score
 454

 E value
 0.0e+00

E value 0.00 Match length 531 % identity 96

NCBI Description Synechocystis sp. PCC6803 complete genome, 13/27,

1576593-1719643

Seq. No. 308835

Seq. ID uC-zmflmo17225b06a1

Method BLASTX
NCBI GI g1652789
BLAST score 575
E value 2.0e-59
Match length 134
% identity 87

NCBI Description (D90908) hypothetical protein [Synechocystis sp.]

Seq. No. 308836

Seq. ID uC-zmflmo17225b10a1

Method BLASTX
NCBI GI g1653351
BLAST score 717
E value 5.0e-76
Match length 163
% identity 93

NCBI Description (D90913) HlyB family [Synechocystis sp.]

Seq. No. 308837

Seq. ID uC-zmflmo17225b12a1

Method BLASTN
NCBI GI g1653348
BLAST score 487
E value 0.0e+00
Match length 526

```
% identity 98
NCBI Description Synechocystis sp. PCC6803 complete genome, 15/27, 1848242-1991549

Seq. No. 308838
Seq. ID 308838
uC-zmflmo17225c04a1
```

Seq. ID uC-zmflmo
Method BLASTN
NCBI GI g1001396
BLAST score 441
E value 0.0e+00
Match length 457
% identity 99

NCBI Description Synechocystis sp. PCC6803 complete genome, 18/27,

2267260-2392728

Seq. No. 308839

Seq. ID uC-zmflmo17225c05a1

Method BLASTN
NCBI GI g1001779
BLAST score 111
E value 4.0e-56
Match length 119
% identity 98

NCBI Description Synechocystis sp. PCC6803 complete genome, 24/27,

3002966-3138603

Seq. No. 308840

Seq. ID uC-zmflmo17225c07a1

Method BLASTN
NCBI GI g1652618
BLAST score 466
E value 0.0e+00
Match length 487
% identity 99

NCBI Description Synechocystis sp. PCC6803 complete genome, 9/27,

1056467-1188885

Seq. No. 308841

Seq. ID uC-zmflmo17225c08a1

Method BLASTX
NCBI GI g1653487
BLAST score 431
E value 1.0e-42
Match length 113
% identity 81

NCBI Description (D90914) zeta-carotene desaturase precursor [Synechocystis

sp.]

Seq. No. 308842

Seq. ID uC-zmflmo17225c09a1

Method BLASTX
NCBI GI g1651674
BLAST score 663
E value 1.0e-69
Match length 139
% identity 91

NCBI Description (D90899) ferrichrome-iron receptor [Synechocystis sp.]

```
308843
Seq. No.
                  uC-zmflmo17225c11a1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g1652225
BLAST score
                   395
                   0.0e + 00
E value
                   395
Match length
% identity
                   Synechocystis sp. PCC6803 complete genome, 6/27,
NCBI Description
                   630555-781448
                   308844
Seq. No.
Seq. ID
                   uC-zmflmo17225d01a1
                   BLASTN
Method
NCBI GI
                   g1001779
BLAST score
                   164
E value
                   3.0e-87
                   204
Match length
% identity
                   Synechocystis sp. PCC6803 complete genome, 24/27,
NCBI Description
                   3002966-3138603
                   308845
Seq. No.
                   uC-zmflmo17225d03a1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g1652844
                   435
BLAST score
                   0.0e+00
E value
Match length
                   446
% identity
                   100
                   Synechocystis sp. PCC6803 complete genome, 11/27,
NCBI Description
                   1311235-1430418
                   308846
Seq. No.
                   uC-zmflmo17225d07a1
Seq. ID
Method
                   BLASTN
                   g1001779
NCBI GI
BLAST score
                   554
                   0.0e + 00
E value
Match length
                   561
                   100
% identity
                   Synechocystis sp. PCC6803 complete genome, 24/27,
NCBI Description
                   3002966-3138603
                   308847
Seq. No.
                   uC-zmflmo17225d08a1
Seq. ID
Method
                   BLASTX
                   g2833462
NCBI GI
                   965
BLAST score
                   1.0e-105
E value
Match length
                   196
% identity
                   100
                   REPLICATIVE DNA HELICASE >gi_1001271_dbj_BAA10516_ (D64003)
NCBI Description
                   replicative DNA helicase [Synechocystis sp.]
Seq. No.
                   308848
```

BLAST score

E value

499 0.0e+00

```
uC-zmflmo17225d10a1
Seq. ID
                  BLASTN
Method
                  g1651650
NCBI GI
BLAST score
                  431
                  0.0e+00
E value
                  475
Match length
                  98
% identity
                  Synechocystis sp. PCC6803 complete genome, 1/27, 1-133859
NCBI Description
                  308849
Seq. No.
                  uC-zmflmo17225d12a1
Seq. ID
                  BLASTX
Method
                  g1256595
NCBI GI
BLAST score
                  901
E value
                  1.0e-97
Match length
                  172
% identity
                  99
NCBI Description (U38915) LytB [Synechocystis PCC6803]
Seq. No.
                  308850
Seq. ID
                  uC-zmflmo17225e01a1
Method
                  BLASTX
NCBI GI
                  g1653704
BLAST score
                  789
                  2.0e-84
E value
Match length
                  167
% identity
                  98
                  (D90915) cation-transporting P-type ATPase [Synechocystis
NCBI Description
                  sp.]
                  308851
Seq. No.
                  uC-zmflmo17225e03a1
Seq. ID
                  BLASTX
Method
                  g1673324
NCBI GI
BLAST score
                  695
E value
                  1.0e-73
                  139
Match length
                  98
% identity
NCBI Description (D64003) hypothetical protein [Synechocystis sp.]
                  308852
Seq. No.
                  uC-zmflmo17225e04a1
Seq. ID
                  BLASTX
Method
                  g1001464
NCBI GI
BLAST score
                  277
E value
                  2.0e-24
                  54
Match length
                  100
% identity
                  (D63999) succinate-semialdehyde dehydrogenase (NADP+)
NCBI Description
                   [Synechocystis sp.]
Seq. No.
                  308853
                  uC-zmflmo17225e05a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1653836
```



```
Match length
% identity
                  Synechocystis sp. PCC6803 complete genome, 27/27,
NCBI Description
                  3418852-3573470
Seq. No.
                  308854
                  uC-zmflmo17225e10a1
Seq. ID
                  BLASTX
Method
                  g1653010
NCBI GI
                  897
BLAST score
                  4.0e-97
E value
                  178
Match length
% identity
                  100
NCBI Description (D90910) sensory transduction histidine kinase
                  [Synechocystis sp.]
                  308855
Seq. No.
Seq. ID
                  uC-zmflmo17225e11a1
                  BLASTN
Method
                  g1001396
NCBI GI
BLAST score
                  433
                                           - 5 -
                  0.0e + 00
E value
                  456
Match length
                  99
% identity
NCBI Description Synechocystis sp. PCC6803 complete genome, 18/27,
                  2267260-2392728
                  308856
Seq. No.
                  uC-zmflmo17225e12a1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1652472
BLAST score
                  774
                   5.0e-83
E value
Match length
                  165
                   99
% identity
NCBI Description (D90905) ethylene response sensor protein [Synechocystis
                            and the second
                  sp.] ·
                  308857
Seq. No.
                  uC-zmflmo17225f03a1
Seq. ID
                  BLASTX
Method
                   q2500722
NCBI GI
BLAST score
                   954
E value
                   1.0e-104
                   187
Match length
                   99
% identity
                   PREPROTEIN TRANSLOCASE SECA SUBUNIT
NCBI Description
                   >gi_1001616_dbj_BAA10347_ (D64002) preprotein translocase
```

SecA subunit [Synechocystis sp.]

308858 Seq. No.

Seq. ID uC-zmflmo17225f06a1 Method BLASTN

NCBI GI q1652492 389 BLAST score 0.0e + 00E value 469 Match length



```
% identity
                  Synechocystis sp. PCC6803 complete genome, 8/27,
NCBI Description
                  920916-1056466
                   308859
Seq. No.
Seq. ID
                  uC-zmflmo17225f09a1
Method
                  BLASTN
                  g1652956
NCBI GI
                   490
BLAST score
                   0.0e + 00
E value
                   538
Match length
% identity
                   98
                   Synechocystis sp. PCC6803 complete genome, 12/27,
NCBI Description
                   1430419-1576592
                   308860
Seq. No.
                   uC-zmflmo17225f10a1
Seq. ID
                   BLASTX
                   g1652100
```

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Method NCBI GI 464 BLAST score 2.0e-46 E value 139 Match length 73 % identity

NCBI Description (D90902) PatA protein [Synechocystis sp.]

. 308861 Seq. No. Seq. ID uC-zmflmo17225f12a1 BLASTN Method g1652956 NCBI GI BLAST score 540 0.0e + 00E value 552 Match length 100 % identity

Synechocystis sp. PCC6803 complete genome, 12/27, NCBI Description

1430419-1576592

Seq. No. 308862

uC-zmflmo17225g01a1 Seq. ID

BLASTN Method q1653348 NCBI GI BLAST score 349 0.0e+00E value Match length 349 100 % identity

Synechocystis sp. PCC6803 complete genome, 15/27, NCBI Description

1848242-1991549

308863 Seq. No.

uC-zmflmo17225g02a1 Seq. ID

BLASTX Method g1653102 NCBI GI 650 BLAST score E value 2.0e-68 Match length 132 98 % identity

(D90911) beta-ketoacyl-acyl carrier protein synthase III NCBI Description

[Synechocystis sp.]

```
308864
Seq. No.
                  uC-zmflmo17225g05a1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2492597
BLAST score
                  743
                  4.0e-79
E value
                  146
Match length
                  99
% identity
                  HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN SLL0182
NCBI Description
                  >gi 1001688 dbj BAA10424 (D64002) ABC transporter
                  [Synechocystis sp.]
                  308865
Seq. No.
                  uC-zmflmo17225g09a1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1001159
                                                            .
                  787
BLAST score
                  3.0e-84
E value
                  152
Match length
                   100
% identity
                   (D64001) methionyl-tRNA formyltransferase [Synechocystis
NCBI Description
                   sp.]
                   308866
Seq. No.
Seq. ID
                   uC-zmflmo17225h01a1
                   BLASTN
Method
NCBI GI
                   g1652956
BLAST score
                   387
                   0.0e+00
E value
                   391
Match length
                   100
% identity
                   Synechocystis sp. PCC6803 complete genome, 12/27,
NCBI Description
                   1430419-1576592
                   308867
Seq. No.
                   uC-zmflmo17225h04a1
Seq. ID
Method
                   BLASTX
                   g1652320
NCBI GI
BLAST score
                   380
                   2.0e-36
E value
Match length
                   75
% identity
                   (D90904) hypothetical protein [Synechocystis sp.]
NCBI Description
                   308868
Seq. No.
                   uC-zmflmo17225h05a1
Seq. ID
Method
                   BLASTN
                   g1652027
NCBI GI
                   122
BLAST score
                   1.0e-62
E value
                   140
Match length
% identity
                   98
                   Synechocystis sp. PCC6803 complete genome, 4/27,
NCBI Description
                   402290-524345
```

1

308869

Seq. No.

```
uC-zmflmo17225h06a1
Seq. ID
                  BLASTX
Method
                  q3024199
NCBI GI
                  883
BLAST score
                  2.0e-95
E value
Match length
                  179
% identity
                   DNA MISMATCH REPAIR PROTEIN MUTS >gi_1652903_dbj_BAA17821_
NCBI Description
                   (D90909) DNA mismatch repair protein [Synechocystis sp.]
                   308870
Seq. No.
Seq. ID
                   uC-zmflmo17225h08a1
                   BLASTX
Method
                   g1006579
NCBI GI
                   752
BLAST score
                   2.0e-84
E value
Match length
                   174
                   97
% identity
                   (D64005) hypothetical protein [Synechocystis sp.]
NCBI Description
                   308871
Seq. No.
Seq. ID
                   uC-zmflmo17225h10a1
                   BLASTX
Method
                   q1001512
NCBI GI
                   300
BLAST score
                   1.0e-30
E value
Match length
                   72
                   95
% identity
                   (D64000) methylenetetrahydrofolate dehydrogenase
NCBI Description
                   [Synechocystis sp.]
                   308872
Seq. No.
                   uC-zmflmo17225h11a1
Seq. ID
                   BLASTN
Method
                   g1651650
NCBI GI
BLAST score
                   432
E value
                   0.0e+00
Match length
                   460
                   99
% identity
                   Synechocystis sp. PCC6803 complete genome, 1/27, 1-133859
NCBI Description
                   308873
Seq. No.
                   uC-zmflmo17225h12a1
Seq. ID
                   BLASTX
Method
```

Method BLASTX
NCBI GI 979703
BLAST score 750
E value 6.0e-80
Match length 134
% identity 99

NCBI Description hypothetical 32K protein (frxC 5' region) - Synechocystis

sp. (PCC 6803) >gi_217091_dbj_BAA01273_ (D10474) ORF278

[Synechocystis sp.]

Seq. No. 308874

Seq. ID uC-zmflmo17226a01a1

Method BLASTX NCBI GI g1001573

```
429
BLAST score
                  1.0e-42
E value
                  93
Match length
                  91
% identity
NCBI Description (D64000) fumarase [Synechocystis sp.]
                  308875
Seq. No.
                  uC-zmflmo17226a02a1
Seq. ID
                  BLASTN
Method
                  g1651768
NCBI GI
                   103
BLAST score
                   3.0e-51
E value
                   147
Match length
                   93
% identity
NCBI Description Synechocystis sp. PCC6803 complete genome, 2/27,
                   133860-271599
                   308876
Seq. No.
                   uC-zmflmo17226a04a1
Seq. ID
                   BLASTX
Method
                   q1652769
NCBI GI
                   855
BLAST score
                   3.0e-92
E value
                   172
Match length
                   99
% identity
                  (D90908) hypothetical protein [Synechocystis sp.]
NCBI Description
                   308877
Seq. No.
                   uC-zmflmo17226a05a1
Seq. ID
                   BLASTX
Method
                   g1001571
NCBI GI
                   383
BLAST score
                   7.0e-37
E value
                   77
Match length
 % identity
                   (D64000) hypothetical protein [Synechocystis sp.]
NCBI Description
                   308878
 Seq. No.
                   uC-zmflmo17226a06a1
 Seq. ID
                   BLASTN
Method
                   q1653715
 NCBI GI
 BLAST score
                   135
                   3.0e-70
 E value
 Match length
                   143
                   99
 % identity
                   Synechocystis sp. PCC6803 complete genome, 26/27,
 NCBI Description
                   3270710-3418851
                   308879
 Seq. No.
                   uC-zmflmo17226a08a1
 Seq. ID
                   BLASTX
 Method
                   q1652593
 NCBI GI
 BLAST score
                   459
 E value
                   9.0e-46
                   110
 Match length
                   85
 % identity
                   (D90906) hypothetical protein [Synechocystis sp.]
 NCBI Description
```

```
308880
Seq. No.
                  uC-zmflmo17226a09a1
Seq. ID
                  BLASTX
Method
                  g1653650
NCBI GI
BLAST score
                  284
E value
                   1.0e-25
                  79
Match length
                   77
% identity
                  (D90915) cation efflux system protein CzcA [Synechocystis
NCBI Description
                  sp.]
                   308881
Seq. No.
                   uC-zmflmo17226a11a1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1001774
                   365
BLAST score
                   1.0e-34
E value
                   76
Match length
                   97
% identity
NCBI Description (D64004) ABC transporter [Synechocystis sp.]
                   308882
Seq. No.
                   uC-zmflmo17226b01a1
Seq. ID
                   BLASTX
Method
                   g1673323
NCBI GI
                   360
BLAST score
                   3.0e-34
E value
                   71
Match length
                   97
% identity
                  (D64003) hypothetical protein [Synechocystis sp.]
NCBI Description
                   308883
Seq. No.
                   uC-zmflmo17226b04a1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q1652663
                   628
BLAST score
E value
                   1.0e-65
                   115
Match length
% identity
NCBI Description (D90907) hypothetical protein [Synechocystis sp.]
Seq. No.
                   308884
Seq. ID
                   uC-zmflmo17226b11a1
                   BLASTN
Method
NCBI GI
                   q1653228
BLAST score
                   485
E value
                   0.0e+00
Match length
                   485
                   100
% identity
                   Synechocystis sp. PCC6803 complete genome, 14/27,
NCBI Description
                   1719644-1848241
Seq. No.
                   308885
                   uC-zmflmo17226b12a1
Seq. ID
Method
                   BLASTN
                   g1653836
NCBI GI
```

BLAST score

E value Match length 404 0.0e+00

411

```
BLAST score
                    0.0e + 00
 E value
                    446
 Match length
                    98
 % identity
                    Synechocystis sp. PCC6803 complete genome, 27/27,
 NCBI Description
                    3418852-3573470
                    308886
 Seq. No.
                    uC-zmflmo17226c01a1
 Seq. ID
 Method
                    BLASTN
 NCBI GI
                    q1653477
 BLAST score
                    428
                    0.0e + 00
 E value
                    442
 Match length
                    100
 % identity
 NCBI Description
                    Synechocystis sp. PCC6803 complete genome, 16/27,
                    1991550-2137258
                    308887
 Seq. No.
                    uC-zmflmo17226c03a1
 Seq. ID
                    BLASTX
 Method
 NCBI GI
                    g2500315
 BLAST score
                    323
                    7.0e-32
 E value
 Match length
                    75
                    97
 % identity
                    50S RIBOSOMAL PROTEIN LŽ7 >gi 1653447 dbj BAA18361_
 NCBI Description
                    (D90913) 50S ribosomal protein L27 [Synechocystis sp.]
                    308888
 Seq. No.
                    uC-zmflmo17226c06a1
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g1653900
                    426
 BLAST score
                    6.0e-42
 E value
                    82
 Match length
 % identity
                    (D90917) hypothetical protein [Synechocystis sp.]
 NCBI Description
                    308889
 Seq. No.
                    uC-zmflmo17226c10a1
 Seq. ID
 Method
                    BLASTN
 NCBI GI
                    q1001779
 BLAST score
                    309
                    1.0e-173
 E value
                    333
 Match length
                    98
 % identity
                    Synechocystis sp. PCC6803 complete genome, 24/27,
 NCBI Description
                    3002966-3138603
                    308890
 Seq. No.
 Seq. ID
                    uC-zmflmo17226d01a1
Method
                    BLASTN
 NCBI GI
                    g1652360
```



```
% identity
                  Synechocystis sp. PCC6803 complete genome, 7/27,
NCBI Description
                  781449-920915
                  308891
Seq. No.
Seq. ID
                  uC-zmflmo17226d04a1
Method
                  BLASTX
NCBI GI
                  q2494656
                  743
BLAST score
                  3.0e-79
E value
                  142
Match length
% identity
                  GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE (G6PD)
NCBI Description
                  >gi 1652530_dbj BAA17451_ (D90906) glucose 6-phosphate
                  dehydrogenase [Synechocystis sp.]
                  308892
Seq. No.
                  uC-zmflmo17226d08a1
Seq. ID
                  BLASTX
Method
                  g2501033
NCBI GI
                  862
BLAST score
                 4.0e−93
E value
                  155
Match length
                  100
% identity
NCBI Description METHIONYL-TRNA SYNTHETASE (METHIONINE--TRNA LIGASE) (METRS)
                   >gi 1001640 dbj BAA10371_ (D64002) methionyl-tRNA
                   synthetase [Synechocystis sp.]
                   308893
Seq. No.
                  uC-zmflmo17226d09a1
Seq. ID
                  BLASTX
Method
                   g1652120
NCBI GI
BLAST score
                   743
                   4.0e-79
E value
                   147
Match length
% identity
NCBI Description (D90902) sensory transduction histidine kinase
                   [Synechocystis sp.]
                   308894
Seq. No.
                   uC-zmflmo17226d11a1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2494254
BLAST score
                   229
                   1.0e-19
E value
                   67
Match length
                   75
 % identity
NCBI Description ELONGATION FACTOR G 2 (EF-G 2) >gi_1653408_dbj_BAA18322_
                   (D90913) elongation factor EF-G [Synechocystis sp.]
```

308895 Seq. No.

uC-zmflmo17226e01a1 Seq. ID

Method BLASTN NCBI GI g1652225 317 BLAST score 1.0e-178 E value 337 -Match length

```
% identity
                  Synechocystis sp. PCC6803 complete genome, 6/27,
NCBI Description
                  630555-781448
                  308896
Seq. No.
                  uC-zmflmo17226e02a1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2500959
                  604
BLAST score
                  9.0e-63
E value
                  176
Match length
                  74
% identity
                  ALANYL-TRNA SYNTHETASE (ALANINE--TRNA LIGASE) (ALARS)
NCBI Description
                  >gi 1653611_dbj_BAA18523_ (D90915) alanyl-tRNA synthetase
                   [Synechocystis sp.]
                  308897
Seq. No.
                  uC-zmflmo17226e03a1
Seq. ID
                  BLASTX
Method
                   g1006612
NCBI GI
                   357
BLAST score
                   6.0e-34
E value
                   71
Match length
                   100
% identity
                   (D64005) phospho-N-acetylmuramoyl-pentapeptide-transferas e
NCBI Description
                   [Synechocystis sp.]
                   308898
Seq. No.
                   uC-zmflmo17226e07a1
Seq. ID
                   BLASTX
Method
                   g1653486
NCBI GI
BLAST score
                   794
                   5.0e-85
E value
Match length
                   163
                   99
% identity
                  (D90914) protease [Synechocystis sp.]
NCBI Description
                   308899
Seq. No.
                   uC-zmflmo17226e09a1
Seq. ID
                   BLASTN
Method
                   g1653477
NCBI GI
BLAST score
                   457
                   0.0e + 00
E value
Match length
                   465
                   100
% identity
                   Synechocystis sp. PCC6803 complete genome, 16/27,
NCBI Description
                   1991550-2137258
                   308900
Seq. No.
                   uC-zmflmo17226e10a1
Seq. ID
                   BLASTN
Method
                   g1001102
NCBI GI
BLAST score
                   516
E value
                   0.0e + 00
Match length
                   520
```

Synechocystis sp. PCC6803 complete genome, 20/27,

100

% identity

NCBI Description



2539000-2644794

```
Seq. No.
                   308901
Seq. ID
                   uC-zmflmo17226e11a1
Method
                   BLASTX
NCBI GI
                   q2494801
BLAST score
                   596
                   7.0e-62
E value
                   110
Match length
                   100
% identity
NCBI Description
                   HYPOTHETICAL 36.0 KD PROTEIN SLR2079
                   >gi 1653050 dbj BAA17967 (D90910) hypothetical protein
                   [Synechocystis sp.]
                   308902
Seq. No.
Seq. ID
                   uC-zmflmo17226e12a1
                   BLASTN
Method
NCBI GI
                   q1653836
BLAST score
                   136
                   9.0e-71
E value
                   192
Match length
% identity
                   93
                   Synechocystis sp. PCC6803 complete genome, 27/27,
NCBI Description
                   3418852-3573470
                   308903
Seq. No.
 Seq. ID
                   uC-zmflmo17226f01a1
                   BLASTX
Method
                   g1652513
NCBI GI
BLAST score
                   481
E value
                   2.0e-48
Match length
                   152
 % identity
                  (D90906) NADH dehydrogenase subunit 4 [Synechocystis sp.]
NCBI Description
 Seq. No.
                   308904
 Seq. ID
                   uC-zmflmo17226f02a1
 Method
                   BLASTX
 NCBI GI
                   g1652110
 BLAST score
                   385
 E value
                   4.0e-37
Match length
                   71
 % identity
                   100
                   (D90902) hypothetical protein [Synechocystis sp.]
 NCBI Description
                   308905
 Seq. No.
                   uC-zmflmo17226f03a1
 Seq. ID
 Method
                   BLASTX
                   g1652476
 NCBI GI
 BLAST score
                   604
                   5.0e-63
 E value
Match length
                   118
 % identity
                   99
                   (D90905) carbonic 3-dehydroquinase [Synechocystis sp.]
 NCBI Description
```

43934

308906

uC-zmflmo17226f05a1

Seq. No.

Seq. ID

Seq. No.

Seq. ID

Method

308911

BLASTX

uC-zmflmo17226q06a1

```
Method
                  BLASTN
                  g1001612
NCBI GI
BLAST score
                  335
E value
                  0.0e + 00
Match length
                  335
                  100
% identity
                  Synechocystis sp. PCC6803 complete genome, 21/27,
NCBI Description
                  2644795-2755702
                  308907
Seq. No.
Seq. ID
                  uC-zmflmo17226f11a1
Method
                  BLASTN
NCBI GI
                  g1652492
BLAST score
                  259
E value
                  1.0e-144
Match length
                  349
% identity
                  94
NCBI Description
                  Synechocystis sp. PCC6803 complete genome, 8/27,
                  920916-1056466
Seq. No.
                  308908
                  uC-zmflmo17226q02a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1652027
BLAST score
                  128
E value
                  6.0e-66
Match length
                  212
% identity
                  90
NCBI Description
                  Synechocystis sp. PCC6803 complete genome, 4/27,
                  402290-524345
                  308909
Seq. No.
Seq. ID
                  uC-zmflmo17226g03a1
Method
                  BLASTX
NCBI GI
                  g2500985
BLAST score
                  293
E value
                  2.0e-26
Match length
                  60
% identity
                  100
NCBI Description
                  PHENYLALANYL-TRNA SYNTHETASE ALPHA CHAIN
                   (PHENYLALANINE--TRNA LIGASE ALPHA CHAIN) (PHERS)
                  >gi 1001185 dbj BAA10328 (D64001) phenylalanyl-tRNA
                  synthetase alpha chain [Synechocystis sp.]
Seq. No.
                  308910
Seq. ID
                  uC-zmflmo17226g05a1
Method
                  BLASTX
NCBI GI
                  g1653665
BLAST score
                  162
E value
                  1.0e-23
Match length
                  61
% identity
NCBI Description
                  (D90915) peptide chain release factor [Synechocystis sp.]
```

Method

NCBI GI

E value

BLAST score

BLASTN

169

q1651650

2.0e-90

```
NCBI GI
                  q1001311
BLAST score
                  346
E value
                  1.0e-32
                  82
Match length
                  83
% identity
                  (D64006) hypothetical protein [Synechocystis sp.]
NCBI Description
                  308912
Seq. No.
                  uC-zmflmo17226g08a1
Seq. ID
Method
                  BLASTX
                  g1263194
NCBI GI
BLAST score
                  181
                   4.0e-13
E value
                  85
Match length
% identity
                   46
NCBI Description
                  (U33094) KpnBI R-M system [Klebsiella pneumoniae]
                  >gi_1586515_prf__2204227A hsdR gene [Klebsiella pneumoniae]
                  308913
Seq. No.
                  uC-zmflmo17226h02a1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1652590
BLAST score
                   387
                   6.0e-38
E value
Match length
                  76
% identity
                   99
                  (D90906) phosphoribosyl aminoidazole succinocarboxamide
NCBI Description
                  synthetase [Synechocystis sp.]
                   308914
Seq. No.
Seq. ID
                  uC-zmflmo17226h04a1
                  BLASTX
Method
NCBI GI
                   q1653010
BLAST score
                  226
                   2.0e-18
E value
Match length
                   44
                                                                                 Ť
                 . 100
% identity
NCBI Description (D90910) sensory transduction histidine kinase
                   [Synechocystis sp.]
Seq. No.
                   308915
Seq. ID
                   uC-zmflmo17226h05a1
Method
                   BLASTN
NCBI GI
                   g1653477
BLAST score
                   356
E value
                   0.0e + 00
Match length
                   375
                   99
% identity
                  Synechocystis sp. PCC6803 complete genome, 16/27,
NCBI Description
                   1991550-2137258
                                                                                  · .
                   308916
Seq. No.
                   uC-zmflmo17226h09a1
Seq. ID
```



```
Match length
                    169
                    100
 % identity
                    Synechocystis sp. PCC6803 complete genome, 1/27, 1-133859
 NCBI Description
 Seq. No.
                    308917
                    uC-zmflmo17226h12a1
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    q3024785
 BLAST score
                    334
 E value
                    1.0e-31
 Match length
                    78
 % identity
                    83
                    EXCINUCLEASE ABC SUBUNIT C >gi 1652700 dbj BAA17620
 NCBI Description
                    (D90907) excinuclease ABC subunit C [Synechocystis sp.]
 Seq. No.
                    308918
 Seq. ID
                    uC-zmflmo17227a04b1
 Method
                    BLASTN
 NCBI GI
                    g1001200
 BLAST score
                    84
 E value
                    5.0e-40
 Match length
                    96
 % identity
                    97
 NCBI Description
                    Synechocystis sp. PCC6803 complete genome, 22/27,
                    2755703-2868766
 Seq. No.
                    308919
 Seq. ID
                    uC-zmflmo17227a05a1
 Method
                    BLASTN
 NCBI GI
                    q1652127
 BLAST score
                    189
 E value
                    1.0e-102
 Match length
                    221
 % identity
                    97
                    Synechocystis sp. PCC6803 complete genome, 5/27,
 NCBI Description
                    524346-630554
                    308920
 Seq. No.
                    uC-zmflmo17227a05b1
 Seq. ID
 Method
                    BLASTN
                    q1652127
 NCBI GI
 BLAST score
                    229
                    1.0e-126
 E value
 Match length
                    389
 % identity
                    90
                    Synechocystis sp. PCC6803 complete genome, 5/27,
 NCBI Description
                    524346-630554
 Seq. No.
                    308921
 Seq. ID
                    uC-zmflmo17227a06b1
 Method
                    BLASTN
- NCBI GI
                    g1653477
                    122
 BLAST score
                    5.0e-62
 E value
 Match length
                    344
 % identity
                    88
```

43937

NCBI Description Synechocystis sp. PCC6803 complete genome, 16/27,



1991550-2137258

```
Seq. No.
                    308922
 Seq. ID
                    uC-zmflmo17227a12a1
 Method
                    BLASTN
 NCBI GI
                    q1001291
 BLAST score
                    181
                    2.0e-97
 E value
 Match length
                    225
 % identity
                    96
                    Synechocystis sp. PCC6803 complete genome, 25/27,
 NCBI Description
                    3138604-3270709
 Seq. No.
                    308923
 Seq. ID
                    uC-zmflmo17227a12b1
 Method
                    BLASTN
. NCBI GI
                    g1652492
 BLAST score
                    80
 E value
                    4.0e-37
 Match length
                    96
 % identity
                    96
 NCBI Description
                    Synechocystis sp. PCC6803 complete genome, 8/27,
                    920916-1056466
 Seq. No.
                    308924
 Seq. ID
                    uC-zmflmo17227b04b1
 Method
                    BLASTN
 NCBI GI
                    q1651768
 BLAST score
                    99
                    9.0e-49
 E value
 Match length
                    139
 % identity
                    93
                    Synechocystis sp. PCC6803 complete genome, 2/27,
 NCBI Description
                    133860-271599
 Seq. No.
                    308925
 Seq. ID
                    uC-zmflmo17227b05a1
 Method
                    BLASTN
 NCBI GI
                    g1652492
 BLAST score
                    271
 E value
                    1.0e-151
 Match length
                    327
 % identity
                    96
                    Synechocystis sp. PCC6803 complete genome, 8/27,
 NCBI Description
                    920916-1056466
 Seq. No.
                    308926
                    uC-zmflmo17227b05b1
 Seq. ID
 Method
                    BLASTN
 NCBI GI
                    g1652492
 BLAST score
                    149
 E value
                   2.0e-78
 Match length
                    229
 % identity
                    91
                    Synechocystis sp. PCC6803 complete genome, 8/27,
 NCBI Description
```

920916-1056466

NCBI GI

BLAST score

g1001612

468

```
Seq. No.
                   308927
Seq. ID
                  uC-zmflmo17227b07b1
Method
                  BLASTX
NCBI GI
                   g1652813
BLAST score
                   358
                   6.0e-34
E value
Match length
                  96
                  79
% identity
                   (D90908) nitrate/nitrite response regulator protein
NCBI Description
                   [Synechocystis sp.]
                  308928
Seq. No.
Seq. ID
                  uC-zmflmo17227b11a1
Method
                  BLASTX
NCBI GI
                  g1652834
BLAST score
                   686
E value
                  2.0e-72
Match length
                  134
% identity
NCBI Description
                  (D90908) hypothetical protein [Synechocystis sp.]
Seq. No.
                  308929
                  uC-zmflmo17227b11b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1256581
BLAST score
                  448
E value
                  0.0e + 00
Match length
                  484
% identity
                   98
NCBI Description
                  Synechocystis sp. lipid A disaccharide synthase (lpxB),
                  ferredoxin (fed), transposase, and MgtC genes, complete cds
                  308930
Seq. No.
Seq. ID
                  uC-zmflmo17227b12a1
Method
                  BLASTX
NCBI GI
                  g1652066
BLAST score
                  446
E value
                  2.0e-44
Match length
                  90
% identity
                  100
NCBI Description (D90902) Na/H antiporter [Synechocystis sp.]
                  308931
Seq. No.
Seq. ID
                  uC-zmflmo17227b12b1
Method
                  BLASTX
NCBI GI
                  g1652066
BLAST score
                  659
E value
                  2.0e-69
Match length
                  130
% identity
                  99
NCBI Description (D90902) Na/H antiporter [Synechocystis sp.]
Seq. No.
                  308932
                  uC-zmflmo17227c02a1
Seq. ID
Method
                  BLASTN
```

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```
E value
                   0.0e + 00
Match length
                  468
% identity
                  100
NCBI Description
                  Synechocystis sp. PCC6803 complete genome, 21/27,
                  2644795-2755702
                  308933
Seq. No.
                  uC-zmflmo17227c02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1001636
BLAST score
                  785
E value
                  5.0e-84
Match length
                  161
% identity
                  93
NCBI Description
                  (D64002) hypothetical protein [Synechocystis sp.]
                  308934
Seq. No.
                  uC-zmflmo17227c03a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q1652844
BLAST score
                   454
                  0.0e+00
È value
Match length
                   466
                  99
% identity
                  Synechocystis sp. PCC6803 complete genome, 11/27,
NCBI Description
                  1311235-1430418
Seq. No.
                  308935
Seq. ID
                  uC-zmflmo17227c06a1
Method
                  BLASTN
NCBI GI
                  q1652492
BLAST score
                  224
E value
                  1.0e-123
Match length
                  252
                  97
% identity
NCBI Description
                  Synechocystis sp. PCC6803 complete genome, 8/27,
                  920916-1056466
                  308936
Seq. No.
Seq. ID
                  uC-zmflmo17227c06b1
Method
                  BLASTX
                  g1652542
NCBI GI
BLAST score
                  390
E value
                  9.0e-38
Match length
                  76
% identity
                  97
NCBI Description (D90906) CbiD protein [Synechocystis sp.]
Seq. No.
                  308937
Seq. ID
                  uC-zmflmo17227c07b1
Method
                  BLASTN
NCBI GI
                  g1001701
BLAST score
                  114
E value
                  8.0e-58
Match length
                  118
% identity
```

43940

NCBI Description Synechocystis sp. PCC6803 complete genome, 23/27,



2868767-3002965

```
Seq. No.
                  308938
Seq. ID
                  uC-zmflmo17227c08b1
Method
                  BLASTN
NCBI GI
                  q1001779
BLAST score
                  210
E value
                  1.0e-115
Match length
                  214
                  100
% identity
                  Synechocystis sp. PCC6803 complete genome, 24/27,
NCBI Description
                  3002966-3138603
                   308939
Seq. No.
                  uC-zmflmo17227c10a1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q1651974
BLAST score
                   699
                   6.0e-74
E value
                   159
Match length
% identity
                   (D90901) ABC transporter [Synechocystis sp.]
NCBI Description
                   308940
Seq. No.
                   uC-zmflmo17227c10b1
Seq. ID
Method
                   BLASTN
NCBI GI
                   q1651897
BLAST score
                   406
                   0.0e + 00
E value
Match length
                   486
% identity
                   Synechocystis sp. PCC6803 complete genome, 3/27,
NCBI Description
                   271600-402289
                   308941
Seq. No.
                   uC-zmflmo17227d01b1
Seq. ID
Method
                   BLASTN
                   g1001291
NCBI GI
BLAST score
                   166
                   1.0e-88
E value
Match length
                   174
                   99
% identity
                   Synechocystis sp. PCC6803 complete genome, 25/27,
NCBI Description
                   3138604-3270709
                   308942
Seq. No.
                   uC-zmflmo17227e05b1
Seq. ID
                   BLASTN
Method
                   g1653604
NCBI GI
BLAST score
                   280
                   1.0e-156
E value
Match length
                   308
                   98
% identity
                   Synechocystis sp. PCC6803 complete genome, 17/27,
NCBI Description
```

Seq. No. 308943

2137259-2267259

```
uC-zmflmo17227e08a1
Seq. ID
                  BLASTN
Method
                  g1653477
NCBI GI
                  450
BLAST score
                  0.0e+00
E value
                  454
Match length
                  100
% identity
                  Synechocystis sp. PCC6803 complete genome, 16/27,
NCBI Description
                  1991550-2137258
                  308944
Seq. No.
                  uC-zmflmo17227e08b1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g1651650
                  436
BLAST score
                   0.0e+00
E value
                   455
Match length
                   99
% identity
                  Synechocystis sp. PCC6803 complete genome, 1/27, 1-133859
NCBI Description
                   308945
Seq. No.
                   uC-zmflmo17227e09a1
Seq. ID
                   BLASTX
Method
                   q1652131
NCBI GI
BLAST score
                   689
                   7.0e-73
E value
Match length
                   133
                   99
% identity
                  (D90903) glutamate-ammonia ligase [Synechocystis sp.]
NCBI Description
                   308946
Seq. No.
                   uC-zmflmo17227e09b1
Seq. ID
                   BLASTX
Method
                   g1652132
NCBI GI
                   280
BLAST score
                   7.0e-35
E value
                   84
Match length
                   92
% identity
                   (D90903) sensory transduction histidine kinase
NCBI Description
                   [Synechocystis sp.]
                   308947
Seq. No.
                   uC-zmflmo17227e11b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g548743
                   268
BLAST score
                   2.0e-23
E value
                   55
Match length
                   98
 % identity
                   50S RIBOSOMAL PROTEIN L11 >gi_1075628_pir__C49316 ribosomal
NCBI Description
                   protein L11 - Synechocystis sp >gi_452792_emb_CAA51491_
                   (X73005) ribosomal protein L11 [Synechocystis PCC6803]
```

Seq. No. 308948

Seq. ID uC-zmflmo17227f02a1

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L11 [Synechocystis sp.]

>gi_1652498_dbj_BAA17419_ (D90906) 50S ribosomal protein

```
BLASTX
Method
                  q3024897
NCBI GI
                  638
BLAST score
                  7.0e-67
E value
                  141
Match length
% identity
                  HYPOTHETICAL 51.0 KD PROTEIN SLL0154
NCBI Description
                  >gi 1001453_dbj_BAA10078_ (D63999) 35.6 kD protein
                  [Synechocystis sp.]
                  308949
Seq. No.
Seq. ID
                  uC-zmflmo17227f02b1
                  BLASTX
Method
NCBI GI
                  q1652449
                   451
BLAST score
                   3.0e-45
E value
Match length
                   99
% identity
                  (D90905) chromosome segregation protein SMC1 [Synechocystis
NCBI Description
                   sp.]
                   308950
Seq. No.
                   uC-zmflmo17227f05b1
Seq. ID
                   BLASTX
Method
                   g1653567
NCBI GI
                   841
BLAST score
                   2.0e-90
E value
                   172
Match length
% identity
NCBI Description (D90914) asparaginase [Synechocystis sp.]
                   308951
Seq. No.
                   uC-zmflmo17227f07b1
Seq. ID
                   BLASTN
Method
                   g1653083
NCBI GI
                   460
BLAST score
                   0.0e+00
E value
Match length
                   464
                   100
 % identity
                   Synechocystis sp. PCC6803 complete genome, 13/27,
NCBI Description
                   1576593-1719643
 Seq. No.
                   308952
                   uC-zmflmo17227f08b1
 Seq. ID
                   BLASTX
 Method
                   g3183105
 NCBI GI
                   380
 BLAST score
                   5.0e-37
 E value
 Match length
                   78
                   97
 % identity
                   ORNITHINE CARBAMOYLTRANSFERASE, ANABOLIC (OTCASE)
 NCBI Description
                   >gi_1001360_dbj_BAA10847_ (D64006) ornithine
                   carbamoyltransferase chain f [Synechocystis sp.]
```

Seq. No. 308953

Seq. ID uC-zmflmo17227f09b1

Method BLASTX

E value

2.0e-13

```
g1651846
NCBI GI
                  286
BLAST score
                   8.0e-26
E value
                  93
Match length
                   33
% identity
NCBI Description
                  (D90900) carbon dioxide concentrating mechanism protein
                  CcmM [Synechocystis sp.]
                   308954
Seq. No.
Seq. ID
                  uC-zmflmo17227g03a1
Method
                  BLASTN
NCBI GI
                   g1652844
                   235
BLAST score
                   1.0e-129
E value
                   259
Match length
                   98
% identity
NCBI Description
                  Synechocystis sp. PCC6803 complete genome, 11/27,
                   1311235-1430418
                   308955
Seq. No.
                   uC-zmflmo17227g05b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q1651671
BLAST score
                   688
                   1.0e-72
E value
                   145
Match length
                   94
% identity
                  (D90899) ferrichrome-iron receptor [Synechocystis sp.]
NCBI Description
                   308956
Seq. No.
                   uC-zmflmo17227g08a1
Seq. ID
Method
                   BLASTN
NCBI GI
                   q1652618
BLAST score
                   407
                   0.0e + 00
E value
Match length
                   439
% identity
                   Synechocystis sp. PCC6803 complete genome, 9/27,
NCBI Description
                   1056467-1188885
Seq. No.
                   308957
                   uC-zmflmo17227g08b1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g1652618
BLAST score
                   257
E value
                   1.0e-142
Match length
                   309
% identity
                   96
                   Synechocystis sp. PCC6803 complete genome, 9/27,
NCBI Description
                   1056467-1188885
                   308958
Seq. No.
Seq. ID
                   uC-zmflmo17227h01b1
                   BLASTN
Method
                   g1652127
NCBI ĞI
BLAST score
                   40
```

```
Match length 64 % identity 91 NCBI Description Synechocystis sp. H
```

308959

NCBI Description Synechocystis sp. PCC6803 complete genome, 5/27, 524346-630554

Seq. ID uC-zmflmo17227h02a1
Method BLASTN
NCBI GI g1651768
BLAST score 279
E value 1.0e-156

Match length 287 % identity 99

Seq. No.

NCBI Description Synechocystis sp. PCC6803 complete genome, 2/27,

133860-271599

Seq. No. 308960

Seq. ID uC-zmflmo17227h02b1

Method BLASTN
NCBI GI g1651768
BLAST score 121
E value 1.0e-61
Match length 229
% identity 88

NCBI Description Synechocystis sp. PCC6803 complete genome, 2/27,

133860-271599

Seq. No. 308961

Seq. ID uC-zmflmo17227h03b1

Method BLASTX
NCBI GI g1652433
BLAST score 278
E value 3.0e-25
Match length 69
% identity 81

NCBI Description (D90905) SrrA [Synechocystis sp.]

Seq. No. 308962

Seq. ID uC-zmflmo17227h08b1

Method BLASTN
NCBI GI g1001102
BLAST score 295
E value 1.0e-165
Match length 331
% identity 97

NCBI Description Synechocystis sp. PCC6803 complete genome, 20/27,

2539000-2644794

Seq. No. 308963

Seq. ID uC-zmflmo17227h09b1

Method BLASTN
NCBI GI g1652127
BLAST score 212
E value 1.0e-116
Match length 264
% identity 95

NCBI Description Synechocystis sp. PCC6803 complete genome, 5/27,

NCBI Description



524346-630554

```
Seq. No.
                   308964
Seq. ID
                   uC-zmflmo17227h10b1
Method
                   BLASTN
NCBI GI
                   q1001102
BLAST score
                   274
E value
                   1.0e-153
Match length
                   300
% identity
NCBI Description
                   Synechocystis sp. PCC6803 complete genome, 20/27,
                   2539000-2644794
                   308965
Seq. No.
Seq. ID
                   uC-zmflmo17228a02a1
Method
                   BLASTN
NCBI GI
                   q1652844
BLAST score
                   363
E value
                   0.0e + 00
Match length
                   415
                   97
% identity
NCBI Description
                   Synechocystis sp. PCC6803 complete genome, 11/27,
                   1311235-1430418
                   308966
Seq. No.
Seq. ID
                   uC-zmflmo17228a03a1
Method
                   BLASTN
NCBI GI
                   g1653836
BLAST score
                   398
E value
                   0.0e + 00
Match length
                   435
                   97
% identity
NCBI Description
                   Synechocystis sp. PCC6803 complete genome, 27/27,
                   3418852-3573470
Seq. No.
                   308967
Seq. ID,
                   uC-zmflmo17228a06a1
Method
                   BLASTN
NCBI GI
                   g1001291
BLAST score
                   101
E value
                   5.0e-50
Match length
                   141
% identity
                   94
NCBI Description
                   Synechocystis sp. PCC6803 complete genome, 25/27,
                   3138604-3270709
Seq. No.
                   308968
Seq. ID
                   uC-zmflmo17228a09a1
Method
                   BLASTX
NCBI GI
                   g2500305
BLAST score
                   494
E value
                   7.0e-50
                   101
Match length
% identity
                   99
```

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50S RIBOSOMAL PROTEIN L23 >gi 1652425 dbj BAA17347

(D90905) 50S ribosomal protein L23 [Synechocystis sp.]

```
308969
 Seq. No.
                   uC-zmflmo17228a10a1
 Seq. ID
Method
                   BLASTN
NCBI GI
                   g1653604
BLAST score
                   148
E value
                   5.0e-78
                   156
Match length
                   99
 % identity
                   Synechocystis sp. PCC6803 complete genome, 17/27,
NCBI Description
                   2137259-2267259
                   308970
 Seq. No.
                   uC-zmflmo17228a11a1
 Seq. ID
                   BLASTX
 Method
 NCBI GI
                   g2492512
 BLAST score
                    646
 E value
                    7.0e-68
 Match length
                    137
 % identity
                    96
                   CELL DIVISION PROTEIN FTSH HOMOLOG 3
 NCBI Description
                    >gi_1652556_dbj_BAA17477_ (D90906) cell division protein
                    FtsH [Synechocystis sp.]
                    308971
 Seq. No.
Seq. ID
                    uC-zmflmo17228a12a1
 Method
                    BLASTX
 NCBI GI
                    q1653852
 BLAST score
                    252
                    5.0e-22
 E value
 Match length
                    50
 % identity
                   (D90917) hypothetical protein [Synechocystis sp.]
 NCBI Description
                    308972
 Seq. No.
                    uC-zmflmo17228b03a1
 Seq. ID
                    BLASTN
 Method
 NCBI GI
                    g1651650
 BLAST score
                    421
                    0.0e + 00
 E value
                    446
 Match length
                    98
 % identity
                    Synechocystis sp. PCC6803 complete genome, 1/27, 1-133859
 NCBI Description
                    308973
 Seq. No.
```

uC-zmflmo17228b06a1 Seq. ID

BLASTN Method NCBI GI g1652225 359 BLAST score 0.0e + 00E value 363 Match length 100 % identity

Synechocystis sp. PCC6803 complete genome, 6/27, NCBI Description

630555-781448

308974 Seq. No.

uC-zmflmo17228b09a1 Seq. ID

Method BLASTX

```
NCBI GI g1652133
BLAST score 588
E value 5.0e-61
Match length 116
% identity 100
NCBI Description (D90903) regulatory components of sensory transduction system [Synechocystis sp.]
```

Seq. No. 308975
Seq. ID uC-zmflmo17228b10a1
Method BLASTN
NCDI CI

NCBI GI g1652127 BLAST score 466 E value 0.0e+00 Match length 470 % identity 100

NCBI Description Synechocystis sp. PCC6803 complete genome, 5/27,

524346-630554

Seq. No. 308976
Seq. ID uC-zmflmo17228b11a1
Method BLASTX
NCBI GI g1084176
BLAST score 265
E value 9.0e-24

E value 9.0 Match length 54 identity 93

NCBI Description glyceraldehyde-3-phosphate dehydrogenase (NADP+)

(phosphorylating) (EC 1.2.1.13) - Synechocystis sp

>gi_785046_emb_CAA60135_ (X86376)

glyceraldehyde-3-phosphate dehydrogenase (NADP+)

(phosphorylating) [Synechocystis sp.]
>gi_1653722_dbj_BAA18633_ (D90916)

glyceraldehyde-3-phosphate dehydrogenase (NADP+)

(phosphorylating) [Synechocystis sp.]

Seq. No. 308977

Seq. ID uC-zmflmo17228b12a1

Method BLASTN
NCBI GI g1001102
BLAST score 115
E value 2.0e-58
Match length 119
% identity 99

NCBI Description Synechocystis sp. PCC6803 complete genome, 20/27,

2539000-2644794

Seq. No. 308978

Seq. ID uC-zmflmo17228c03a1

Method BLASTX
NCBI GI g1006595
BLAST score 870
E value 5.0e-94
Match length 172
% identity 100

NCBI Description (D64005) DNA polymerase I [Synechocystis sp.]

```
308979
Seq. No.
Seq. ID
                  uC-zmflmo17228c10a1
Method
                  BLASTN
NCBI GI
                   g1653477
BLAST score
                   181
                   2.0e-97
E value
                   294
Match length
                   92
% identity
                  Synechocystis sp. PCC6803 complete genome, 16/27,
NCBI Description
                   1991550-2137258
                   308980
Seq. No.
                   uC-zmflmo17228c11a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1652438
BLAST score
                   601
E value
                   1.0e-62
Match length
                   110
% identity
                   100
                   (D90905) hypothetical protein [Synechocystis sp.]
NCBI Description
                   308981
Seq. No.
                   uC-zmflmo17228d02a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1001322
BLAST score
                   525
E value
                   1.0e-53
Match length
                   137
% identity
                   78
                   (D64006) NADH dehydrogenase subunit 5 [Synechocystis sp.]
NCBI Description
                   308982
Seq. No.
                   uC-zmflmo17228d03a1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g1001396
BLAST score
                   444
                   0.0e+00
E value
Match length
                   444
                   100
% identity
                   Synechocystis sp. PCC6803 complete genome, 18/27,
NCBI Description
                   2267260-2392728
                   308983
Seq. No.
                   uC-zmflmo17228d04a1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g1652956
BLAST score
                   243
E value
                   1.0e-134
Match length
                   243
% identity
                   100
NCBI Description
                   Synechocystis sp. PCC6803 complete genome, 12/27,
                   1430419-1576592
                   308984
Seq. No.
```

Seq. ID

uC-zmflmo17228d07a1

Method NCBI GI BLASTN g1652225

E value

Match length

6.0e-64

140

```
BLAST score
                  472
E value
                  0.0e+00
Match length
                  476
                  100
% identity
NCBI Description
                  Synechocystis sp. PCC6803 complete genome, 6/27,
                  630555-781448
                  308985
Seq. No.
                  uC-zmflmo17228d08a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2498704
BLAST score
                  485
                  7.0e-49
E value
                  92
Match length
% identity
                  100
NCBI Description
                  PUTATIVE OXPPCYCLE PROTEIN OPCA >gi 1652850 dbj BAA17768
                   (D90909) OpcA [Synechocystis sp.]
                  308986
Seq. No.
Seq. ID
                  uC-zmflmo17228d11a1
Method
                  BLASTN
NCBI GI
                  q1652844
BLAST score
                  251
E value
                  1.0e-139
Match length
                   440
                  99
% identity
NCBI Description
                  Synechocystis sp. PCC6803 complete genome, 11/27,
                  1311235-1430418
Seq. No.
                   308987
Seq. ID
                  uC-zmflmo17228e01a1
Method
                  BLASTN
NCBI GI
                   q1653604
BLAST score
                   390
E value
                   0.0e+00
Match length
                   394
% identity
                   100
                  Synechocystis sp. PCC6803 complete genome, 17/27,
NCBI Description
                   2137259-2267259
                   308988
Seq. No.
Seq. ID
                   uC-zmflmo17228e02a1
Method
                  BLASTX
NCBI GI
                   q1653153
BLAST score
                   614
                   4.0e-64
E value
Match length
                   129
                   97
% identity
                  (D90911) acriflavin resistance protein [Synechocystis sp.]
NCBI Description
Seq. No.
                   308989
Seq. ID
                  uC-zmflmo17228e05a1
Method
                  BLASTX
NCBI GI
                  q1703272
BLAST score
                   613
```



```
% identity
                  PUTATIVE METHIONINE AMINOPEPTIDASE A (MAP) (PEPTIDASE M)
NCBI Description
                  >gi 1001226 dbj BAA10466 (D64003) methionine
                  aminopeptidase [Synechocystis sp.]
                  308990
Seq. No.
Seq. ID
                  uC-zmflmo17228e06a1
Method
                  BLASTX
NCBI GI
                  q1652280
BLAST score
                  718
E value
                  3.0e-76
Match length
                  147
% identity
                  97
NCBI Description
                  (D90904) ribonuclease II [Synechocystis sp.]
Seq. No.
                  308991
Seq. ID
                  uC-zmflmo17228e09a1
Method
                  BLASTN
NCBI GI
                  q1651897
BLAST score
                  473
E value
                  0.0e + 00
Match length
                  477
% identity
                  100
NCBI Description
                  Synechocystis sp. PCC6803 complete genome, 3/27,
                  271600-402289
Seq. No.
                  308992
Seq. ID
                  uC-zmflmo17228e12a1
Method
                  BLASTX
NCBI GI
                  g1653786
BLAST score
                  638
E value
                  5.0e-67
Match length
                  122
% identity
                  99
NCBI Description
                  (D90916) mannose-1-phosphate quanyltransferase
                  [Synechocystis sp.]
                  308993
Seq. No.
Seq. ID
                  uC-zmflmo17228f01a1
                  BLASTX
Method
                  g2506756
NCBI GI
BLAST score
                  716
                  5.0e-76
E value
Match length
                  138
                  99
% identity
NCBI Description
                  HYPOTHETICAL 34.8 KD PROTEIN SLL0191 (ORF60-3)
                  >gi 1001611 dbj BAA10239 (D64000) hypothetical protein
                  [Synechocystis sp.]
Seq. No.
                  308994
Seq. ID
                  uC-zmflmo17228f04a1
Method
                  BLASTN
```

Method BLASTN
NCBI GI g1001200
BLAST score 431
E value 0.0e+00
Match length 447
% identity 99



NCBI Description Synechocystis sp. PCC6803 complete genome, 22/27, 2755703-2868766 308995 Seq. No. Seq. ID uC-zmflmo17228f07a1 Method BLASTX NCBI GI g1652945 BLAST score 625 E value 2.0e-65 122 Match length % identity NCBI Description (D90909) water channel protein [Synechocystis sp.] 308996 Seq. No. uC-zmflmo17228g05a1 Seq. ID Method BLASTN NCBI GI g1653083 BLAST score 119 7.0e-61 E value 119 Match length 100 % identity NCBI Description Synechocystis sp. PCC6803 complete genome, 13/27, 1576593-1719643 308997 Seq. No. Seq. ID uC-zmflmo17228g08a1 Method BLASTX NCBI GI g2833460 BLAST score 282 E value 1.0e-25 Match length 56 % identity RIBOFLAVIN-SPECIFIC DEAMINASE >qi 1001153 dbj BAA10295 NCBI Description (D64001) riboflavin biosynthesis protein [Synechocystis sp.] Seq. No. 308998 Seq. ID uC-zmflmo17228g09a1 Method BLASTN NCBI GI g1651650 BLAST score 451 0.0e + 00E value 483 Match length 98 % identity Synechocystis sp. PCC6803 complete genome, 1/27, 1-133859 NCBI Description 308999 Seq. No. uC-zmflmo17228g10a1 Seq. ID Method BLASTX g2497264 NCBI GI BLAST score 514 E value 2.0e-52 102 Match length 100 % identity 3-ISOPROPYLMALATE DEHYDROGENASE (BETA-IPM DEHYDROGENASE) NCBI Description (IMDH) (3-IPM-DH) >gi 1653112 dbj BAA18028 (D90911)

3-isopropylmalate dehydrogenase [Synechocystis sp.]

```
309000
Seq. No.
Seq. ID
                  uC-zmflmo17228g11a1
Method
                  BLASTX
NCBI GI
                  g2494263
BLAST score
                  775
                  7.0e-83
E value
Match length
                  153
% identity
                  99
NCBI Description
                  PEPTIDE CHAIN RELEASE FACTOR 3 (RF-3)
                  >gi 1652592 dbj BAA17513 (D90906) peptide-chain-release
                  factor 3 [Synechocystis sp.]
                  309001
Seq. No.
Seq. ID
                  uC-zmflmo17228h01a1
Method
                  BLASTN
NCBI GI
                  g1001200
BLAST score
                  172
E value
                   6.0e-92
Match length
                  326
% identity
                  98
                  Synechocystis sp. PCC6803 complete genome, 22/27,
NCBI Description
                  2755703-2868766
                  309002
Seq. No.
Seq. ID
                  uC-zmflmo17228h04a1
Method
                  BLASTX
NCBI GI
                  g1001827
BLAST score
                  731
E value
                  1.0e-77
Match length
                  160
% identity
                  89
                  (D64005) sensory transduction histidine kinase
NCBI Description
                   [Synechocystis sp.]
                  309003
Seq. No.
                  uC-zmflmo17228h06a1
Seq. ID
Method
                  BLASTN
                  g1001102
NCBI GI
BLAST score
                   407
E value
                  0.0e+00
Match length
                   407
                   100
% identity
                  Synechocystis sp. PCC6803 complete genome, 20/27,
NCBI Description
                  2539000-2644794
                   309004
Seq. No.
                  uC-zmflmo17228h11a1
Seq. ID
Method
                  BLASTN
NCBI GI
                   g1653477
BLAST score
                   445
E value
                  0.0e + 00
Match length
                   445
```

43953

Synechocystis sp. PCC6803 complete genome, 16/27,

100

1991550-2137258

% identity NCBI Description

Seq. ID Method

```
309005
Seq. No.
Seq. ID
                   uC-zmflmo17229a01b1
Method
                   BLASTN
NCBI GI
                   g1001701
BLAST score
                   335
E value
                   0.0e + 00
Match length
                   351
% identity
                   99
                   Synechocystis sp. PCC6803 complete genome, 23/27,
NCBI Description
                   2868767-3002965
                   309006
Seq. No.
Seq. ID
                   uC-zmflmo17229a04b1
Method
                   BLASTN
                   g1653715
NCBI GI
BLAST score
                   168
                   8.0e<sup>2</sup>90
E value
                   172
Match length
% identity
                   99
NCBI Description
                  Synechocystis sp. PCC6803 complete genome, 26/27,
                   3270710-3418851
Seq. No.
                   309007
Seq. ID
                   uC-zmflmo17229a06b1
Method
                   BLASTX
NCBI GI
                   g2494041
BLAST score
                   591
E value
                   3.0e-61
Match length
                   137
                   82
% identity
NCBI Description
                  DIAMINOPIMELATE EPIMERASE >gi 1653875 dbj BAA18785
                   (D90917) diaminopimelate epimerase [Synechocystis sp.]
Seq. No.
                   309008
Seq. ID
                   uC-zmflmo17229a09b1
Method
                   BLASTX
NCBI GI
                   g1653629
BLAST score
                   556
E value
                   3.0e-57
Match length
                   126
% identity
                  (D90915) hypothetical protein [Synechocystis sp.]
NCBI Description
Seq. No.
                   309009
Seq. ID
                   uC-zmflmo17229a11a1
Method
                   BLASTN
NCBI GI
                   q1653836
BLAST score
                   268
                   1.0e-149
E value
Match length
                   304
                   97
% identity
                   Synechocystis sp. PCC6803 complete genome, 27/27,
NCBI Description
                   3418852-3573470
Seq. No.
                   309010
```

43954

uC-zmflmo17229a12b1

BLASTN

```
NCBI GI
                  q1652956
BLAST score
                  170
E value
                  9.0e - 91
Match length
                  250
% identity
                  92
                  Synechocystis sp. PCC6803 complete genome, 12/27,
NCBI Description
                  1430419-1576592
Seq. No.
                  309011
Seq. ID
                  uC-zmflmo17229b02b1
Method
                  BLASTN
NCBI GI
                  g1653715
BLAST score
                  58
E value
                  8.0e-24
Match length
                  261
% identity
                  81
                  Synechocystis sp. PCC6803 complete genome, 26/27,
NCBI Description
                  3270710-3418851
Seq. No.
                  309012
Seq. ID
                  uC-zmflmo17229b03b1
Method
                  BLASTX
NCBI GI
                  g2500055
BLAST score
                  596
E value
                  5.0e-62
Match length
                  124
% identity
                   98
NCBI Description
                  DNA REPAIR PROTEIN RADA HOMOLOG (DNA REPAIR PROTEIN SMS
                  HOMOLOG) >gi 1653575 dbj BAA18488 (D90914) sms protein
                   [Synechocystis sp.]
Seq. No.
                  309013
Seq. ID
                  uC-zmflmo17229b05a1
Method
                  BLASTN
NCBI GI
                  g1652027
BLAST score
                  241
E value
                  1.0e-133
Match length
                  395
% identity
                  88
NCBI Description
                  Synechocystis sp. PCC6803 complete genome, 4/27,
                  402290-524345
Seq. No.
                  309014
Seq. ID
                  uC-zmflmo17229b05b1
Method
                  BLASTN
NCBI GI
                  g1652027
BLAST score
                  335
E value
                  0.0e+00
Match length
                  479
% identity
                  93
NCBI Description
                  Synechocystis sp. PCC6803 complete genome, 4/27,
                  402290-524345
```

Seq. No.

309015

uC-zmflmo17229b06a1

Seq. ID Method

BLASTX .

NCBI GI

g1001819

E value

Match length

3.0e-46

92

```
BLAST score
                   386
E value
                  2.0e-37
Match length
                  144
% identity
                  55
NCBI Description
                  (D64005) cation efflux system protein [Synechocystis sp.]
                  309016
Seq. No.
Seq. ID
                  uC-zmflmo17229b09b1
Method
                  BLASTX
NCBI GI
                  q1653805
BLAST score
                  489
                  1.0e-49
E value
Match length
                  90
                  99
% identity
NCBI Description
                  (D90916) hypothetical protein [Synechocystis sp.]
                  309017
Seq. No.
                  uC-zmflmo17229b11b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1652614
BLAST score
                  838
E value
                  3.0e-90
Match length
                  159
% identity
                  99
NCBI Description
                  (D90906) naphthoate synthase [Synechocystis sp.]
                  309018
Seq. No.
Seq. ID
                  uC-zmflmo17229c06b1
Method
                  BLASTX
NCBI GI
                  g208131
BLAST score
                  159
                  1.0e-10
E value
                  89
Match length
                   45
% identity
NCBI Description
                  (M77169) beta-galactosidase alpha-peptide [Cloning vector]
                  >gi_3132861 (U90554) beta-galactosidase alpha peptide
                   [Shuttle vector pJIR1456] >gi 3132864 (U90555)
                  beta-galactosidase alpha peptide [Shuttle vector pJIR1457]
Seq. No.
                  309019
Seq. ID
                  uC-zmflmo17229c11b1
Method
                  BLASTN
NCBI GI
                  q1652360
BLAST score
                  258
E value
                  1.0e-143
Match length
                  291
% identity
                  97
NCBI Description
                  Synechocystis sp. PCC6803 complete genome, 7/27,
                  781449-920915
Seq. No.
                  309020
Seq. ID
                  uC-zmflmo17229d03b1
Method
                  BLASTX
NCBI GI
                  g2500435
BLAST score
                  462
```

```
% identity
                  30S RIBOSOMAL PROTEIN S10 >gi 1653406 dbj BAA18320
NCBI Description
                  (D90913) 30S ribosomal protein S10 [Synechocystis sp.]
Seq. No.
                  309021
Seq. ID
                  uC-zmflmo17229d06b1
Method
                  BLASTN
NCBI GI
                  q1652956
BLAST score
                 · 62
E value
                  2.0e-26
Match length
                  173
% identity
                  84
NCBI Description Synechocystis sp. PCC6803 complete genome, 12/27,
                  1430419-1576592
Seq. No.
                  309022
Seq. ID
                  uC-zmflmo17229d07a1
Method
                  BLASTX
NCBI GI
                  q1652323
BLAST score
                  380
E value
                  2.0e-36
Match length
                  90
% identity
                  84
                  (D90904) fibrillin [Synechocystis sp.]
NCBI Description
Seq. No.
                  309023
Seq. ID
                  uC-zmflmo17229d07b1
Method
                  BLASTX
NCBI GI
                  q1652788
BLAST score
                  914
                  5.0e-99
E value
Match length
                  196
                  93
% identity
NCBI Description
                  (D90908) phosphotransacetylase [Synechocystis sp.]
                  309024
Seq. No.
                  uC-zmflmo17229d09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1001504
BLAST score
                  425
E value
                  4.0e-42
Match length
                  84
                  99
% identity
                  (D64000) Ycf38 [Synechocystis sp.]
NCBI Description
Seq. No.
                  309025
Seq. ID
                  uC-zmflmo17229e02a1
Method
                  BLASTN
NCBI GI
                  g1001200
BLAST score
                  425
E value
                  0.0e+00
Match length
                  429
```

Seq. No. 309026

% identity

NCBI Description

100

2755703-2868766

Synechocystis sp. PCC6803 complete genome, 22/27,

NCBI GI

```
uC-zmflmo17229e02b1
Seq. ID
Method
                  BLASTN
                  g1001200
NCBI GI
BLAST score
                  420
                  0.0e + 00
E value
                  460
Match length
                  98
% identity
                  Synechocystis sp. PCC6803 complete genome, 22/27,
NCBI Description
                  2755703-2868766
                  309027
Seq. No.
                  uC-zmflmo17229e05b1
Seq. ID
                  BLASTX
Method
                  q1653066
NCBI GI
BLAST score
                  632
E value
                  2.0e-68
                  132
Match length
% identity
                  99
                  (D90910) hypothetical protein [Synechocystis sp.]
NCBI Description
Seq. No.
                   309028
                   uC-zmflmo17229e06a1
Seq. ID
Method
                  BLASTX
                   q2500783
NCBI GI
BLAST score
                   468
E value
                   8.0e-47
Match length
                   94
% identity
                   99
                  SERINE HYDROXYMETHYLTRANSFERASE (SERINE METHYLASE) (SHMT)
NCBI Description
                   >gi 1652200 dbj BAA17124 (D90903) serine
                  hydroxymethyltransferase [Synechocystis sp.]
                   309029
Seq. No.
                   uC-zmflmo17229e06b1
Seq. ID
                  BLASTX
Method
NCBI GI
                   g1001519
BLAST score
                   827
                   6.0e-89
E value
Match length
                   169
% identity
                   99
                  (D64000) hypothetical protein [Synechocystis sp.]
NCBI Description
                   309030
Seq. No.
                   uC-zmflmo17229e07a1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g1653715
BLAST score
                   437
                   0.0e+00
E value
                   441
Match length
% identity
                   100
NCBI Description
                  Synechocystis sp. PCC6803 complete genome, 26/27,
                   3270710-3418851
                   309031
Seq. No.
Seq. ID
                   uC-zmflmo17229e07b1
Method
                   BLASTX
```

43958

g3123046

BLAST score

E value Match length 468 5.0e-47



```
BLAST score
                   3.0e-89
E value
                   155
Match length
                   100
% identity
NCBI Description
                   HYPOTHETICAL 28.9 KD PROTEIN SLL0249
                   >gi 1653029 dbj BAA17946 (D90910) hypothetical protein
                   [Synechocystis sp.]
                   309032
Seq. No.
                   uC-zmflmo17229f05a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1651875
BLAST score
                   537
                   5.0e-55
E value
                   148
Match length
% identity
                   75
NCBI Description (D90900) hypothetical protein [Synechocystis sp.]
                   309033
Seq. No.
                   uC-zmflmo17229f05b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1651875
                   818
BLAST score
                   3.0e-89
E value
Match length
                   168
                   97
% identity
NCBI Description (D90900) hypothetical protein [Synechocystis sp.]
                   309034
Seq. No.
Seq. ID
                   uC-zmflmo17229f08a1
                   BLASTX
Method
NCBI GI
                   g1001494
BLAST score
                   618
E value
                   2.0e-64
Match length
                   120
                   100
% identity
                   (D64000) protein-export membrane protein SecF
NCBI Description
                   [Synechocystis sp.]
                   309035
Seq. No.
Seq. ID
                   uC-zmflmo17229f08b1
Method
                   BLASTX
NCBI GI
                   g1001494
BLAST score
                   918
                   2.0e-99
E value
Match length
                   191
% identity
                   98
NCBI Description
                   (D64000) protein-export membrane protein SecF
                   [Synechocystis sp.]
                   309036
Seq. No.
Seq. ID
                   uC-zmflmo17229f10b1
Method
                   BLASTX
                   g2493001
NCBI GI
```



```
% identity
                  CATION-TRANSPORTING ATPASE PACS >gi 1652345 dbj BAA17268
NCBI Description
                   (D90904) cation-transporting ATPase [Synechocystis sp.]
Seq. No.
                   309037
Seq. ID
                  uC-zmflmo17229f12b1
Method
                  BLASTX
NCBI GI
                   q1653480
BLAST score
                   872
E value
                   8.0e-95
Match length
                   181
                   98
% identity
                   (D90914) phosphoenolpyruvate carboxylase [Synechocystis
NCBI Description
Seq. No.
                   309038
                   uC-zmflmo17229g03b1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g1001612
BLAST score
                   227
                   1.0e-125
E value
Match length
                   242
                   99
% identity
                   Synechocystis sp. PCC6803 complete genome, 21/27,
NCBI Description
                   2644795-2755702
Seq. No.
                   309039
Seq. ID
                   uC-zmflmo17229g09b1
Method
                   BLASTN
NCBI GI
                   q1001200
BLAST score
                   331
E value
                   0.0e + 00
Match length
                   351
% identity
                   99
                   Synechocystis sp. PCC6803 complete genome, 22/27,
NCBI Description
                   2755703-2868766
                   309040
Seq. No.
Seq. ID
                   uC-zmflmo17229g12b1
Method
                   BLASTN
NCBI GI
                   q1652618
BLAST score
                   396
E value
                   0.0e + 00
Match length
                   479
% identity
                   96
                   Synechocystis sp. PCC6803 complete genome, 9/27,
NCBI Description
                   1056467-1188885
                   309041
Seq. No.
                   uC-zmflmo17229h01a1
Seq. ID
```

Method BLASTX NCBI GI g1001593 BLAST score 395 2.0e-38 E value Match length 76 % identity 97

(D64000) glucose inhibited division protein A NCBI Description



```
[Synechocystis sp.]
Seq. No.
                  309042
Seq. ID
                  uC-zmflmo17229h01b1
Method
                  BLASTX
                  g1651711
NCBI GI
BLAST score
                  822
E value
                  2.0e-88
Match length
                  163
                  97
% identity
NCBI Description
                  (D90899) hypothetical protein [Synechocystis sp.]
                  309043
Seq. No.
Seq. ID
                  uC-zmflmo17229h02b1
Method
                  BLASTN
NCBI GI
                  g1001612
BLAST score
                  399
E value
                  0.0e + 00
Match length
                  543
% identity
                  93
NCBI Description
                  Synechocystis sp. PCC6803 complete genome, 21/27,
                  2644795-2755702
Seq. No.
                  309044
Seq. ID
                  uC-zmflmo17229h03a1
Method
                  BLASTN
NCBI GI
                  g1651650
BLAST score
                  202
E value
                  1.0e-110
```

Match length 250

% identity 95

NCBI Description Synechocystis sp. PCC6803 complete genome, 1/27, 1-133859

309045 Seq. No. Seq. ID uC-zmflmo17229h03b1 Method BLASTN

NCBI GI g1651650 BLAST score 280 E value 1.0e-156 Match length 535 % identity 89

NCBI Description Synechocystis sp. PCC6803 complete genome, 1/27, 1-133859

Seq. No. 309046

Seq. ID uC-zmflmo17229h04b1

Method BLASTN NCBI GI q1653228 BLAST score 70 E value 6.0e-31 Match length 189 % identity 85

NCBI Description Synechocystis sp. PCC6803 complete genome, 14/27,

1719644-1848241

309047 Seq. No.

Seq. ID uC-zmflmo17229h06b1

Method BLASTX



```
g2493590
NCBI GI -
BLAST score
                  370
E value
                  2.0e-35
Match length
                  103
% identity
                  77
                  PROBABLE CELL DIVISION PROTEIN FTSW
NCBI Description
                  >gi 1653355 dbj BAA18269 (D90913) rod-shape-determining
                  protein [Synechocystis sp.]
Seq. No.
                  309048
                  uC-zmflmo17229h07b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1653083
BLAST score
                  138
E value
                  1.0e-71
Match length
                  310
% identity
                  86
                  Synechocystis sp. PCC6803 complete genome, 13/27,
NCBI Description
                  1576593-1719643
Seq. No.
                  309049
Seq. ID
                  uC-zmflmo17229h09b1
Method
                  BLASTX
NCBI GI
                  g1001320
BLAST score
                  289
E value
                  6.0e-26
Match length
                  70
% identity
                  79
NCBI Description
                  (D64006) nitrate transport protein NrtD [Synechocystis sp.]
                  309050
Seq. No.
                  uC-zmflmo17229h11a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1653477
BLAST score
                  244
E value
                  1.0e-135
Match length
                  349
                  92
% identity
                  Synechocystis sp. PCC6803 complete genome, 16/27,
NCBI Description
                  1991550-2137258
                  309051
Seq. No.
Seq. ID
                  uC-zmflmo17229h11b1
Method
                  BLASTN
NCBI GI
                  g1653477
BLAST score
                  313
E value
                  1.0e-176
Match length
                  432
                  93
% identity
NCBI Description
                  Synechocystis sp. PCC6803 complete genome, 16/27,
                  1991550-2137258
                  309052
```

Seq. No.

Seq. ID uC-zmflmo17230a01a1

Method BLASTN NCBI GI g1653083 BLAST score 398

```
E value
                  0.0e + 00
Match length
                  402
                  100
% identity
                  Synechocystis sp. PCC6803 complete genome, 13/27,
NCBI Description
                  1576593-1719643
                  309053
Seq. No.
                  uC-zmflmo17230a02a1
Seq. ID
Method .
                  BLASTX
                  g1651823
NCBI GI
BLAST score
                  514
                  2.0e-52
E value
                  98
Match length
                  98
% identity
                  (D90900) hypothetical protein [Synechocystis sp.]
NCBI Description
                  309054
Seq. No.
                  uC-zmflmo17230a02b1
Seq. ID
                  BLASTX
Method
                  q1651822
NCBI GI
BLAST score
                  616
                  1.0e-67
E value
Match length
                  158
% identity
                  81
                  (D90900) ABC transporter [Synechocystis sp.]
NCBI Description
                  309055
Seq. No.
                  uC-zmflmo17230a04a1
Seq. ID
                  BLASTN
Method
                  g1652027
NCBI GI
BLAST score
                  120
                  6.0e-61
E value
                  253
Match length
                  85
% identity
                  Synechocystis sp. PCC6803 complete genome, 4/27,
NCBI Description
                  402290-524345
                  309056
Seq. No.
                  uC-zmflmo17230a09a1
Seq. ID
Method
                  BLASTX
                  g2494280
NCBI GI
BLAST score
                  552
                   6.0e-57
E value
                  112
Match length
                  99
% identity
                  ELONGATION FACTOR TS (EF-TS) >gi_1653231_dbj_BAA18146_
NCBI Description
                   (D90912) elongation factor TS [Synechocystis sp.]
Seq. No.
                   309057
```

uC-zmflmo17230a09b1 Seq. ID

Method BLASTN NCBI GI g1653228 BLAST score 528 0.0e+00E value 560 Match length % identity 99

NCBI Description Synechocystis §p. PCC6803 complete genome, 14/27,

43963

....



1719644-1848241

```
309058
Seq. No.
Seq. ID
                   uC-zmflmo17230a10b1
Method
                   BLASTX
                   q3126967
NCBI GI
                   515
BLAST score
                   2.0e-52
E value
                   108
Match length
% identity
                   17
                   (AF061807) polyubiquitin [Elaeagnus umbellata]
NCBI Description
                   309059
Seq. No.
                   uC-zmflmo17230b06b1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g1652725
BLAST score
                   347
E value
                   0.0e + 00
Match length
                   386
% identity
                   98
NCBI Description
                   Synechocystis sp. PCC6803 complete genome, 10/27,
                   1188886-1311234
                   309060
Seq. No.
                   uC-zmflmo17230b08b1
Seq. ID
Method
                   BLASTX
                   g2117937
NCBI GI
BLAST score
                   403
E value
                   3.0e-39
                   123
Match length
% identity
                   68
                   UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) -
NCBI Description
                   barley >gi 1212996 emb CAA62689 (X91347) UDP-glucose
                   pyrophosphorylase [Hordeum vulgare]
Seq. No.
                   309061
                   uC-zmflmo17230c03b1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g1652618
BLAST score
                   179
                   2.0e-96
E value
Match length
                   199
                   97
% identity
                   Synechocystis sp. PCC6803 complete genome, 9/27,
NCBI Description
                   1056467-1188885
                   309062
Seq. No.
                   uC-zmflmo17230c06a1
Seq. ID
Method
                   BLASTX
                   g3122978
NCBI GI
BLAST score
                   482
E value
                   1.0e-48
Match length
                   93
                   97
% identity
                   PROBABLE TRNA
NCBI Description
```

(5-METHYLAMINOMETHYL-2-THIOURIDYLATE)-METHYLTRANSFERASE >gi 1652889 dbj BAA17807 (D90909) hypothetical protein

.~



[Synechocystis sp.]

```
309063
Seq. No.
Seq. ID
                  uC-zmflmo17230c06b1
Method
                  BLASTX
NCBI GI
                  q3123068
BLAST score
                   462
                  1.0e-46
E value
Match length
                  87
% identity
                   98
```

NCBI Description HYPOTHETICAL 50.4 KD PROTEIN SLR0863

>gi 1652888 dbj BAA17806 (D90909) hypothetical protein

[Synechocystis sp.]

Seq. No. 309064 Seq. ID uC-zmf

Seq. ID uC-zmflmo17230c07a1

Method BLASTX
NCBI GI g3915463
BLAST score 247
E value 5.0e-21
Match length 47
% identity 98

NCBI Description HYPOTHETICAL 33.1 KD PROTEIN SLR1592

>gi 1652063 dbj BAA16988 (D90902) hypothetical protein

[Synechocystis sp.]

Seq. No. 309065

Seq. ID uC-zmflmo17230c07b1

Method BLASTX
NCBI GI g3915463
BLAST score 716
E value 6.0e-76
Match length 159
% identity 85

NCBI Description HYPOTHETICAL 33.1 KD PROTEIN SLR1592

>gi_1652063_dbj_BAA16988 (D90902) hypothetical protein

[Synechocystis sp.]

Seq. No. 309066

Seq. ID uC-zmflmo17230c09b1

Method BLASTX
NCBI GI g3914388
BLAST score 485
E value 4.0e-49
Match length 92
% identity 100

NCBI Description 2,3-BISPHOSPHOGLYCERATE-INDEPENDENT PHOSPHOGLYCERATE MUTASE

(PHOSPHOGLYCEROMUTASE) (BPG-INDEPENDENT PGAM)

>gi_1653699_dbj_BAA18611_ (D90915)

2,3-bisphosphoglycerate-independent phosphoglycerate mutase

[Synechocystis sp.]

Seq. No. 309067

Seq. ID uC-zmflmo17230d03a1

Method BLASTN
NCBI GI g1652360
BLAST score 419

% identity

96

```
0.0e + 00
E value
Match length
                   419
% identity
                   100
NCBI Description
                   Synechocystis sp. PCC6803 complete genome, 7/27,
                   781449-920915
Seq. No.
                   309068
Seq. ID
                   uC-zmflmo17230d03b1
Method
                   BLASTN
NCBI GI
                   g1652360
BLAST score
                   379
E value
                   0.0e + 00
Match length
                   432
                   97
% identity
NCBI Description
                   Synechocystis sp. PCC6803 complete genome, 7/27,
                   781449-920915
Seq. No.
                   309069
Seq. ID
                   uC-zmflmo17230e06a1
Method
                   BLASTX
NCBI GI
                   g1001505
BLAST score
                   374
E value
                   2.0e-43
Match length
                   106
% identity
                   92
NCBI Description (D64000) ABC transporter [Synechocystis sp.]
Seq. No.
                   309070
Seq. ID
                   uC-zmflmo17230e06b1
Method
                   BLASTN
NCBI GI
                   q1001484
BLAST score
                   222
E value
                   1.0e-122
Match length
                   327
% identity
                   91
NCBI Description
                  Synechocystis sp. PCC6803 complete genome, 19/27,
                   2392729-2538999
Seq. No.
                   309071
Seq. ID
                   uC-zmflmo17230e07a1
Method
                   BLASTX
NCBI GI
                   g1652137
BLAST score
                   824
E value
                   1.0e-88
Match length
                   162
% identity
                   100
NCBI Description (D90903) hypothetical protein [Synechocystis sp.]
                   309072
Seq. No.
                   uC-zmflmo17230e07b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1652137
BLAST score
                   821
E value
                   3.0e-88
Match length
                   162
```

43966

NCBI Description (D90903) hypothetical protein [Synechocystis sp.]



```
309073
 Seq. No.
                   uC-zmflmo17230e08b1
 Seq. ID
Method
                   BLASTX
NCBI GI
                   q3023956
BLAST score
                   235
E value
                   1.0e-19
Match length
                   117
% identity
                   5
                   VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1 >gi 607003
NCBI Description
                   (L28125) beta transducin-like protein [Podospora anserina]
                   309074
Seq. No.
 Seq. ID
                   uC-zmflmo17230e10b1
Method
                   BLASTX
NCBI GI
                   g1001819
BLAST score
                   574
                   2.0e-59
E value
Match length
                   119
 % identity
                   98
NCBI Description
                   (D64005) cation efflux system protein [Synechocystis sp.]
                   309075
Seq. No.
                   uC-zmflmo17230e11b1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g1653604
BLAST score
                   220
E value
                   1.0e-121
Match length
                   239
% identity
                   98
NCBI Description
                   Synechocystis sp. PCC6803 complete genome, 17/27,
                   2137259-2267259
                   309076
Seq. No.
Seq. ID
                   uC-zmflmo17230f07a1
Method
                   BLASTX
NCBI GI
                   g1653666
BLAST score
                   667
E value
                   2.0e-70
Match length
                   135
% identity
                   99
NCBI Description
                   (D90915) chloride channel protein [Synechocystis sp.]
Seq. No.
                   309077
Seq. ID
                   uC-zmflmo17230f07b1
Method
                   BLASTX
NCBI GI
                   g2493811
BLAST score
                   386
E value
                   3.0e-37
Match length
                   76
% identity
                   95
NCBI Description
                   COPROPORPHYRINOGEN III OXIDASE, AEROBIC
                   (COPROPORPHYRINOGENASE) (COPROGEN OXIDASE)
```

Seq. No. 309078

oxidase [Synechocystis sp.]

>gi_1651937_dbj_BAA16863_ (D90901) coproporphyrinogen III



```
uC-zmflmo17230f09a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2500554
BLAST score
                  358
E value
                  4.0e-34
Match length
                  71
% identity
                  RIBONUCLEASE III (RNASE III) >qi 1653550 dbj BAA18463
NCBI Description
                   (D90914) ribonuclease III [Synechocystis sp.]
                  309079
Seq. No.
Seq. ID
                  uC-zmflmo17230f09b1
Method
                  BLASTN
NCBI GI
                  q1653477
BLAST score
                  420
E value
                  0.0e + 00
Match length
                  481
% identity
                  98
NCBI Description
                  Synechocystis sp. PCC6803 complete genome, 16/27,
                  1991550-2137258
Seq. No.
                  309080
Seq. ID
                  uC-zmflmo17230f12b1
Method
                  BLASTN
NCBI GI
                  g1652725
BLAST score
                  232
E value
                  1.0e-128
Match length
                  236
                  100
% identity
NCBI Description
                  Synechocystis sp. PCC6803 complete genome, 10/27,
                  1188886-1311234
Seq. No.
                  309081
                  uC-zmflmo17230g03b1
Seq. ID
Method
                  BLASTN
NCBI GI
                   g1652844
BLAST score
                  156
E value
                  1.0e-82
Match length
                  184
                  96
% identity
NCBI Description
                  Synechocystis sp. PCC6803 complete genome, 11/27,
                  1311235-1430418
                  309082
Seq. No.
                  uC-zmflmo17230g04a1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2500257
BLAST score
                  523
                  2.0e-53
E value
Match length
                  100
                  100
% identity
NCBI Description
                  50S RIBOSOMAL PROTEIN L13 >gi 1652400 dbj BAA17322
```

NCBI Description 50S RIBOSOMAL PROTEIN L13 >gi_1652400_dbj_BAA17322_ (D90905) 50S ribosomal protein L13 [Synechocystis sp.]

Seq. No. 309083

Seq. ID uC-zmflmo17230g04b1

Method BLASTX

Match length

73

```
g2500426
NCBI GI
BLAST score
                  546
E value
                  6.0e-56
Match length
                  109
% identity
                  99
                  30S RIBOSOMAL PROTEIN S9 >gi 1652399 dbj BAA17321 (D90905)
NCBI Description
                  30S ribosomal protein S9 [Synechocystis sp.]
Seq. No.
                  309084
Seq. ID
                  uC-zmflmo17230g07a1
Method
                  BLASTX
NCBI GI
                  g1652111
BLAST score
                  539
E value
                  3.0e-55
Match length
                  106
% identity
                  98
NCBI Description
                  (D90902) enoyl-[acyl-carrier-protein] reductase
                  [Synechocystis sp.]
                  309085
Seq. No.
                  uC-zmflmo17230g07b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q1652027
BLAST score
                  363
                  0.0e + 00
E value
                  433
Match length
% identity
                  96
NCBI Description Synechocystis sp. PCC6803 complete genome, 4/27,
                  402290-524345
Seq. No.
                  309086
Seq. ID
                  uC-zmflmo17230q08b1
Method
                  BLASTX
NCBI GI
                  q1652463
BLAST score
                  344
E value
                  5.0e-33
Match length
                  73
% identity
                  93
NCBI Description (D90905) serine protease HtrA [Synechocystis sp.]
Seq. No.
                  309087
                  uC-zmflmo17230g09b1
Seq. ID
Method
                  BLASTX
                  q1653367
NCBI GI
BLAST score
                  354
                  1.0e-33
E value
Match length
                  77
% identity
                  92
NCBI Description (D90913) hypothetical protein [Synechocystis sp.]
                  309088
Seq. No.
                  uC-zmflmo17230h05b1
Seq. ID
Method
                  BLASTX
                  g1652587
NCBI GI
BLAST score
                  370
E value
                  6.0e-36
```



% identity NCBI Description (D90906) cytoplasmic membrane protein for maltose uptake [Synechocystis sp.] 309089 Seq. No. Seq. ID uC-zmflmo17230h08a1 Method BLASTN NCBI GI g1653228 BLAST score 429 E value 0.0e+00 Match length 433 % identity 100 NCBI Description Synechocystis sp. PCC6803 complete genome, 14/27, 1719644-1848241 309090 Seq. No. Seq. ID uC-zmflmo17230h08b1 Method BLASTN NCBI GI q1001701 BLAST score 353 E value 0.0e+00 Match length 428 % identity 94 NCBI Description Synechocystis sp. PCC6803 complete genome, 23/27, 2868767-3002965 309091 Seq. No. Seq. ID uC-zmflmo17230h10b1 Method BLASTN g1001102 NCBI GI BLAST score 171 E value 1.0e-91 Match length 179 % identity 99 NCBI Description Synechocystis sp. PCC6803 complete genome, 20/27, 2539000-2644794 Seq. No. 309092 Seq. ID uC-zmflmo17231a04a1 Method BLASTX NCBI GI q2501028 BLAST score 370 E value 5.0e-36 Match length 75 % identity 99 NCBI Description LEUCYL-TRNA SYNTHETASE (LEUCINE--TRNA LIGASE) (LEURS) >gi_1652380_dbj_BAA17302_ (D90905) leucyl-tRNA synthetase [Synechocystis sp.]

Seq. No. 309093

Seq. ID uC-zmflmo17231a05a1

Method BLASTN NCBI GI g1651768 BLAST score 221 E value 1.0e-121 Match length 261 % identity 97

Seq. No.

Seq. ID

309099

uC-zmflmo17231b06a1



```
NCBI Description
                  Synechocystis sp. PCC6803 complete genome, 2/27,
                   133860-271599
Seq. No.
                   309094
Seq. ID
                   uC-zmflmo17231a06a1
Method
                   BLASTX
NCBI GI
                   q1651923
BLAST score
                   388
E value
                   7.0e-38
Match length
                   97
% identity
                   85
NCBI Description
                  (D90901) UDP-glucose dehydrogenase [Synechocystis sp.]
Seq. No.
                   309095
Seq. ID
                   uC-zmflmo17231a08a1
Method
                   BLASTN
NCBI GI
                   g1001612
BLAST score
                   374
E value
                   0.0e + 00
Match length
                   374
% identity
                   100
NCBI Description
                  Synechocystis sp. PCC6803 complete genome, 21/27,
                   2644795-2755702
Seq. No.
                   309096
Seq. ID
                   uC-zmflmo17231b01a1
Method
                   BLASTX
NCBI GI
                   g1001742
BLAST score
                   554
E value
                   4.0e-57
Match length
                  123
% identity
                  88
NCBI Description
                  (D64004) hypothetical protein [Synechocystis sp.]
Seq. No.
                  309097
Seq. ID
                  uC-zmflmo17231b03a1
Method
                  BLASTX
                   g1653948
NCBI GI
BLAST score
                   398
E value
                   4.0e-39
Match length
                  84
% identity
                  99
NCBI Description
                  (D90917) hypothetical protein [Synechocystis sp.]
                  309098
Seq. No.
Seq. ID
                  uC-zmflmo17231b05a1
Method
                  BLASTN
NCBI GI
                  g1001612
BLAST score
                  217
E value
                  1.0e-119
Match length
                  341
% identity
                  96
NCBI Description
                  Synechocystis sp. PCC6803 complete genome, 21/27,
                  2644795-2755702
```

Seq. ID

NCBI GI

Method

```
Method
                   BLASTN
NCBI GI
                   g1652956
BLAST score
                   283
E value
                   1.0e-158
Match length
                   388
% identity
                   93
NCBI Description
                  Synechocystis sp. PCC6803 complete genome, 12/27,
                   1430419-1576592
                   309100
Seq. No.
Seq. ID
                   uC-zmflmo17231b08a1
Method
                  BLASTN
NCBI GI
                   g1652027
BLAST score
                   403
E value
                   0.0e+00
Match length
                   411
% identity
                   100
NCBI Description
                  Synechocystis sp. PCC6803 complete genome, 4/27,
                   402290-524345
Seq. No.
                   309101
Seq. ID
                  uC-zmflmo17231b09a1
Method
                  BLASTN
NCBI GI
                   q1001200
BLAST score
                   407
E value
                   0.0e + 00
Match length
                   434
% identity
                   99
NCBI Description
                  Synechocystis sp. PCC6803 complete genome, 22/27,
                  2755703-2868766
Seq. No.
                  309102
Seq. ID
                  uC-zmflmo17231b12a1
Method
                  BLASTX
NCBI GI
                  q1653810
BLAST score
                  513
E value
                  3.0e-52
Match length
                  98
% identity
                  100
NCBI Description
                  (D90916) hypothetical protein [Synechocystis sp.]
                  309103
Seq. No.
Seq. ID
                  uC-zmflmo17231c04a1
Method
                  BLASTX
NCBI GI
                  q2500722
BLAST score
                  481
                  3.0e-60
E value
Match length
                  125
% identity
                  98
                  PREPROTEIN TRANSLOCASE SECA SUBUNIT
NCBI Description
                  >gi_1001616_dbj BAA10347 (D64002) preprotein translocase
                  SecA subunit [Synechocystis sp.]
Seq. No.
                  309104
```

43972

uC-zmflmo17231c05a1

BLASTX

g1653960

BLAST score

E value

729

2.0e-77



```
BLAST score
                  532
E value
                  4.0e-75
Match length
                  155
% identity
                  88
NCBI Description
                  (D90917) DNA polymerase III alpha subunit [Synechocystis
                  309105
Seq. No.
Seq. ID
                  uC-zmflmo17231c06a1
Method
                  BLASTN
NCBI GI
                  g1652956
BLAST score
                  369
E value
                  0.0e+00
Match length
                  398
% identity
                  98
NCBI Description
                  Synechocystis sp. PCC6803 complete genome, 12/27,
                  1430419-1576592
Seq. No.
                  309106
Seq. ID
                  uC-zmflmo17231c12a1
Method
                  BLASTX
NCBI GI
                  q1653170
BLAST score
                  778
E value
                  3.0e-83
Match length
                  152
% identity
                  100
NCBI Description
                  (D90911) sensory transduction histidine kinase
                  [Synechocystis sp.]
                  309107
Seq. No.
Seq. ID
                  uC-zmflmo17231d01a1
Method
                  BLASTN
NCBI GI
                  q1652844
BLAST score
                  337
E value
                  0.0e+00
Match length
                  366
% identity
                  98
NCBI Description
                  Synechocystis sp. PCC6803 complete genome, 11/27,
                  1311235-1430418
Seq. No.
                  309108
Seq. ID
                  uC-zmflmo17231d02a1
Method
                  BLASTN
NCBI GI
                  q1652027
BLAST score
                  312
                  1.0e-175
E value
Match length
                  328
% identity
                  99
NCBI Description
                 Synechocystis sp. PCC6803 complete genome, 4/27,
                  402290-524345
                  309109
Seq. No.
Seq. ID
                  uC-zmflmo17231d03a1
Method
                  BLASTX
NCBI GI
                  g1652763
```



Match length 140 % identity 100

NCBI Description (D90908) 5-oxo-1,2,5-tricarboxilic-3-penten acid

decarboxilase/isomer [Synechocystis sp.]

Seq. No. 309110

Seq. ID uC-zmflmo17231d04a1

Method BLASTN
NCBI GI g1001396
BLAST score 281
E value 1.0e-157
Match length 296
% identity 99

NCBI Description Synechocystis sp. PCC6803 complete genome, 18/27,

2267260-2392728

Seq. No. 309111

Seq. ID uC-zmflmo17231d05a1

Method BLASTX
NCBI GI g1237023
BLAST score 305
E value 4.0e-28
Match length 91
% identity 78

NCBI Description (D13960) virginiamycin acetyltransferase [Synechocystis

sp.] >gi_1653264_dbj_BAA18179_ (D90912) acetyltransferase

[Synechocystis sp.]

Seq. No. 309112

Seq. ID uC-zmflmo17231d06a1

Method BLASTN
NCBI GI g1651768
BLAST score 333
E value 0.0e+00
Match length 385
% identity 98

NCBI Description Synechocystis sp. PCC6803 complete genome, 2/27,

133860-271599

Seq. No. 309113

Seq. ID uC-zmflmo17231d09a1

Method BLASTX
NCBI GI g1001111
BLAST score 280
E value 6.0e-25
Match length 76
% identity 76

NCBI Description (D64001) hypothetical protein [Synechocystis sp.]

Seq. No. 309114

Seq. ID uC-zmflmo17231d11a1

Method BLASTN
NCBI GI g1652956
BLAST score 365
E value 0.0e+00
Match length 365
% identity 100

```
NCBI Description
                   Synechocystis sp. PCC6803 complete genome, 12/27,
                   1430419-1576592
                   309115
Seq. No.
Seq. ID
                   uC-zmflmo17231e02a1
Method
                   BLASTN
NCBI GI
                   g1653836
BLAST score
                   335
E value
                   0.0e + 00
Match length
                   368
% identity
                   97
NCBI Description
                   Synechocystis sp. PCC6803 complete genome, 27/27,
                   3418852-3573470
Seq. No.
                   309116
Seq. ID
                   uC-zmflmo17231e04a1
Method
                   BLASTX
NCBI GI
                   g2499001
BLAST score
                   461
E value
                   3.0e-46
Match length
                   90
% identity
                   100
NCBI Description
                  PROBABLE THIAMIN-PHOSPHATE PYROPHOSPHORYLASE (TMP
                   PYROPHOSPHORYLASE) (TMP-PPASE) (THIAMIN-PHOSPHATE SYNTHASE)
                   >gi 1652058_dbj BAA16983_ (D90902) thiamin biosynthetic
                   bifunctional enzyme [Synechocystis sp.]
Seq. No.
                   309117
Seq. ID
                   uC-zmflmo17231e05a1
Method
                   BLASTX
NCBI GI
                   g1652106
BLAST score
                   577
E value
                   7.0e-60
Match length
                  117
% identity
                   97
NCBI Description (D90902) PleD [Synechocystis sp.]
Seq. No.
                  309118
Seq. ID
                  uC-zmflmo17231e09a1
Method
                  BLASTN
NCBI GI
                   g1001484
BLAST score
                  245
E value
                  1.0e-135
Match length
                  257
                  99
% identity
NCBI Description
                  Synechocystis sp. PCC6803 complete genome, 19/27,
                  2392729-2538999
Seq. No.
                  309119
Seq. ID
                  uC-zmflmo17231f01a1
Method
                  BLASTN
NCBI GI
                  g1652956
BLAST score
                  242
E value
                  1.0e-134
Match length
                  254
% identity
                  99
```

43975

NCBI Description Synechocystis sp. PCC6803 complete genome, 12/27,



1430419-1576592

```
Seq. No.
                     309120
   Seq. ID
                     uC-zmflmo17231f03a1
   Method
                     BLASTX
   NCBI GI
                     q2498449
   BLAST score
                     628
   E value
                     9.0e-66
  Match length
                     127
   % identity
                     99
   NCBI Description
                     PHOSPHORIBOSYLFORMIMINO-5-AMINOIMIDAZOLE CARBOXAMIDE
                     RIBOTIDE ISOMERASE >gi 1653757 dbj BAA18668 (D90916)
                     phosphorybosilformimino-5-amino-
                     phosphorybosil-4-imidazolecarboxamideisomerase
                     [Synechocystis sp.]
Seq. No.
                     309121
   Seq. ID
                     uC-zmflmo17231f06a1
  Method
                     BLASTN
  NCBI GI
                     q1652844
  BLAST score
                     349
  E value
                     0.0e + 00
  Match length
                     353
   % identity
                     100
   NCBI Description
                     Synechocystis sp. PCC6803 complete genome, 11/27,
                     1311235-1430418
   Seq. No.
                     309122
   Seq. ID
                     uC-zmflmo17231f10a1
  Method
                     BLASTN
  NCBI GI
                     g1653083
  BLAST score
                     359
  E value
                     0.0e + 00
  Match length
                     363
   % identity
                     100
  NCBI Description
                     Synechocystis sp. PCC6803 complete genome, 13/27,
                     1576593-1719643
   Seq. No.
                     309123
   Seq. ID
                     uC-zmflmo17231f11a1
  Method
                     BLASTX
  NCBI GI
                     g1652471
  BLAST score
                     695
  E value
                     1.0e-73
  Match length
                     133
   % identity
                     100
  NCBI Description (D90905) CobN protein [Synechocystis sp.]
  Seq. No.
                     309124
  Seq. ID
                     uC-zmflmo17231g04a1
  Method
                     BLASTX
  NCBI GI
                     g1171075
  BLAST score
                     744
```

43976

3.0e-79

NCBI Description UDP-N-ACETYLMURAMOYLALANYL-D-GLUTAMYL-2,

146

99

E value Match length

% identity

Seq. ID

Method

NCBI GI

E value

Seq. No.

Seq. ID

Method

NCBI GI

E value

Seq. No.

Seq. ID

Method

NCBI GI

E value

BLAST score

Match length

% identity

BLAST score

Match length

% identity

BLAST score

Match length

% identity



```
6-DIAMINOPIMELATE--D-ALANYL-D-ALANYL LIGASE
                   (UDP-MURNAC-PENTAPEPTIDE SYNTHETASE)
                   (D-ALANYL-D-ALANINE-ADDING ENZYME) >gi 1084179 pir S49610
                  UDP-N-acetylmuramoylalanyl-D-glutamyl-\overline{2},
                  6-diaminopimelate--D-alanyl-D-alanine ligase (EC 6.3.2.15)
                  - Synechocystis sp. (PCC 6803) >gi 575416 emb CAA44303
                   (X62437) UDP-N-acetylmuramoylalanyl-D-glutamyl-2,
                  6-diaminopimelate--D-alanyl-D-alanine ligase [Synechocystis
                  sp.]
                  309125
                  uC-zmflmo17231g05a1
                  BLASTX
                  g2492985
                  651
                  2.0e-68
                  132
                  98
NCBI Description
                  GLUTAMATE RACEMASE >gi 1652867 dbj BAA17785 (D90909)
                  glutamate racemase [Synechocystis sp.]
                  309126
                  uC-zmflmo17231g08a1
                  BLASTX
                  g1707936
                  633
                  2.0e-66
                  116
                  99
NCBI Description
                  1,4-ALPHA-GLUCAN BRANCHING ENZYME (GLYCOGEN BRANCHING
                  ENZYME) >gi_1001448_dbj_BAA10073_ (D63999) 1,4-alpha-glucan
                  branching enzyme [Synechocystis sp.]
                  309127
                  uC-zmflmo17231g11a1
                  BLASTX
                  g1653541
                  642
                  3.0e-67
                  124
                  100
NCBI Description
                  (D90914) hypothetical protein [Synechocystis sp.]
                  309128
                  uC-zmflmo17231g12a1
                  BLASTX
```

Seq. No.

Seq. ID

Method NCBI GI g1652952 BLAST score 655 E value 6.0e-69 Match length 125

% identity 99 NCBI Description

(D90909) transposase [Synechocystis sp.]

Seq. No. 309129

Seq. ID uC-zmflmo17231h02a1

Method BLASTN NCBI GI g1653604

```
BLAST score
                  288
                  1.0e-161
E value
Match length
                  313
% identity
                  97
NCBI Description
                  Synechocystis sp. PCC6803 complete genome, 17/27,
                  2137259-2267259
                  309130
Seq. No.
                  uC-zmflmo17231h05a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1001291
BLAST score
                   407
E value
                  0.0e+00
Match length
                   435
% identity
                  98
NCBI Description
                  Synechocystis sp. PCC6803 complete genome, 25/27,
                  3138604-3270709
Seq. No.
                  309131
Seq. ID
                  uC-zmflmo17231h07a1
Method
                  BLASTN
NCBI GI
                  q1653604
BLAST score
                  81
E value
                  3.0e-38
Match length
                  117
% identity
                  92
NCBI Description
                  Synechocystis sp. PCC6803 complete genome, 17/27,
                  2137259-2267259
Seq. No.
                  309132
Seq. ID
                  uC-zmflmo17231h09a1
Method
                  BLASTX
NCBI GI
                  g1001656
BLAST score
                   420
E value
                  2.0e-41
Match length
                  94
% identity
                  87
NCBI Description
                  (D64002) mannosyl transferase [Synechocystis sp.]
Seq. No.
                  309133
                  uC-zmflmo17231h10a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1001469
BLAST score
                  309
E value
                  3.0e-29
Match length
                  105
% identity
                  74
NCBI Description
                  (D63999) cell division cycle protein [Synechocystis sp.]
Seq. No.
                  309134
Seq. ID
                  uC-zmflmo17231h11a1
Method
                  BLASTX
NCBI GI
                  g1653247
BLAST score
                  737
E value
                  4.0e-86
Match length
                  149
% identity
                  43
```

Method

NCBI GI

BLASTX

g2995384



```
NCBI Description
                  (D90912) hypothetical protein [Synechocystis sp.]
                  309135
Seq. No.
                  uC-zmflmo17231h12a1
Seq. ID
                  BLASTN
Method
NCBI GI
                  q1651650
BLAST score
                  365
                  0.0e + 00
E value
                   476
Match length
% identity
                  99
                  Synechocystis sp. PCC6803 complete genome, 1/27, 1-133859
NCBI Description
                  309136
Seq. No.
                  uC-zmflmo17233d12a1
Seq. ID
Method
                  BLASTN
                   g902583
NCBI GI
BLAST score
                   102
                   2.0e-50
E value
                  216
Match length
% identity
                  86
                  Zea mays clone MubG1 ubiquitin gene, complete cds
NCBI Description
                   309137
Seq. No.
                  uC-zmflmo17234e05a1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3264611
BLAST score
                   218
                   9.0e-18
E value
Match length
                   42
                   98
% identity
                  (AF061511) seven in absentia homolog [Zea mays]
NCBI Description
                   309138
Seq. No.
                   uC-zmflmo17235b08b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1899060
BLAST score
                   237
                   7.0e-25
E value
Match length
                   96
% identity
                   64
NCBI Description
                  (U79669) endosperm C-24 sterol methyltransferase [Zea mays]
                   309139
Seq. No.
                   uC-zmflmo17235b12b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4504909
BLAST score
                   293
                   2.0e-26
E value
                   129
Match length
                   47
% identity
NCBI Description
                  karyopherin (importin) beta 3 >gi_2102696 (U72761)
                   karyopherin beta 3 [Homo sapiens]
                   309140
Seq. No.
                   uC-zmflmo17235c07b1
Seq. ID
```

```
BLAST score
E value
                  2.0e-14
Match length
                  57
% identity
                  72
NCBI Description
                 (AJ004810) cytochrome P450 monooxygenase [Zea mays]
                  309141
Seq. No.
                  uC-zmflmo17235d09b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3123270
BLAST score
                  327
                  2.0e-30
E value
Match length
                  82
% identity
                  80
NCBI Description
                  40S RIBOSOMAL PROTEIN S4 (SCAR PROTEIN SS620)
                  >gi 2463335 emb CAA75242 (Y15009) ribosomal protein S4
                  [Oryza sativa]
                  309142
Seq. No.
Seq. ID
                  uC-zmflmo17235g07b1
Method
                  BLASTX
NCBI GI
                  g2499708
BLAST score
                  301
E value
                  3.0e-27
Match length
                  119
% identity
                  63
NCBI Description
                  PHOSPHOLIPASE D PRECURSOR (PLD) (CHOLINE PHOSPHATASE)
                  (PHOSPHATIDYLCHOLINE-HYDROLYZING PHOSPHOLIPASE D)
                  >gi 1020409 dbj BAA11135 (D73410) phospholipase D [Zea
                  mays]
                  309143
Seq. No.
Seq. ID
                  uC-zmflmo17236a07b1
Method
                  BLASTX
NCBI GI
                  g3341693
BLAST score
                  238
E value
                  7.0e-20
Match length
                  104
% identity
                  53
NCBI Description
                  (AC003672) unknown protein [Arabidopsis thaliana]
Seq. No.
                  309144
Seq. ID
                  uC-zmflmo17236c11b1
Method
                  BLASTN
NCBI GI
                  g22292
BLAST score
                  82
E value
                  3.0e-38
Match length
                  300
% identity
                  82
NCBI Description Z.mays mRNA for glycine-rich protein
```

Seq. ID uC-zmflmo17236d01b1

Method BLASTN
NCBI GI g311238
BLAST score 46
E value 1.0e-16



Match length % identity 88

NCBI Description Z.mays cat1 gene for catalase

309146 Seq. No.

uC-zmflmo17236f05b1 Seq. ID

Method BLASTX NCBI GI g4510345 BLAST score 181 E value 3.0e-13 Match length 116 % identity 37

NCBI Description (AC006921) unknown protein [Arabidopsis thaliana]

Seq. No. 309147

Seq. ID uC-zmflmo17236g02a1

Method BLASTX NCBI GI g2499708 BLAST score 148 1.0e-09 E value Match length 40 75 % identity

NCBI Description PHOSPHOLIPASE D PRECURSOR (PLD) (CHOLINE PHOSPHATASE)

(PHOSPHATIDYLCHOLINE-HYDROLYZING PHOSPHOLIPASE D)

>gi_1020409 dbj BAA11135 (D73410) phospholipase D [Zea

mays]

Seq. No. 309148

Seq. ID uC-zmflmo17236g02b1

Method BLASTX NCBI GI q417154 BLAST score 576 E value 1.0e-59 Match length 127 % identity 93

NCBI Description HEAT SHOCK PROTEIN 82 >gi_100685_pir__S25541 heat shock

protein 82 - rice (strain Taichung Native One)

>gi_20256_emb_CAA77978_ (Z11920) heat shock protein 82

(HSP82) [Oryza sativa]

Seq. No. 309149

Seq. ID uC-zmflmo17238a03b1

Method BLASTX NCBI GI g2564249 BLAST score 590 E value 4.0e-61 Match length 180 % identity 59

(Y08686) serine palmitoyltransferase, subunit II [Homo NCBI Description

sapiens] >gi_3043576_dbj_BAA25452_ (AB011098) KIAA0526 protein [Homo sapiens] >gi_4186182 (AF111168) serine palmitoyl transferase, subunit II [Homo sapiens]

Seq. No. 309150

Seq. ID uC-zmflmo17238c05b1

Method BLASTX NCBI GI g3688173

BLAST score 182 1.0e-13 E value Match length 58 % identity 62

NCBI Description (AL031804) putative protein [Arabidopsis thaliana]

Seq. No.

309151

Seq. ID

uC-zmflmo17238c07b1

BLASTX Method NCBI GI g542596 BLAST score 189 E value 4.0e-14 Match length 58 % identity 64

NCBI Description

Tid(56) protein - fruit fly (Drosophila melanogaster) >gi 456627 emb CAA54837 (X77822) Tid(56) [Drosophila

melanogaster] >qi 1487972 emb CAA64528 (X95241)

lethal(2)tumorous imaginal discs [Drosophila melanogaster]

>gi 4007007 emb CAA66720_ (X98094) lethal(2)tumorous

imaginal discs [Drosophila melanogaster]

309152 Seq. No.

Seq. ID uC-zmflmo17238e10b1

Method BLASTX NCBI GI q115771 BLAST score 656 7.0e-69 E value Match length 148 % identity 85

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-1) (LHCP) >gi 82682 pir S04453 chlorophyll

a/b-binding protein precursor - maize

>gi 22224 emb CAA32900 (X14794) chlorophyll a/b-binding

preprotein (AA 1 - 262) [Zea mays]

Seq. No. 309153

Seq. ID uC-zmflmo17238f01b1

Method BLASTX NCBI GI g3157951 BLAST score 411 E value 3.0e-40Match length 88 91 % identity

NCBI Description (AC002131) Contains similarity to vesicle trafficking

protein gb U91538 from Mus musculus. ESTs gb F15494 and gb F14097 come from this gene. [Arabidopsis thaliana]

Seq. No. 309154

Seq. ID uC-zmflmo17238f05a1

Method BLASTX NCBI GI g3880399 BLAST score 170 5.0e-12 E value Match length 76 % identity 43

NCBI Description (Z71267) predicted using Genefinder; cDNA EST yk275h2.3

comes from this gene; cDNA EST yk309g11.3 comes from this



gene; cDNA EST yk309g11.5 comes from this gene; cDNA EST yk275h2.5 comes from this gene [Caenorhabditis elegans]

Seq. No. 309155

Seq. ID uC-zmflmo17238g02a1

Method BLASTX
NCBI GI g2911886
BLAST score 163
E value 2.0e-12
Match length 57

% identity 58

NCBI Description (AF047663) contains similarity to signal recognition particle subunit 54 (SRP54)-type domains (Pfam; SRP54, score; 71.31); partial CDS [Caenorhabditis elegans]

309156

Method BLASTN
NCBI GI g4185305
BLAST score 110
E value 4.0e-55
Match length 186

% identity 90

NCBI Description Zea mays cosmid IV.1E1 22-kDa alpha zein protein 21

(sz22-21) gene, complete cds; retrotransposon Opie-2 gag protein, polyprotein, and copia protein genes, complete

cds; and unknown genes

Seq. No. 309157

Seq. ID uC-zmflmo17240a04b1

Method BLASTN
NCBI GI g1839588
BLAST score 61
E value 1.0e-25
Match length 116
% identity 88

NCBI Description PRm 3=chitinase {clone CHEM 5} [Zea mays=maize, cv. INRA

258, mercuric chloride-treated, leaves, mRNA Partial, 945

nt]

Seq. No. 309158

Seq. ID uC-zmflmo17240a05b1

Method BLASTN
NCBI GI g2641618
BLAST score 59
E value 1.0e-24
Match length 146
% identity 87

NCBI Description Zea mays ubiquitin-conjugating enzyme protein E2 (ubc7)

mRNA, complete cds

Seq. No. 309159

Seq. ID uC-zmflmo17240a12b1

Method BLASTX
NCBI GI g1352830
BLAST score 162
E value 5.0e-13



Match length 99 % identity 55

NCBI Description VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A (V-ATPASE 69 KD

SUBUNIT) >gi 1049253 (U36436) vacuolar ATPase 69 kDa

subunit [Zea mays]

Seq. No. 309160

Seq. ID uC-zmflmo17240b06b1

Method BLASTN
NCBI GI g2370460
BLAST score 62
E value 3.0e-26
Match length 166
% identity 86

NCBI Description Sorghum bicolor mRNA for putative glycoprotein

Seq. No.

Seq. ID uC-zmflmo17240b07b1

309161

Method BLASTX
NCBI GI g498643
BLAST score 547
E value 4.0e-56
Match length 143
% identity 80

NCBI Description (U10270) G-box binding factor 1 [Zea mays]

Seq. No. 309162

Seq. ID uC-zmflmo17240d07b1

Method BLASTX
NCBI GI g4559351
BLAST score 268
E value 2.0e-23
Match length 163
% identity 35

NCBI Description (AC006585) hypothetical protein [Arabidopsis thaliana]

Seq. No. 309163

Seq. ID uC-zmflmo17240f01b1

Method BLASTX
NCBI GI g112994
BLAST score 318
E value 4.0e-31
Match length 81
% identity 93

NCBI Description GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN

>gi_82685_pir__S04536 embryonic abundant protein,
glycine-rich - maize >gi 22313 emb CAA31077 (X12564)

ABA-inducible gene protein [Zea mays]

>gi_226091_prf__1410284A abscisic acid inducible gene [Zea

mays]

Seq. No. 309164

Seq. ID uC-zmflmo17240f08b1

Method BLASTX NCBI GI g2281705 BLAST score 290 E value 5.0e-26

```
Match length
                  151
                  43
% identity
NCBI Description
                  (AF013979) ethylene responsive factor [Oryza sativa]
                  309165
Seq. No.
                  uC-zmflmo17240f09a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4160401
BLAST score
                  222
E value
                  1.0e-121
Match length
                  310
% identity
                  93
NCBI Description
                  Zea mays eIF-5 gene, exons 1-2
```

Seq. No. 309166 Seq. ID uC-zmflmo17240g03b1

Method BLASTX
NCBI GI g3258569
BLAST score 217
E value 2.0e-17
Match length 108
% identity 46

NCBI Description (U89959) Similar to yeast general negative regulator of

transcription subunit 1 [Arabidopsis thaliana]

Seq. No. 309167

Seq. ID uC-zmflmo17240g05a1

Method BLASTX
NCBI GI g4006871
BLAST score 171
E value 4.0e-12
Match length 72
% identity 51

NCBI Description (Z99707) patatin-like protein [Arabidopsis thaliana]

Seq. No. 309168

Seq. ID uC-zmflmo17240g05b1

Method BLASTX
NCBI GI g4335745
BLAST score 248
E value 4.0e-21
Match length 141
% identity 39

NCBI Description (AC006284) putative hydrolase (contains an

esterase/lipase/thioesterase active site serine domain

(prosite: PS50187) [Arabidopsis thaliana]

Seq. No. 309169

Seq. ID uC-zmflmo17240h12b1

Method BLASTX
NCBI GI g1621268
BLAST score 546
E value 6.0e-56
Match length 127
% identity 78

NCBI Description (Z81012) unknown [Ricinus communis]



```
Seq. No.
                  309170
Seq. ID
                  uC-zmflmo17241b09a1
Method
                  BLASTN
NCBI GI
                  g168434
BLAST score
                  52
E value
                  1.0e-20
Match length
                  60
% identity
                  97
NCBI Description Z.mays catalase isozyme 3 (CAT-3) mRNA, complete cds
                  309171
Seq. No.
                  uC-zmflmo17241e01a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4234851
BLAST score
                  301
                  1.0e-169
E value
Match length
                  333
% identity
                  97
NCBI Description Zea mays copia-like retrotransposon Sto-4, partial sequence
Seq. No.
                  309172
                  uC-zmflmo17242b07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g485742
BLAST score
                  489
E value
                  3.0e-49
Match length
                  112
% identity
                  88
NCBI Description
                  (L32791) pyrophosphatase [Beta vulgaris]
Seq. No.
                  309173
Seq. ID
                  uC-zmflmo17242b11b1
Method
                  BLASTX
NCBI GI
                  g4539333
BLAST score
                  193
E value
                  6.0e-19
Match length
                  121
% identity
                  53
NCBI Description
                  (AL035539) putative amino acid transport protein
                  [Arabidopsis thaliana]
                  309174
Seq. No.
Seq. ID
                  uC-zmflmo17242b12b1
Method
                  BLASTN
NCBI GI
                  g4007864
BLAST score
                  234
E value
                  1.0e-129
Match length
                  342
% identity
                  28
NCBI Description Zea mays HRGP gene, AC1503 line
```

Seq. ID uC-zmflmo17242g12b1

Method BLASTX
NCBI GI g4580990
BLAST score 323
E value 7.0e-30



```
Match length
                    144
                    42
 % identity
 NCBI Description
                   (AF120335) putative transposase [Arabidopsis thaliana]
 Seq. No.
                    309176
                   uC-zmflmo17242h08b1
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                    q2443887
 BLAST score
                    262
 E value
                    1.0e-22
 Match length
                    151
 % identity
                    45
                   (AC002294) Similar to transcription factor
 NCBI Description
                   gb_Z46606_1658307 and others [Arabidopsis thaliana]
 Seq. No.
                    309177
 Seq. ID
                    uC-zmflmo17243d02a1
 Method
                   BLASTX
 NCBI GI
                    q3063445
 BLAST score
                    147
 E value
                    3.0e-09
 Match length
                   70
 % identity
                    49
                   (AC003981) F22013.7 [Arabidopsis thaliana]
 NCBI Description
Seq. No. *
                   309178
                   uC-zmflmo17244c08a1
 Seq. ID
 Method
                   BLASTN
 NCBI GI
                    q22312
 BLAST score
                    154
                    3.0e-81
 E value
 Match length
                    248
                    82
 % identity
 NCBI Description
                   Maize ABA-inducible gene for glycine-rich protein ( ABA =
                   abscisic acid)
                    309179
 Seq. No.
 Seq. ID
                   uC-zmflmo17244g12a1
 Method
                   BLASTN
 NCBI GI
                    g1185553
 BLAST score
                    78
                    6.0e-36
 E value
 Match length
                   156
                    47
 % identity
 NCBI Description
                   Zea mays glyceraldehyde-3-phosphate dehydrogenase (gpc2)
                    gene, complete cds
 Seq. No.
                    309180
 Seq. ID
                   uC-zmflmo17245a12b1
 Method
                   BLASTX
 NCBI GI
                   g3335349
 BLAST score
                   158
```

E value 7.0e-16 Match length 136 % identity 43

NCBI Description (AC004512) Similar to gb U46691 putative chromatin structure regulator (SUPT6H) from Homo sapiens. ESTs



gb_T42908, gb AA586170 and gb AA395125 come from this gene. [Arabidopsis thaliana]

Seq. No. 309181 uC-zmflmo17245b11b1 Seq. ID Method BLASTN NCBI GI g3821780 BLAST score 34 E value 2.0e-09 Match length 34 100 % identity NCBI Description Xenopus laevis cDNA clone 27A6-1 Seq. No. 309182 Seq. ID uC-zmflmo17245c03b1 Method BLASTN

g4007864 NCBI GI BLAST score 51 E value 5.0e-20 Match length 67 % identity 94

NCBI Description Zea mays HRGP gene, AC1503 line

309183 Seq. No. Seq. ID uC-zmflmo17245d06b1 Method BLASTX NCBI GI g4220475 BLAST score 175 E value 4.0e-13 Match length 74

% identity NCBI Description

(AC006069) hypothetical protein [Arabidopsis thaliana]

309184 Seq. No.

Seq. ID uC-zmflmo17245d10a1

47

Method BLASTX NCBI GI g100598 BLAST score 382 E value 2.0e-38 Match length 115 % identity 76

NCBI Description ubiquitin / ribosomal protein S27a-1 - barley >gi 167073

(M60175) ubiquitin [Hordeum vulgare]

Seq. No. 309185

Seq. ID uC-zmflmo17245g10b1

Method BLASTX NCBI GI g115771 BLAST score 469 E value 5.0e-47 Match length 117 % identity 78

CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR NCBI Description

(CAB-1) (LHCP) >gi_82682_pir__S04453 chlorophyll a/b-binding protein precursor - maize

>gi_22224_emb_CAA32900_ (X14794) chlorophyll a/b-binding preprotein (AA 1 - 262) [Zea mays]

309191

```
Seq. No.
                  309186
                  uC-zmflmo17246a07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3913018
BLAST score
                  160
                  5.0e-11
E value
Match length
                  44
                  75
% identity
NCBI Description
                  FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR
                  (ALDP) >gi 218155 dbj BAA02730 (D13513) chloroplastic
                  aldolase [Oryza sativa]
                  309187
Seq. No.
Seq. ID
                  uC-zmflmo17246c03b1
Method
                  BLASTN
NCBI GI
                  g257040
BLAST score
                  259
E value
                  1.0e-144
Match length
                  362
% identity
                  71
NCBI Description hydroxyproline-rich glycoprotein [maize, Genomic, 1703 nt]
Seq. No.
                  309188
Seq. ID
                  uC-zmflmo17246c05b1
Method
                  BLASTX
NCBI GI
                  g1076746
BLAST score
                  256
E value
                  4.0e-24
Match length
                  66
                  87
% identity
NCBI Description
                  heat shock protein 70 - rice (fragment)
                  >gi 763160 emb CAA47948 (X67711) heat shock protein 70
                  [Oryza sativa]
Seq. No.
                  309189
Seq. ID
                  uC-zmflmo17246c07b1
Method
                  BLASTX
NCBI GI
                  g2394306
BLAST score
                  237
E value
                  2.0e-20
Match length
                  65
% identity
                  65
NCBI Description
                  (AF017269) 73 kDA subunit of cleavage and polyadenylation
                  specificity factor [Homo sapiens]
                  309190
Seq. No.
                  uC-zmflmo17246d10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4204259
BLAST score
                  433
E value
                  7.0e-43
Match length
                  114
                  73
% identity
NCBI Description (AC005223) 18074 [Arabidopsis thaliana]
```



```
uC-zmflmo17246f02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4206306
BLAST score
                  284
                  5.0e-26
E value
Match length
                  60
                  87
% identity
NCBI Description
                  (AF049110) prpol [Zea mays]
                  309192
Seq. No.
                  uC-zmflmo17246h05b1
Seq. ID
Method
                  BLASTX
                  g3281853
NCBI GI
BLAST score
                  301
E value
                  2.0e-27
Match length
                  93
% identity
NCBI Description
                  (AL031004) putative protein [Arabidopsis thaliana]
Seq. No.
                  309193
                  uC-zmflmo17248a08a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g22091
BLAST score
                  49
                  4.0e-19
E value
Match length
                  93
% identity
                  89
NCBI Description
                  Z.diploperennis gene for hydroxyproline-rich glycoprotein
                  309194
Seq. No.
                  uC-zmflmo17248b10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2499819
BLAST score
                  223
                  2.0e-18
E value
Match length
                  96
                  59
% identity
                  ASPARTIC PROTEINASE ORYZASIN 1 PRECURSOR
NCBI Description
                  >gi_2130068 pir S66516 aspartic proteinase 1 precursor -
                  rice >gi_1030715_dbj_BAA06876_ (D32165) aspartic protease
                   [Oryza sativa] >gi 1711289 dbj BAA06875 (D32144) aspartic
                  protease [Oryza sativa]
                  309195
Seq. No.
                  uC-zmflmo17248b12b1
Seq. ID
Method
                  BLASTX
                  g2832641
NCBI GI
BLAST score
                  163
E value
                  2.0e-11
Match length
                  94
% identity
                  40
NCBI Description
                  (AL021710) glycolate oxidase - like protein [Arabidopsis
```

thaliana]

Seq. No. 309196

Seq. ID uC-zmflmo17248c12b1

Method BLASTX

```
q2894308
NCBI GI
BLAST score
                  167
E value
                  1.0e-24
Match length
                  92
                  13
% identity
                  (AJ223330) polyubiquitin [Nicotiana tabacum]
NCBI Description
                  309197
Seq. No.
                  uC-zmflmo17248d05b1
Seq. ID
```

Method BLASTX
NCBI GI g4539346
BLAST score 144
E value 1.0e-12
Match length 94
% identity 47

NCBI Description (AL035539) putative protein [Arabidopsis thaliana]

 Seq. No.
 309198

 Seq. ID
 uC-zmflmo17248d12b1

 Method
 BLASTX

 NCBI GI
 g4378875

 BLAST score
 302

 E value
 1.0e-27

 Match length
 114

Match length 114 % identity 54

NCBI Description (AF124360) delta-12 desaturase [Brassica carinata]

Seq. No. 309199

Seq. ID uC-zmflmo17248e07a1

Method BLASTX
NCBI GI g4539291
BLAST score 254
E value 5.0e-22
Match length 108
% identity 47

NCBI Description (AL049480) putative protein [Arabidopsis thaliana]

Seq. No. 309200

Seq. ID uC-zmflmo17248e09a1

Method BLASTN
NCBI GI g22091
BLAST score 284
E value 1.0e-159
Match length 340
% identity 97

NCBI Description Z.diploperennis gene for hydroxyproline-rich glycoprotein

Seq. No. 309201

Seq. ID uC-zmflmo17248e12b1

Method BLASTX
NCBI GI g3426048
BLAST score 180
E value 2.0e-13
Match length 98
% identity 45

NCBI Description (AC005168) putative hydroxymethylglutaryl-CoA lyase

precursor [Arabidopsis thaliana]

Seq. ID

```
Seq. No.
                   309202
Seq. ID
                  uC-zmflmo17248f03b1
Method
                  BLASTX
NCBI GI
                  q4538929
BLAST score
                   270
E value
                  1.0e-23
Match length
                  73
% identity
                   66
NCBI Description
                   (AL049483) putative nucleic acid binding protein
                   [Arabidopsis thaliana]
Seq. No.
                  309203
Seq. ID
                  uC-zmflmo17248h07b1
Method
                  BLASTX
NCBI GI
                  g2827002
BLAST score
                   450
E value
                  7.0e-45
Match length
                  139
% identity
                   69
NCBI Description
                  (AF005993) HSP70 [Triticum aestivum]
Seq. No.
                  309204
Seq. ID
                  uC-zmflmo17248h09b1
Method
                  BLASTX
NCBI GI
                  g70645
BLAST score
                  520
E value
                   4.0e-53
Match length
                  131
% identity
NCBI Description
                  ubiquitin precursor - garden pea >gi 20589 emb CAA34886
                   (X17020) polyubiquitin (AA 1-381) [Pisum sativum]
                  >gi_4115339 (L81142) ubiquitin [Pisum sativum]
                  >gi_226707_prf__1603402A poly-ubiquitin [Pisum sativum]
Seq. No.
                  309205
Seq. ID
                  uC-zmflmo17249e03a1
Method
                  BLASTX
NCBI GI
                  g3786007
BLAST score
                  173
                  2.0e-12
E value
Match length
                  92
% identity
                  42
NCBI Description
                  (AC005499) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  309206
Seq. ID
                  uC-zmflmo17250c06a1
Method
                  BLASTN
NCBI GI
                  q483409
BLAST score
                  131
E value
                  9.0e-68
Match length
                  167
% identity
                  95
NCBI Description
                  Zea Mays calmodulin-binding protein mRNA, 3'end
Seq. No.
                  309207
```

43992

uC-zmflmo17251a01a1



```
Method
                   BLASTX
NCBI GI
                   q1653449
BLAST score
                   693
E value
                   2.0e-73
Match length
                   141
                   94
% identity
                   (D90913) alpha-isopropylmalate synthase [Synechocystis sp.]
NCBI Description
Seq. No.
                   309208
Seq. ID
                   uC-zmflmo17251a02a1
Method
                   BLASTN
NCBI GI
                   q1652225
BLAST score
                   392
                   0.0e+00
E value
                   428
Match length
% identity
                   98
NCBI Description
                   Synechocystis sp. PCC6803 complete genome, 6/27,
                   630555-781448
Seq. No.
                   309209
Seq. ID
                   uC-zmflmo17251a04a1
Method
                   BLASTN
NCBI GI
                   g1001396
BLAST score
                   323
E value
                   0.0e + 00
Match length
                   347
                   98
% identity
NCBI Description
                   Synechocystis sp. PCC6803 complete genome, 18/27,
                   2267260-2392728
Seq. No.
                   309210
Seq. ID
                   uC-zmflmo17251a05a1
Method
                   BLASTN
NCBI GI
                   q1653348
BLAST score
                   293
E value
                   1.0e-164
Match length
                   348
% identity
                   96
NCBI Description
                   Synechocystis sp. PCC6803 complete genome, 15/27,
                   1848242-1991549
Seq. No.
                   309211
Seq. ID
                   uC-zmflmo17251a06a1
Method
                   BLASTN
NCBI GI
                   g1001701
BLAST score
                   339
E value
                   0.0e+00
Match length
                   387
                   96
% identity
NCBI Description
                   Synechocystis sp. PCC6803 complete genome, 23/27,
                   2868767-3002965
                   309212
Seq. No.
Seq. ID
                   uC-zmflmo17251a07a1
Method
                  BLASTX
NCBI GI
```

43993

g1651698

198

BLAST score



```
E value
                  3.0e-15
Match length
                  63
% identity
                  63
NCBI Description
                  (D90899) hypothetical protein [Synechocystis sp.]
                  309213
Seq. No.
                  uC-zmflmo17251b08a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1001102
BLAST score
                  447
                  0.0e + 00
E value
                  455
Match length
                  100
% identity
NCBI Description
                  Synechocystis sp. PCC6803 complete genome, 20/27,
                  2539000-2644794
                  309214
Seq. No.
Seq. ID
                  uC-zmflmo17251c01a1
Method
                  BLASTN
NCBI GI
                  g1652225
BLAST score
                  393
                  0.0e+00
E value
                  409
Match length
                  99
% identity
NCBI Description
                  Synechocystis sp. PCC6803 complete genome, 6/27,
                  630555-781448
                  309215
Seq. No.
Seq. ID
                  uC-zmflmo17251c02a1
Method
                  BLASTX
NCBI GI
                  g1001327
BLAST score
                  450
                  5.0e-45
E value
Match length
                  106
% identity
                  84
NCBI Description (D64006) ExsB [Synechocystis sp.]
Seq. No.
                  309216
                  uC-zmflmo17251c04a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1001598
                  495
BLAST score
E value
                  3.0e-50
Match length
                  118
% identity
                  86
NCBI Description
                  (D64000) transposase [Synechocystis sp.]
                  >gi_1651758_dbj_BAA16686_ (D90899) transposase
                  [Synechocystis sp.] >gi_1652984_dbj_BAA17901_ (D90910)
                  transposase [Synechocystis sp.] >gi_1653064_dbj_BAA17981_
                  (D90910) transposase [Synechocystis sp.]
                  >gi 1653236_dbj_BAA18151_ (D90912) transposase
                  [Synechocystis sp.] >gi_1653394_dbj_BAA18308_ (D90913)
                  transposase [Synechocystis sp.] >gi_1653686_dbj_BAA18598_
                  (D90915) transposase [Synechocystis sp.]
```

Seq. ID uC-zmflmo17251c06a1

Method

NCBI GI

BLAST score

BLASTN

462

g1651897



```
Method
                   BLASTN
NCBI GI
                   g1653477
BLAST score
                   404
E value
                   0.0e+00
                   436
Match length
                   98
% identity
                  Synechocystis sp. PCC6803 complete genome, 16/27,
NCBI Description
                   1991550-2137258
                   309218
Seq. No.
                  uC-zmflmo17251c08a1
Seq. ID
Method
                  BLASTN
NCBI GI
                   g1001701
BLAST score
                   439
                  0.0e+00
E value
Match length
                   447
                   100
% identity
                  Synechocystis sp. PCC6803 complete genome, 23/27,
NCBI Description
                   2868767-3002965
                   309219
Seq. No.
                  uC-zmflmo17251c10a1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1477448
                   304
BLAST score
E value
                   6.0e-37
                  93
Match length
                   89
% identity
NCBI Description
                  (X96599) magnesium chelatase [Synechocystis sp.]
                   309220
Seq. No.
                   uC-zmflmo17251d02a1
Seq. ID
Method
                  BLASTN
NCBI GI
                   g1001484
BLAST score
                   458
E value
                   0.0e + 00
Match length
                   462
% identity
                   100
NCBI Description
                  Synechocystis sp. PCC6803 complete genome, 19/27,
                   2392729-2538999
                   309221
Seq. No.
                   uC-zmflmo17251d04a1
Seq. ID
Method
                  BLASTN
NCBI GI
                   g1001200
BLAST score
                   297
E value
                   1.0e-166
Match length
                   318
% identity
                   98
NCBI Description
                  Synechocystis sp. PCC6803 complete genome, 22/27,
                   2755703-2868766
Seq. No.
                   309222
Seq. ID
                   uC-zmflmo17251d07a1
```



```
0.0e+00
E value
Match length
                  474
% identity
                   99
                  Synechocystis sp. PCC6803 complete genome, 3/27,
NCBI Description
                  271600-402289
                  309223
Seq. No.
                  uC-zmflmo17251d11a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1652844
BLAST score
                   458
                  0.0e + 00
E value
Match length
                   466
% identity
                   100
                  Synechocystis sp. PCC6803 complete genome, 11/27,
NCBI Description
                   1311235-1430418
                   309224
Seq. No.
                   uC-zmflmo17251e01a1
Seq. ID
                   BLASTN
Method
                   g1001200
NCBI GI
BLAST score
                   355
                   0.0e + 00
E value
Match length
                   387
% identity
                   98
                   Synechocystis sp. PCC6803 complete genome, 22/27,
NCBI Description
                   2755703-2868766
                   309225
Seq. No.
                   uC-zmflmo17251e02a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1653693
BLAST score
                   220
                   2.0e-18
E value
Match length
                   59
                   66
% identity
                  (D90915) hypothetical protein [Synechocystis sp.]
NCBI Description
                   309226
Seq. No.
Seq. ID
                   uC-zmflmo17251e04a1
Method
                   BLASTN
NCBI GI
                   q1652360
BLAST score
                   400
                   0.0e + 00
E value
Match length
                   429
                   98
% identity
                   Synechocystis sp. PCC6803 complete genome, 7/27,
NCBI Description
                   781449-920915
                   309227
Seq. No.
                   uC-zmflmo17251e05a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1673303
                   292
BLAST score
E value
                   3.0e-26
```

43996

59

98

Match length

% identity



```
NCBI Description
                  (D64001) transposase [Synechocystis sp.]
Seq. No.
                   309228
                   uC-zmflmo17251e07a1
Seq. ID
Method
                   BLASTN
                   g1001612
NCBI GI
BLAST score
                   342
E value
                   0.0e+00
Match length
                   428
                   93
% identity
                  Synechocystis sp. PCC6803 complete genome, 21/27,
NCBI Description
                   2644795-2755702
Seq. No.
                   309229
Seq. ID
                   uC-zmflmo17251e09a1
Method
                   BLASTX
NCBI GI
                   q1653644
BLAST score
                   619
                   1.0e-64
E value
Match length
                   154
% identity
                   80
NCBI Description
                  (D90915) high-affinity branched-chain amino acid transport
                  protein BraE [Synechocystis sp.]
Seq. No.
                   309230
Seq. ID
                   uC-zmflmo17251e10a1
Method
                   BLASTX
NCBI GI
                   q1652790
BLAST score
                   607
E value
                   4.0e-63
Match length
                   120
% identity
                   98
NCBI Description
                  (D90908) sugar fermentation stimulation protein
                   [Synechocystis sp.]
Seq. No.
                   309231
                   uC-zmflmo17251f01a1
Seq. ID
Method
                   BLASTX
                   g1651888
NCBI GI
BLAST score
                   576
E value
                   1.0e-59
Match length
                   116
% identity
                   96
NCBI Description
                   (D90900) peptide methionine sulfoxide reductase
                   [Synechocystis sp.]
Seq. No.
                   309232
Seq. ID
                   uC-zmflmo17251f04a1
Method
                  BLASTX
                   g1001708
NCBI GI
BLAST score
                   846
E value
                   4.0e-91
Match length
                  164
% identity
                   98
```

43997

NCBI Description (D64004) NifS [Synechocystis sp.]

```
uC-zmflmo17251f05a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q1653715
BLAST score
                  486
                  0.0e+00
E value
Match length
                  551
% identity
                  97
NCBI Description
                  Synechocystis sp. PCC6803 complete genome, 26/27,
                  3270710-3418851
Seq. No.
                  309234
Seq. ID
                  uC-zmflmo17251f08a1
Method
                  BLASTX
                  g1651976
NCBI GI
BLAST score
                  653
E value
                  1.0e-68
Match length
                  147
% identity
                  88
NCBI Description
                  (D90901) CDP-glucose 4,6-dehydratase [Synechocystis sp.]
Seq. No.
                  309235
Seq. ID
                  uC-zmflmo17251f11a1
Method
                  BLASTX
NCBI GI
                  g1653455
BLAST score
                  930
E value
                  1.0e-101
Match length
                  183
                  98
% identity -
NCBI Description (D90913) delta-1-pyrroline-5-carboxylate dehydrogenase
                  [Synechocystis sp.]
Seq. No.
                  309236
Seq. ID
                  uC-zmflmo17251g02a1
Method
                  BLASTN
NCBI GI
                  g1652725
BLAST score
                  225
E value
                  1.0e-124
Match length
                  229
                  100
% identity
NCBI Description
                  Synechocystis sp. PCC6803 complete genome, 10/27,
                  1188886-1311234
Seq. No.
                  309237
Seq. ID
                  uC-zmflmo17251g04a1
Method
                  BLASTX
NCBI GI
                  g2496196
BLAST score
                  157
E value
                  2.0e-10
Match length
                  125
% identity
NCBI Description
                  HYPOTHETICAL PROTEIN MJECS02 >gi_2129058_pir__B64516
                  hypothetical protein MJECS02 - Methanococcus jannaschii
                  plasmid pURB801 >gi 1522636 (L77119) M. jannaschii
                  predicted coding region MJECS02 [Methanococcus jannaschii]
```

Seq. ID uC-zmflmo17251g05a1

NCBI GI

BLAST score



```
Method
                   BLASTX
NCBI GI
                   g1653093
BLAST score
                   410
E value
                   5.0e-40
Match length
                   82
                   99
% identity
NCBI Description
                  (D90911) hypothetical protein [Synechocystis sp.]
                   309239
Seq. No.
                   uC-zmflmo17251g06a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2496791
BLAST score
                   508
E value
                   2.0e-51
                   104
Match length
% identity
                   93
NCBI Description
                  HYPOTHETICAL 20.1 KD PROTEIN SLR0053
                   >gi 1001136 dbj BAA10278 (D64001) hypothetical protein
                   [Synechocystis sp.]
Seq. No.
                   309240
Seq. ID
                   uC-zmflmo17251g07a1
Method
                  BLASTN
NCBI GI
                   g1653715
BLAST score
                   382
E value
                   0.0e + 00
Match length
                   398
                   99
% identity
NCBI Description
                  Synechocystis sp. PCC6803 complete genome, 26/27,
                   3270710-3418851
Seq. No.
                   309241
Seq. ID
                  uC-zmflmo17251g08a1
Method
                  BLASTN
NCBI GI
                   g1653083
BLAST score
                   333
E value
                   0.0e + 00
Match length
                   383
% identity
                   99
NCBI Description
                  Synechocystis sp. PCC6803 complete genome, 13/27,
                   1576593-1719643
Seq. No.
                   309242
Seq. ID
                  uC-zmflmo17251g12a1
Method
                  BLASTX
NCBI GI
                  q1001295
BLAST score
                   424
E value
                  3.0e-47
Match length
                  100
% identity
                   94
NCBI Description (D64006) sucrose phosphate synthase [Synechocystis sp.]
Seq. No.
                  309243
Seq. ID
                  uC-zmflmo17251h07a1
Method
                  BLASTX
```

g1652513

```
E value
                  7.0e-75
Match length
                  143
% identity
                  99
NCBI Description
                  (D90906) NADH dehydrogenase subunit 4 [Synechocystis sp.]
Seq. No.
                  309244
Seq. ID
                  uC-zmflmo17251h09a1
Method
                  BLASTN
NCBI GI
                  q1001396
BLAST score
                  309
E value
                  1.0e-173
Match length
                  338
% identity
                  97
                  Synechocystis sp. PCC6803 complete genome, 18/27,
NCBI Description
                  2267260-2392728
Seq. No.
                  309245
Seq. ID
                  uC-zmflmo17252a02a1
Method
                  BLASTN
NCBI GI
                  g1001200
BLAST score
                  509
                  0.0e+00
E value
                                       45
Match length
                  532
% identity
                  99
                  Synechocystis sp. PCC6803 complete genome, 22/27,
NCBI Description
                  2755703-2868766
Seq. No.
                  309246
Seq. ID
                  uC-zmflmo17252a03a1
Method
                  BLASTX
NCBI GI
                  q1652160
BLAST score
                  396
E value
                  1.0e-38
```

Match length 82 % identity 90

(D90903) hypothetical protein [Synechocystis sp.] NCBI Description

Seq. No. 309247

Seq. ID uC-zmflmo17252a07a1

Method BLASTN NCBI GI q1771977 BLAST score 85 2.0e-40 E value Match length 141 % identity 90

NCBI Description Synechocystis sp. DNA photolyase (phrA) gene, complete cds

Seq. No. 309248

Seq. ID uC-zmflmo17252a09a1

Method BLASTN NCBI GI g1652127 BLAST score 364 E value 0.0e + 00Match length 395 99 % identity

NCBI Description Synechocystis sp. PCC6803 complete genome, 5/27,

524346-630554



```
309249
Seq. No.
Seq. ID
                   uC-zmflmo17252b01a1
Method
                   BLASTN
NCBI GI
                   g1001102
BLAST score
                   400
E value
                   0.0e + 00
Match length
                   408
% identity
                   100
NCBI Description
                   Synechocystis sp. PCC6803 complete genome, 20/27,
                   2539000-2644794
Seq. No.
                   309250
Seq. ID
                   uC-zmflmo17252b03a1
Method
                   BLASTX
NCBI GI
                   q1001789
BLAST score
                   769
                   4.0e-82
E value
Match length
                   157
% identity
                   94
NCBI Description
                  (D64005) PleD gene product [Synechocystis sp.]
Seq. No.
                   309251
Seq. ID
                   uC-zmflmo17252b07a1
Method
                   BLASTN
NCBI GI
                   g1001701
BLAST score
                   213
E value
                   1.0e-116
Match length
                   225
                   99
% identity
NCBI Description
                  Synechocystis sp. PCC6803 complete genome, 23/27,
                   2868767-3002965
Seq. No.
                   309252
Seq. ID
                  uC-zmflmo17252b11a1
Method
                  BLASTX
NCBI GI
                   g1653736
BLAST score
                   858
E value
                   1.0e-92
Match length
                   168
% identity
                  99
NCBI Description
                  (D90916) transcriptional regulatory protein [Synechocystis
                  sp.]
Seq. No.
                   309253
Seq. ID
                  uC-zmflmo17252b12a1
Method
                  BLASTX
NCBI GI
                   g3122222
BLAST score
                  717
E value
                  4.0e-76
Match length
                  143
% identity
                  99
                  HISTIDINOL DEHYDROGENASE (HDH) >gi_1652156_dbj_BAA17080_
NCBI Description
                   (D90903) histidinol dehydrogenase [Synechocystis sp.]
```

Seq. ID uC-zmflmo17252c01a1

309254

```
Method
                  BLASTX
NCBI GI
                  g1652006
BLAST score
                  494
E value
                  3.0e-50
Match length
                  98
% identity
                  94
                  (D90901) UDPglucose 4-epimerase [Synechocystis sp.]
NCBI Description
                  309255
Seq. No.
Seq. ID
                  uC-zmflmo17252c05a1
Method
                  BLASTX
NCBI GI
                  q1651708
BLAST score
                  706
                  8.0e-75
E value
                  137
Match length
% identity
                  95
NCBI Description
                  (D90899) hypothetical protein [Synechocystis sp.]
                  309256
Seq. No.
Seq. ID
                  uC-zmflmo17252c06a1
                  BLASTN
Method
NCBI GI
                  q1001291
BLAST score
                  297
                  1.0e-166
E value
                  337
Match length
                  97
% identity
NCBI Description
                  Synechocystis sp. PCC6803 complete genome, 25/27,
                  3138604-3270709
Seq. No.
                  309257
Seq. ID
                  uC-zmflmo17252c08a1
Method
                  BLASTX
NCBI GI
                  q1421161
BLAST score
                  201
E value
                  1.0e-15
Match length
                  95
% identity
                   49
                  Chain A, Fasciculin2 - Mouse Acetylcholinesterase Complex
NCBI Description
                  309258
Seq. No.
Seq. ID
                  uC-zmflmo17252c10a1
Method
                  BLASTX
NCBI GI
                  g1652061
BLAST score
                  317
                   4.0e-29
E value
Match length
                   64
```

% identity 98

NCBI Description (D90902) hypothetical protein [Synechocystis sp.]

309259 Seq. No.

uC-zmflmo17252c11a1 Seq. ID

Method BLASTX NCBI GI g2499969 216 BLAST score 3.0e-17 E value Match length 40 % identity 100



309260

309261

NCBI Description

PHOTOSYSTEM I REACTION CENTRE SUBUNIT VIII

>gi_2119842_pir__A57482 photosystem I protein psaI
Synechocystis sp. (PCC 6803) >gi_404812 (L24773)

photosystem I small subunit [Synechocystis sp.]

>gi_1653864_dbj_BAA18774_ (D90917) photosystem I subunit

VIII [Synechocystis sp.] >gi_1944320_dbj_BAA19609_ (D38131)

PsaI [Synechocystis sp.]

Seq. ID uC-zmflmo17252d01a1
Method BLASTX
NCBI GI g1652588
BLAST score 505
E value 1.0e-53
Match length 129
% identity 86

Seq. No.

Seq. No.

NCBI Description (D90906) protein kinase PknA [Synechocystis sp.]

Seq. ID uC-zmflmo17252d04a1
Method BLASTN
NCBI GI g1001291
BLAST score 466
E value 0.0e+00
Match length 473
% identity 100

NCBI Description Synechocystis sp. PCC6803 complete genome, 25/27,

3138604-3270709

Seq. No. 309262

Seq. ID uC-zmflmo17252d06a1

Method BLASTX
NCBI GI g1653877
BLAST score 210
E value 5.0e-17
Match length 49
% identity 90

NCBI Description (D90917) hypothetical protein [Synechocystis sp.]

Seq. No. 309263

Seq. ID uC-zmflmo17252d07a1

Method BLASTN
NCBI GI g1001396
BLAST score 360
E value 0.0e+00
Match length 412
% identity 96

NCBI Description Synechocystis sp. PCC6803 complete genome, 18/27,

2267260-2392728

Seq. No. 309264

Seq. ID uC-zmflmo17252d08a1

Method BLASTN
NCBI GI g1651897
BLAST score 366
E value 0.0e+00
Match length 378

% identity

96



```
% identity
NCBI Description
                  Synechocystis sp. PCC6803 complete genome, 3/27,
                   271600-402289
Seq. No.
                   309265
Seq. ID
                  uC-zmflmo17252d09a1
Method
                  BLASTX
NCBI GI
                  g2506309
BLAST score
                  588
E value
                   4.0e-61
Match length
                  116
% identity
                  96
NCBI Description
                  CYTOCHROME C OXIDASE POLYPEPTIDE I (CYTOCHROME AA3 SUBUNIT
                  1) (OXIDASE AA(3) SUBUNIT 1) >gi_1652367_dbj_BAA17289
                   (D90905) cytochrome c oxidase subunit I [Synechocystis sp.]
Seq. No.
                   309266
                  uC-zmflmo17252d11a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1652731
BLAST score
                  308
E value
                  3.0e-28
Match length
                  64
% identity
                  94
NCBI Description
                  (D90908) hypothetical protein [Synechocystis sp.]
                  309267
Seq. No.
Seq. ID
                  uC-zmflmo17252d12a1
Method
                  BLASTN
NCBI GI
                  g1653836
BLAST score
                  193
E value
                  1.0e-104
Match length
                  252
% identity
                  94
NCBI Description
                  Synechocystis sp. PCC6803 complete genome, 27/27,
                  3418852-3573470
Seq. No.
                  309268
Seq. ID
                  uC-zmflmo17252e01a1
Method
                  BLASTX
NCBI GI
                  q1001685
BLAST score
                  394
E value
                  4.0e-38
Match length
                  76
% identity
                  100
NCBI Description
                  (D64002) heterodisulfide reductase subunit B [Synechocystis
                  sp.]
Seq. No.
                  309269
Seq. ID
                  uC-zmflmo17252e02a1
Method
                  BLASTN
NCBI GI
                  g1001200
BLAST score
                  298
E value
                  1.0e-167
Match length
                  358
```

44004

NCBI Description Synechocystis sp. PCC6803 complete genome, 22/27,



2755703-2868766

```
309270
Seq. No.
Seq. ID
                  uC-zmflmo17252e03a1
Method
                   BLASTN
NCBI GI
                   q1653348
BLAST score
                   203
E value
                   1.0e-110
Match length
                   243
% identity
                   96
                  Synechocystis sp. PCC6803 complete genome, 15/27,
NCBI Description
                   1848242-1991549
                   309271
Seq. No.
                  uC-zmflmo17252e04a1
Seq. ID
Method
                  BLASTN
NCBI GI
                   a1652618
BLAST score
                   507
E value
                   0.0e + 00
Match length
                   539
% identity
                   99
NCBI Description
                  Synechocystis sp. PCC6803 complete genome, 9/27,
                  1056467-1188885
Seq. No.
                   309272
Seq. ID
                  uC-zmflmo17252e05a1
Method
                  BLASTN
NCBI GI
                  a1653228
BLAST score
                   412
E value
                  0.0e+00
Match length
                   428
                   99
% identity
NCBI Description
                  Synechocystis sp. PCC6803 complete genome, 14/27,
                  1719644-1848241
Seq. No.
                   309273
Seq. ID
                  uC-zmflmo17252e06a1
Method
                  BLASTX
NCBI GI
                  q3024481
BLAST score
                   408
E value
                   5.0e-40
                  83
Match length
% identity
                   96
NCBI Description
                  PHOSPHORIBOSYLAMINE--GLYCINE LIGASE (GARS) (GLYCINAMIDE
                  RIBONUCLEOTIDE SYNTHETASE) (PHOSPHORIBOSYLGLYCINAMIDE
                  SYNTHETASE) >gi_1653412_dbj_BAA18326_ (D90913) glycinamide
                  ribonucleotide synthetase [Synechocystis sp.]
                  309274
Seq. No.
Seq. ID
                  uC-zmflmo17252e07a1
Method
                  BLASTX
```

Method BLASTX
NCBI GI g1001645
BLAST score 503
E value 6.0e-51
Match length 100
% identity 99

NCBI Description (D64002) hypothetical protein [Synechocystis sp.]

Seq. ID

309280

uC-zmflmo17252f10a1

```
309275
Seq. No.
Seq. ID
                  uC-zmflmo17252e08a1
Method
                  BLASTN
NCBI GI
                  g1001291
BLAST score
                  178
E value
                  8.0e-96
Match length
                  194
% identity
                   98
NCBI Description
                  Synechocystis sp. PCC6803 complete genome, 25/27,
                  3138604-3270709
Seq. No.
                  309276
Seq. ID
                  uC-zmflmo17252e11a1
Method
                  BLASTX
NCBI GI
                  g3024729
BLAST score
                  910
E value
                  1.0e-98
Match length
                  178
% identity
                  97
NCBI Description
                  THIAMIN BIOSYNTHESIS PROTEIN THIC >qi 1208488 dbj BAA10656
                   (D64004) ThiC protein [Synechocystis sp.]
Seq. No.
                  309277
Seq. ID
                  uC-zmflmo17252f03a1
Method
                  BLASTN
NCBI GI
                  g1653477
BLAST score
                   439
E value
                  0.0e + 00
Match length
                   487
                  98
% identity
NCBI Description
                  Synechocystis sp. PCC6803 complete genome, 16/27,
                  1991550-2137258
                  309278
Seq. No.
Seq. ID
                  uC-zmflmo17252f04a1
Method
                  BLASTX
NCBI GI
                  g1652262
BLAST score
                  362
E value
                  1.0e-34
Match length
                  74
% identity
                  96
NCBI Description
                  (D90904) cytochrome oxidase d subunit I [Synechocystis sp.]
Seq. No.
                  309279
Seq. ID
                  uC-zmflmo17252f08a1
Method
                  BLASTN
NCBI GI
                  g1001396
BLAST score
                  255
E value
                  1.0e-141
Match length
                  323
% identity
                  40
NCBI Description
                  Synechocystis sp. PCC6803 complete genome, 18/27,
                  2267260-2392728
```

Match length

139

```
Method
NCBI GI
                   q1653939
BLAST score
                   684
E value
                   3.0e-72
Match length
                   140
                   95
% identity
NCBI Description
                  (D90917) HrEpiB [Synechocystis sp.]
Seq. No.
Seq. ID
                  uC-zmflmo17252f11a1
Method
                  BLASTX
NCBI GI
                  q1653942
BLAST score
                   690
E value
                   6.0e-73
Match length
                  129
                   99
% identity
NCBI Description (D90917) hypothetical protein [Synechocystis sp.] 4
Seq. No.
                   309282
Seq. ID
                  uC-zmflmo17252g01a1
Method
                  BLASTN
NCBI GI
                  g1651650
BLAST score
                  118
E value
                   6.0e-60
Match length
                  222
% identity
NCBI Description Synechocystis sp. PCC6803 complete genome, 1/27, 1-133859
Seq. No.
                  309283
Seq. ID
                  uC-zmflmo17252g02a1
Method
                  BLASTN
NCBI GI
                  q1651768
BLAST score
                  419
E value
                  0.0e + 00
Match length
                  427
% identity
                  100
NCBI Description
                  Synechocystis sp. PCC6803 complete genome, 2/27,
                  133860-271599
Seq. No.
                  309284
Seq. ID
                  uC-zmflmo17252q05a1
Method
                  BLASTX
NCBI GI
                  g2494149
BLAST score
                  294
E value
                  6.0e-27
Match length
                  88
% identity
                  68
NCBI Description
                  DNA PRIMASE >gi_1653314_dbj_BAA18229_ (D90912) DNA primase
                  [Synechocystis sp.]
Seq. No.
                  309285
Seq. ID
                  uC-zmflmo17252g07a1
Method
                  BLASTX
NCBI GI
                  g1653189
BLAST score
                  613
E value
                  5.0e-64
```

Match length

% identity

135

95



```
% identity
NCBI Description
                   (D90911) D-alanyl-D-alanine carboxypeptidase [Synechocystis
                   sp.]
Seq. No.
                   309286
Seq. ID
                   uC-zmflmo17252g09a1
Method
                   BLASTN
NCBI GI
                   q1653083
BLAST score
                   353
E value
                   0.0e+00
Match length
                   393
% identity
                   97
NCBI Description
                   Synechocystis sp. PCC6803 complete genome, 13/27,
                   1576593-1719643
Seq. No.
                   309287
Seq. ID
                   uC-zmflmo17252g10a1
Method
                   BLASTX
NCBI GI
                   g3183456
BLAST score
                   739
E value
                   1.0e-78
Match length
                   159
% identity
                   91
NCBI Description
                   HYPOTHETICAL 38.3 KD PROTEIN SLR1938
                   >gi 1653689 dbj BAA18601 (D90915) hypothetical protein
                   [Synechocystis sp.]
Seq. No.
                   309288
Seq. ID
                   uC-zmflmo17252h05a1
Method
                   BLASTX
NCBI GI
                   g1001150
BLAST score
                   434
E value
                   2.0e-43
Match length
                   90
% identity
                   96
NCBI Description
                   (D64001) general secretion pathway protein E [Synechocystis
                   sp.]
Seq. No.
                   309289
Seq. ID
                   uC-zmflmo17252h07a1
Method
                   BLASTX
NCBI GI
                   g1652666
BLAST score
                   333
E value
                   9.0e-32
Match length
                   73
% identity
                   93
                  (D90907) glycogen phosphorylase [Synechocystis sp.]
NCBI Description
Seq. No.
                   309290
Seq. ID
                   uC-zmflmo17252h10a1
Method
                  BLASTX
NCBI GI
                   g131406
BLAST score
                   659
E value
                   2.0e-69
```

44008

NCBI Description NADH-UBIQUINONE OXIDOREDUCTASE SUBUNIT K HOMOLOG 1

>gi_79727_pir__S04437 psbG1 protein - Synechocystis sp.
(PCC 6803) >gi_48047_emb_CAA35485_ (X17439) PSII-G protein
(AA 1 - 248) [Synechocystis PCC6803]

75^{2,0}

>gi_1653370_dbj_BAA18284_ (D90913) NADH-ubiquinone oxidoreductase subunit PsbG [Synechocystis sp.]

Seq. No. 309291

Seq. ID uC-zmflmo17253a02a1

Method BLASTX
NCBI GI g1652457
BLAST score 500
E value 6.0e-51
Match length 99
% identity 96

NCBI Description (D90905) rehydrin [Synechocystis sp.]

Seq. No. 309292

Seq. ID uC-zmflmo17253a03a1

Method BLASTN
NCBI GI g1651897
BLAST score 444
E value 0.0e+00
Match length 480
% identity 98

NCBI Description Synechocystis sp. PCC6803 complete genome, 3/27,

271600-402289

Seq. No. 309293

Seq. ID uC-zmflmo17253a05a1

Method BLASTX
NCBI GI g1001553
BLAST score 417
E value 6.0e-41
Match length 76
% identity 100

NCBI Description (D64000) hypothetical protein [Synechocystis sp.]

Seq. No. 309294

Seq. ID uC-zmflmo17253a06a1

Method BLASTN
NCBI GI g1653715
BLAST score 215
E value 1.0e-118
Match length 247
% identity 97

NCBI Description Synechocystis sp. PCC6803 complete genome, 26/27,

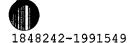
3270710-3418851

Seq. No. 309295

Seq. ID uC-zmflmo17253a09a1

Method BLASTN
NCBI GI g1653348
BLAST score 505
E value 0.0e+00
Match length 533
% identity 99

NCBI Description Synechocystis sp. PCC6803 complete genome, 15/27,



```
Seq. No.
                  309296
Seq. ID
                  uC-zmflmo17253b02a1
Method
                  BLASTN
                  g1001484
NCBI GI
BLAST score
                  177
E value
                  4.0e-95
Match length
                  253
% identity
                  93
NCBI Description
                  Synechocystis sp. PCC6803 complete genome, 19/27,
                  2392729-2538999
Seq. No.
                  309297
                  uC-zmflmo17253b05a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1651766
BLAST score
                  235
E value
                  9.0e-20
                  46
Match length .
% identity
                  98
NCBI Description
                  (D90899) hypothetical protein [Synechocystis sp.]
Seq. No.
                  309298
Seq. ID
                  uC-zmflmo17253b06a1
Method
                  BLASTN
NCBI GI
                  g1653604
BLAST score
                  446
E value
                  0.0e + 00
Match length
                  481
% identity
                  98
NCBI Description
                  Synechocystis sp. PCC6803 complete genome, 17/27,
                  2137259-2267259
Seq. No.
                  309299
Seq. ID
                  uC-zmflmo17253b08a1
Method
                  BLASTN
NCBI GI
                  g1653836
BLAST score
                  273
E value
                  1.0e-152
Match length
                  342
% identity
                  94
                  Synechocystis sp. PCC6803 complete genome, 27/27,
NCBI Description
                  3418852-3573470
Seq. No.
                  309300
Seq. ID
                  uC-zmflmo17253b09a1
Method
                  BLASTX
NCBI GI
                  q1001641
BLAST score
                  694
E value
                  2.0e-73
Match length
                  143
```

Seq. No. 309301

% identity

NCBI Description

Seq. ID uC-zmflmo17253c01a1

(D64002) hypothetical protein [Synechocystis sp.]

Seq. ID

Method

NCBI GI

```
Method
 NCBI GI
                   a2829607
 BLAST score
                   448
 E value
                   7.0e-45
 Match length
                   98
 % identity
                   86
 NCBI Description
                   D-ALANINE--D-ALANINE LIGASE (D-ALANYLALANINE SYNTHETASE)
                   >gi_1652758_dbj_BAA17677 (D90908) D-alanine:D-alanine
                   ligase-related protein [Synechocystis sp.]
 Seq. No.
                   309302
 Seq. ID
                   uC-zmflmo17253c02a1
Method
                   BLASTN
 NCBI GI
                   g1653604
 BLAST score
                   153
E value
                   6.0e-81
Match length
                   165
 % identity
                   98
NCBI Description
                   Synechocystis sp. PCC6803 complete genome, 17/27,
                   2137259-2267259
                   309303
 Seq. No.
 Seq. ID
                   uC-zmflmo17253c03a1
Method
                   BLASTN
 NCBI GI
                   g1651768
BLAST score
                   471
E value
                   0.0e + 00
Match length
                   483
 % identity
                   99
NCBI Description
                   Synechocystis sp. PCC6803 complete genome, 2/27,
                   133860-271599
Seq. No.
                   309304
 Seq. ID
                   uC-zmflmo17253c04a1
Method
                   BLASTX
 NCBI GI
                   g1706336
BLAST score
                   711
E value
                   2.0e-75
Match length
                   141
 % identity
NCBI Description
                   UROPORPHYRINOGEN DECARBOXYLASE >gi 1001337 dbj BAA10824
                   (D64006) uroporphyrinogen decarboxylase [Synechocystis sp.]
Seq. No.
                   309305
 Seq. ID
                   uC-zmflmo17253c07a1
Method
                   BLASTX
NCBI GI
                   g1001715
BLAST score
                   376
E value
                   4.0e-36
Match length
                   90
 % identity
                   80
NCBI Description
                   (D64004) hypothetical protein [Synechocystis sp.]
                   309306
Seq. No.
```

44011

uC-zmflmo17253c09a1

BLASTX

g731325

```
BLAST score
E value
                  7.0e-28
Match length
                  56
                  100
% identity
                  HYPOTHETICAL 9.0 KD PROTEIN IN AROC 3'REGION
NCBI Description
                  >gi_1075615_pir__B49316 aroC 3'-region hypothetical protein
                   - Synechocystis sp >gi_452799_emb_CAA47856_ (X67516) orf81
                   [Synechocystis sp.]
                  309307
Seq. No.
                  uC-zmflmo17253c10a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q1001291
BLAST score
                  249
E value
                  1.0e-138
Match length
                  269
                  98
% identity
                  Synechocystis sp. PCC6803 complete genome, 25/27,
NCBI Description
                  3138604-3270709
                  309308
Seq. No.
                  uC-zmflmo17253d01a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1651768
BLAST score
                   426
E value
                  0.0e+00
                   430
Match length
                  100
% identity
                  Synechocystis sp. PCC6803 complete genome, 2/27,
NCBI Description
                  133860-271599
Seq. No.
                   309309
                  uC-zmflmo17253d02a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1001476
BLAST score
                   657
E value
                   4.0e-69
Match length
                   141
% identity
                   93
NCBI Description
                   (D63999) 3-ketoacyl-acyl carrier protein reductase
                   [Synechocystis sp.]
Seq. No.
                   309310
Seq. ID
                  uC-zmflmo17253d03a1
Method
                  BLASTN
NCBI GI
                   g1652127
BLAST score
                   386
E value
                   0.0e+00
Match length
                   407
% identity
                   98
                  Synechocystis sp. PCC6803 complete genome, 5/27,
NCBI Description
                   524346-630554
```

Seq. No.

309311

Seq. ID uC-zmflmo17253d06a1

Method BLASTX NCBI GI g2494061



```
BLAST score
                  1.0e-83
E value
Match length
                  154
                   97
% identity
                  PUTATIVE DIHYDROFLAVONOL-4-REDUCTASE (DFR)
NCBI Description
                   (DIHYDROKAEMPFEROL 4-REDUCTASE) >gi_1652316_dbj_BAA17239_
                   (D90904) dihydroflavonol 4-reductase [Synechocystis sp.]
                   309312
Seq. No.
                   uC-zmflmo17253d08a1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g1653348
BLAST score
                   416
                   0.0e+00
E value
Match length
                   456
                   98
% identity
                   Synechocystis sp. PCC6803 complete genome, 15/27,
NCBI Description
                   1848242-1991549
                   309313
Seq. No.
                   uC-zmflmo17253d09a1
Seq. ID
                   BLASTX
Method
                   g1651723
NCBI GI
BLAST score
                   617
                   3.0e-64
E value
                   118
Match length
                   99
% identity
                   (D90899) phosphoglycerate mutase [Synechocystis sp.]
NCBI Description
                   309314
Seq. No.
                   uC-zmflmo17253d11a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1208483
BLAST score
                   481
E value
                   2.0e-48
                   165
Match length
                   85
% identity
                   (D64004) hypothetical protein [Synechocystis sp.]
NCBI Description
                   309315
Seq. No.
                   uC-zmflmo17253e01a1
Seq. ID
                   BLASTN
Method
                   q1652360
NCBI GI
                   165
BLAST score
E value
                   5.0e-88
                   221
Match length
% identity
                   Synechocystis sp. PCC6803 complete genome, 7/27,
NCBI Description
                   781449-920915
Seq. No.
                   309316
Seq. ID
                   uC-zmflmo17253e04a1
Method
                   BLASTX
NCBI GI
                   g96774
BLAST score
                   169
E value
                   1.0e-11
Match length
                   128
```

```
% identity 36
NCBI Description hypothetical protein - Salmonella typhimurium
```

Seq. No. 309317
Seq. ID uC-zmflmo17253e06a1
Method BLASTX
NCBI GI g1652076

NCBI GI g1652076
BLAST score 341
E value 5.0e-32
Match length 63
% identity 98

NCBI Description (D90902) hypothetical protein [Synechocystis sp.]

Seq. No. 309318
Seq. ID uC-zmflmo17253e11a1
Method BLASTX
NCRI CT 2405354

NCBI GI g2495354
BLAST score 736
E value 2.0e-78
Match length 149
% identity 99

NCBI Description DNAK PROTEIN 1 (HEAT SHOCK PROTEIN 70) (HSP70)

>gi_1001148_dbj_BAA10290_ (D64001) DnaK [Synechocystis sp.]

Seq. No. 309319

Seq. ID uC-zmflmo17253f01a1

Method BLASTX
NCBI GI g1653061
BLAST score 452
E value 2.0e-45
Match length 94
% identity 90

NCBI Description (D90910) squalene-hopene-cyclase [Synechocystis sp.]

Seq. No. 309320

Seq. ID uC-zmflmo17253f05a1

Method BLASTX
NCBI GI g3123109
BLAST score 774
E value 9.0e-83
Match length 156
% identity 97

NCBI Description HYPOTHETICAL 69.1 KD PROTEIN SLL1178

>gi_1653353_dbj_BAA18267 (D90913) nodulation protein

[Synechocystis sp.]

Seq. No. 309321

Seq. ID uC-zmflmo17253f07a1

Method BLASTN
NCBI GI g1652225
BLAST score 265
E value 1.0e-147
Match length 309
% identity 96

NCBI Description Synechocystis sp. PCC6803 complete genome, 6/27,

630555-781448

```
Seq. No.
Seq. ID
                  uC-zmflmo17253f09a1
                  BLASTN
Method
                  q1652725
NCBI GI
BLAST score
                  246
                  1.0e-136
E value
Match length
                  274
% identity
                   97
                  Synechocystis sp. PCC6803 complete genome, 10/27,
NCBI Description
                  1188886-1311234
                   309323
Seq. No.
                  uC-zmflmo17253f10a1
Seq. ID
Method
                  BLASTX
                  g1653576
NCBI GI
BLAST score
                   353
                   3.0e-33
E value
Match length
                   76
% identity
                   92
                  (D90914) hypothetical protein [Synechocystis sp.]
NCBI Description
                   309324
Seq. No.
                  uC-zmflmo17253g06a1
Seq. ID
Method
                  BLASTX
                   g3025124
NCBI GI
BLAST score
                   364
                   3.0e - 35
E value
Match length
                   75
                   95
% identity
                  HYPOTHETICAL 17.7 KD PROTEIN SLR1419
NCBI Description
                   >gi 1653717 dbj BAA18628 (D90916) hypothetical protein
                   [Synechocystis sp.]
Seq. No.
                   309325
Seq. ID
                   uC-zmflmo17253g11a1
Method
                   BLASTX
NCBI GI
                   q3025124
                   291
BLAST score
                   8.0e-27
E value
```

Match length 64 % identity 89

HYPOTHETICAL 17.7 KD PROTEIN SLR1419 NCBI Description

>gi 1653717 dbj BAA18628 (D90916) hypothetical protein

[Synechocystis sp.]

309326 Seq. No.

uC-zmflmo17253h03a1 Seq. ID

Method BLASTX NCBI GI q1651845 BLAST score 682 E value 4.0e-72 Match length 136 % identity

NCBI Description (D90900) hypothetical protein [Synechocystis sp.]

>gi 1096875 prf 2112351B ccmN gene [Synechocystis sp.]

Seq. No. 309327

```
uC-zmflmo17253h07a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1652225
BLAST score
                  287
                  1.0e-160
E value
                  337
Match length
                  96
% identity
NCBI Description
                  Synechocystis sp. PCC6803 complete genome, 6/27,
                  630555-781448
Seq. No.
                  309328
                  uC-zmflmo17253h09a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1653083
BLAST score
                  310
                  1.0e-174
E value
Match length
                  343
                  97
% identity
NCBI Description Synechocystis sp. PCC6803 complete genome, 13/27,
                  1576593-1719643
                  309329
Seq. No.
                  uC-zmflmo17255a01b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1001102
BLAST score
                  314
                  1.0e-176
E value
Match length
                  366
                  96
% identity
NCBI Description
                  Synechocystis sp. PCC6803 complete genome, 20/27,
                  2539000-2644794
                  309330
Seq. No.
Seq. ID
                  uC-zmflmo17255a02a1
Method
                  BLASTX
NCBI GI
                  g1653382
BLAST score
                  462
                  3.0e-46
E value
Match length
                  91
% identity
                  99
                  (D90913) hypothetical protein [Synechocystis sp.]
NCBI Description
Seq. No.
                  309331
                  uC-zmflmo17255a02b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1001701
BLAST score
                  475
E value
                  0.0e+00
Match length
                  510
                  98
% identity
NCBI Description
                  Synechocystis sp. PCC6803 complete genome, 23/27,
```

2868767-3002965

Seq. No. 309332

Seq. ID uC-zmflmo17255a03b1

Method BLASTX NCBI GI g1651818

```
BLAST score
E value
                  2.0e-87
Match length
                  164
                  98
% identity
NCBI Description (D90900) MorR protein [Synechocystis sp.]
                  309333
Seq. No.
                  uC-zmflmo17255a04b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1652360
BLAST score
                  192
                  1.0e-104
E value
Match length
                  271
% identity
                  93
                  Synechocystis sp. PCC6803 complete genome, 7/27,
NCBI Description
                  781449-920915
                  309334
Seq. No.
                  uC-zmflmo17255a05b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1653715
BLAST score
                  478
                  0.0e+00
E value
Match length
                  559
% identity
                  97
NCBI Description
                  Synechocystis sp. PCC6803 complete genome, 26/27,
                  3270710-3418851
                  309335
Seq. No.
Seq. ID
                  uC-zmflmo17255a06b1
Method
                  BLASTN
NCBI GI
                  q1653836
BLAST score
                  454
E value
                  0.0e+00
Match length
                  482
% identity
                  99
NCBI Description
                  Synechocystis sp. PCC6803 complete genome, 27/27,
                  3418852-3573470
Seq. No.
                  309336
                  uC-zmflmo17255a07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2495391
                  798
BLAST score
E value
                  2.0e-85
Match length
                  174
                  94
% identity
NCBI Description
                  PROBABLE NITROGEN ASSIMILATION TRANSCRIPTIONAL ACTIVATOR
```

>gi 1653610 dbj BAA18522 (D90915) transcriptional

activator protein NtcB [Synechocystis sp.]

Seq. No. 309337

Seq. ID uC-zmflmo17255a11b1

Method BLASTN NCBI GI g1652492 BLAST score 382 E value 0.0e+00

```
Match length
                  96
% identity
                  Synechocystis sp. PCC6803 complete genome, 8/27,
NCBI Description
                  920916-1056466
                  309338
Seq. No.
                  uC-zmflmo17255a12b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3122863
BLAST score
                  613
                  8.0e-64
E value
                  148
Match length
                  86
% identity
NCBI Description
                  D-3-PHOSPHOGLYCERATE DEHYDROGENASE (PGDH)
                  >gi 1652961_dbj_BAA17878_ (D90910) phosphoglycerate
                  dehydrogenase [Synechocystis sp.]
                  309339
Seq. No.
                  uC-zmflmo17255b03a1
Seq. ID
                  {\tt BLASTX}
Method
                  g1653669
NCBI GI
                  309
BLAST score
                  3.0e-28
E value
                  67
Match length
                  94
% identity
                  (D90915) hypothetical protein [Synechocystis sp.]
NCBI Description
Seq. No.
                  309340
                  uC-zmflmo17255b04a1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1208487
                  278
BLAST score
                  1.0e-24
E value
                  57
Match length
                  98
% identity
                  (D64004) transposase [Synechocystis sp.]
NCBI Description
                  309341
Seq. No.
                  uC-zmflmo17255b08a1
Seq. ID
                  BLASTX
                  g1652329
                  711
                  2.0e-75
Match length
                  152
```

```
Method
NCBI GI
BLAST score
E value
```

91 % identity

NCBI Description (D90904) NADH dehydrogenase subunit 4 [Synechocystis sp.]

309342 Seq. No.

Seq. ID uC-zmflmo17255b09b1

BLASTN Method NCBI GI g1652725 BLAST score 182 5.0e-98 E value Match length 226 95 % identity

Synechocystis sp. PCC6803 complete genome, 10/27, NCBI Description

1188886-1311234



```
309343
Seq. No.
                  uC-zmflmo17255b10a1
Seq. ID
                  BLASTN
Method
                   q1653083
NCBI GI
BLAST score
                   398
E value
                   0.0e + 00
Match length
                   398
                   100
% identity
                  Synechocystis sp. PCC6803 complete genome, 13/27,
NCBI Description
                   1576593-1719643
                   309344
Seq. No.
                   uC-zmflmo17255c04a1
Seq. ID
Method
                   BLASTN
                   g1001102
NCBI GI
BLAST score
                   413
E value
                   0.0e + 00
Match length
                   440
                   98
% identity
                   Synechocystis sp. PCC6803 complete genome, 20/27,
NCBI Description
                   2539000-2644794
                   309345
Seq. No.
                   uC-zmflmo17255c05a1
Seq. ID
Method
                   BLASTN
                   g1653836
NCBI GI
BLAST score
                   385
                   0.0e + 00
E value
Match length
                   397
                   99
% identity
                   Synechocystis sp. PCC6803 complete genome, 27/27,
NCBI Description
                   3418852-3573470
Seq. No.
                   309346
                   uC-zmflmo17255c07a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1651785
BLAST score
                   653
E value
                   1.0e-68
Match length
                   128
                   99
% identity
                  (D90900) hypothetical protein [Synechocystis sp.]
NCBI Description
Seq. No.
                   309347
                   uC-zmflmo17255d03a1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g1652225
BLAST score
                   428
E value
                   0.0e + 00
Match length
                   439
% identity
                   100
                   Synechocystis sp. PCC6803 complete genome, 6/27,
NCBI Description
                   630555-781448
```

309348

uC-zmflmo17255d05a1

Seq. No.

Seq. ID

```
Method
NCBI GI
                  q1652235
BLAST score
                  581
                  3.0e-60
E value
                  131
Match length
                  88
% identity
                  (D90904) potassium channel [Synechocystis sp.]
NCBI Description
                  309349
Seq. No.
                  uC-zmflmo17255d06a1
Seq. ID
Method
                  BLASTX
                  g2492610
NCBI GI
BLAST score
                  788
E value
                  2.0e-84
Match length
                  160
                  98
% identity
                  ACETYL-COENZYME A CARBOXYLASE CARBOXYL TRANSFERASE SUBUNIT
NCBI Description
                  BETA >gi 79730 pir JQ1238 zinc finger protein -
                  Synechocystis sp >gi 217109 dbj BAA00893 (D10004) zinc
                  finger protein [Synechocystis sp.] >gi_243477_bbs_77776
                   (S77740) putative zinc finger protein [Synechocystis, PCC
                  6803, Peptide, 326 aa] [Synechocystis]
                  >gi 1001466 dbj BAA10092 (D63999) acetyl-CoA carboxylase
                  beta subunit [Synechocystis sp.]
                  309350
Seq. No.
                  uC-zmflmo17255d07a1
Seq. ID
                  BLASTN
Method
                  g1652618
NCBI GI
BLAST score
                  364
                  0.0e+00
E value
                  388
Match length
                  98
% identity
                  Synechocystis sp. PCC6803 complete genome, 9/27,
NCBI Description
                  1056467-1188885
                   309351
Seq. No.
                  uC-zmflmo17255d09a1
Seq. ID
Method
                  BLASTN
NCBI GI
                   g1652027
BLAST score
                   158
                   6.0e-84
E value
                   162
Match length
                   99
% identity
                  Synechocystis sp. PCC6803 complete genome, 4/27,
NCBI Description
                   402290-524345
                   309352
Seq. No.
Seq. ID
                   uC-zmflmo17255d10a1
Method
                   BLASTX
NCBI GI
                   g130286
```

BLAST score 504 4.0e-51 E value Match length 126 79 % identity

PLASTOCYANIN PRECURSOR >gi 97669 pir S13733 plastocyanin -NCBI Description Synechocystis sp >gi_47402_emb_CAA38038 (X54105)



plastocyanin [Synechocystis PCC6803]
>gi_1001599_dbj_BAA10227_ (D64000) plastocyanin
[Synechocystis sp.]

Seq. ID uC-zmflmo17255d11b1
Method BLASTN
NCBI GI g1652725
BLAST score 134
E value 1.0e-69

Match length 182 % identity 94

Seq. No.

NCBI Description Synechocystis sp. PCC6803 complete genome, 10/27,

1188886-1311234

Seq. No. 309354

Seq. ID uC-zmflmo17255e01b1

Method BLASTN
NCBI GI g1652360
BLAST score 241
E value 1.0e-133
Match length 257
% identity 98

NCBI Description Synechocystis sp. PCC6803 complete genome, 7/27,

781449-920915

Seq. No. 309355

Seq. ID uC-zmflmo17255e02a1

Method BLASTN
NCBI GI g1652360
BLAST score 348
E value 0.0e+00
Match length 383
% identity 97

NCBI Description Synechocystis sp. PCC6803 complete genome, 7/27,

781449-920915

Seq. No. 309356

Seq. ID uC-zmflmo17255e03a1

Method BLASTX
NCBI GI g1653558
BLAST score 343
E value 3.0e-32
Match length 94
% identity 80

NCBI Description (D90914) hypothetical protein [Synechocystis sp.]

Seq. No. 309357

Seq. ID uC-zmflmo17255e04a1

Method BLASTX
NCBI GI g1001663
BLAST score 457
E value 1.0e-45
Match length 90
% identity 99

NCBI Description (D64002) rare lipoprotein A [Synechocystis sp.]

E value

4.0e-78

```
309358
Seq. No.
                  uC-zmflmo17255e05a1
Seq. ID
                  BLASTN
Method
                  q1651650
NCBI GI
BLAST score
                  106
E value
                  8.0e-53
                  187
Match length
                  88
% identity
NCBI Description Synechocystis sp. PCC6803 complete genome, 1/27, 1-133859
Seq. No.
                  309359
                  uC-zmflmo17255e09a1
Seq. ID
                  BLASTX
Method
                  q1652190
NCBI GI
                   743
BLAST score
E value
                   4.0e-79
Match length
                   149
                   10
% identity
NCBI Description (D90903) Fat protein [Synechocystis sp.]
                   309360
Seq. No.
Seq. ID
                   uC-zmflmo17255e09b1
                   BLASTX
Method
                   q1653558
NCBI GI
                   243
BLAST score
                   4.0e-21
E value
Match length
                   50
% identity
                  (D90914) hypothetical protein [Synechocystis sp.]
NCBI Description
                   309361
Seq. No.
Seq. ID
                   uC-zmflmo17255e11a1
Method
                   BLASTX
NCBI GI
                   g1652104
BLAST score
                   774
E value
                   9.0e-83
Match length
                   155
% identity
                   99
                   (D90902) hypothetical protein [Synechocystis sp.]
NCBI Description
Seq. No.
                   309362
Seq. ID
                   uC-zmflmo17255e12b1
Method
                   BLASTN
                   q1653477
NCBI GI
BLAST score
                   379
                   0.0e+00
E value
Match length
                   383
                   100
% identity
                   Synechocystis sp. PCC6803 complete genome, 16/27,
NCBI Description
                   1991550-2137258
Seq. No.
                   309363
                   uC-zmflmo17255f01b1
Seq. ID
                   BLASTX
Method
                   g1652746
NCBI GI
BLAST score
                   656
```

NCBI Description

```
Match length
% identity
                   89
                  (D90908) hypothetical protein [Synechocystis sp.]
NCBI Description
                  309364
Seq. No.
                  uC-zmflmo17255f02a1
Seq. ID
Method
                  BLASTX
                  g1653786
NCBI GI
BLAST score
                   492
E value
                  5.0e-53
Match length
                  115
                  94
% identity
NCBI Description
                  (D90916) mannose-1-phosphate guanyltransferase
                   [Synechocystis sp.]
Seq. No.
                   309365
                  uC-zmflmo17255f02b1
Seq. ID
Method
                  BLASTN
                  g1653715
NCBI GI
BLAST score
                   60
                   3.0e-25
E value
                   204
Match length
                   89
% identity
NCBI Description
                  Synechocystis sp. PCC6803 complete genome, 26/27,
                   3270710-3418851
                   309366
Seq. No.
                   uC-zmflmo17255f06a1
Seq. ID
Method
                  BLASTN
                   g1651650
NCBI GI
BLAST score
                   412
E value
                   0.0e + 00
Match length
                   449
% identity
                   98
NCBI Description Synechocystis sp. PCC6803 complete genome, 1/27, 1-133859
Seq. No.
                   309367
Seq. ID
                   uC-zmflmo17255f08a1
Method
                   BLASTX
NCBI GI
                   g1001516
BLAST score
                   318
E value
                   1.0e-29
Match length
                   103
                   77
% identity
NCBI Description
                   (D64000) sensory transduction histidine kinase
                   [Synechocystis sp.]
Seq. No.
                   309368
Seq. ID
                   uC-zmflmo17255f09a1
Method
                   BLASTX
NCBI GI
                   q1652817
BLAST score
                   577
E value
                   1.0e-59
Match length
                   114
% identity
                   100
                  (D90908) hypothetical protein [Synechocystis sp.]
```

```
Seq. No.
                   309369
                  uC-zmflmo17255f11a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1653226
                  451
BLAST score
                  7.0e-45
E value
Match length
                  86
                  100
% identity
                  (D90911) hypothetical protein [Synechocystis sp.]
NCBI Description
                  309370
Seq. No.
                  uC-zmflmo17255f12b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2500971
BLAST score
                   640
                  5.0e-67
E value
Match length
                  129
                   98
% identity
                  ASPARTYL-TRNA SYNTHETASE (ASPARTATE--TRNA LIGASE) (ASPRS)
NCBI Description
                  >qi 1652993 dbj BAA17910 (D90910) aspartyl-tRNA synthetase
                   [Synechocystis sp.]
Seq. No.
                   309371
                  uC-zmflmo17255g01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1652312
BLAST score
                   894
                  1.0e-96
E value
                   177
Match length
% identity
                   97
                  (D90904) serine/threonine protein kinase [Synechocystis
NCBI Description
                   sp.]
Seq. No.
                   309372
                   uC-zmflmo17255g04a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1653455
BLAST score
                   470
                   2.0e-47
E value
Match length
                   101
% identity
                   91
                   (D90913) delta-1-pyrroline-5-carboxylate dehydrogenase
NCBI Description
                   [Synechocystis sp.]
```

Seq. No. 309373

Seq. ID uC-zmflmo17255g06a1

Method BLASTX
NCBI GI g1653428
BLAST score 300
E value 3.0e-27
Match length 68
% identity 82

NCBI Description (D90913) hypothetical protein [Synechocystis sp.]

Seq. No. 309374

Seq. ID uC-zmflmo17255g08a1

Method BLASTN

```
q1652618
NCBI GI
BLAST score
                  266
E value
                  1.0e-148
                  314
Match length
% identity
                   96
                  Synechocystis sp. PCC6803 complete genome, 9/27,
NCBI Description
                  1056467-1188885
                  309375
Seq. No.
Seq. ID
                  uC-zmflmo17255g09a1
Method
                  BLASTX
                   q1001154
NCBI GI
                   518
BLAST score
                   6.0e-53
E value
                   114
Match length
% identity
                   89
NCBI Description (D64001) processing protease [Synechocystis sp.]
Seq. No.
                   309376
                   uC-zmflmo17255g12b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q1001687
                   476
BLAST score
                   1.0e-47
E value
                   104
Match length
                   92
% identity
NCBI Description (D64002) hypothetical protein [Synechocystis sp.]
                   309377
Seq. No.
                   uC-zmflmo17255h01b1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g1652225
BLAST score
                   342
E value
                   0.0e+00
Match length
                   457
                   94
% identity
                   Synechocystis sp. PCC6803 complete genome, 6/27,
NCBI Description
                   630555-781448
                   309378
Seq. No.
                   uC-zmflmo17255h02b1
Seq. ID
                   BLASTN
Method
```

Method BLASTN
NCBI GI g1651650
BLAST score 509
E value 0.0e+00
Match length 529
% identity 99

NCBI Description Synechocystis sp. PCC6803 complete genome, 1/27, 1-133859

Seq. No. 309379

Seq. ID uC-zmflmo17255h03b1

Method BLASTX
NCBI GI g1652384
BLAST score 355
E value 4.0e-34
Match length 73
% identity 92



```
(D90905) ABC transporter [Synechocystis sp.]
NCBI Description
                  309380
Seq. No.
                  uC-zmflmo17255h04b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1652923
                  762
BLAST score
                  3.0e-81
E value
                  163
Match length
                   91
% identity
                   (D90909) peptidyl-prolyl cis-trans isomerase [Synechocystis
NCBI Description
                   309381
Seq. No.
                   uC-zmflmo17255h05b1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g1653604
BLAST score
                   249
E value
                   1.0e-138
                   277
Match length
                   97
% identity
                   Synechocystis sp. PCC6803 complete genome, 17/27,
NCBI Description
                   2137259-2267259
                   309382
Seq. No.
                   uC-zmflmo17255h06b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1653540
                   675
BLAST score
                   4.0e-71
E value
                   127
Match length
% identity
                   97
                   (D90914) hypothetical protein [Synechocystis sp.]
NCBI Description
                   309383
Seq. No.
                   uC-zmflmo17255h07b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1651864
BLAST score
                   430
E value
                   1.0e-42
Match length
                   99
% identity
                   87
                   (D90900) pyridoxal phosphate biosynthetic protein PdxJ
NCBI Description
                   [Synechocystis sp.]
Seq. No.
                   309384
                   uC-zmflmo17255h08b1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g1001484
BLAST score
                   409
                   0.0e + 00
E value
                   433
Match length
% identity
                   99
                   Synechocystis sp. PCC6803 complete genome, 19/27,
NCBI Description
```

Seq. No. 309385

2392729-2538999

```
uC-zmflmo17255h09b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1653288
BLAST score
                   704
E value
                   2.0e-74
Match length
                   146
% identity
                   98
                   (D90912) hypothetical protein [Synechocystis sp.]
NCBI Description
                   309386
Seq. No.
                   uC-zmflmo17255h11b1
Seq. ID
                   BLASTN
Method
                   g1651768
NCBI GI
BLAST score
                   306
E value
                   1.0e-172
Match length
                   338
                   98
% identity
                   Synechocystis sp. PCC6803 complete genome, 2/27,
NCBI Description
                   133860-271599
Seq. No.
                   309387
                   uC-zmflmo17256a01b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1651846
BLAST score
                   523
E value
                   8.0e-77
Match length
                   157
% identity
                   26
                  (D90900) carbon dioxide concentrating mechanism protein
NCBI Description
                   CcmM [Synechocystis sp.]
                   309388
Seq. No.
                   uC-zmflmo17256a03b1
Seq. ID
                   BLASTN
Method
                   g1652225
NCBI GI
BLAST score
                   378
                   0.0e+00
E value
Match length
                   382
                   100
% identity
                   Synechocystis sp. PCC6803 complete genome, 6/27,
NCBI Description
                   630555-781448
                   309389
Seq. No.
                   uC-zmflmo17256a09b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2499885
BLAST score
                   628
E value
                   1.0e-65
Match length
                   129
```

% identity 98

NCBI Description PUTATIVE PROTEASE SLR0021 >gi 1001581 dbj BAA10208_

(D64000) protease IV [Synechocystis sp.]

309390 Seq. No.

uC-zmflmo17256a10b1 Seq. ID

Method BLASTN NCBI GI g1653477

```
BLAST score
                  0.0e + 00
E value
                  507
Match length
% identity
                  97
                  Synechocystis sp. PCC6803 complete genome, 16/27,
NCBI Description
                  1991550-2137258
                  309391
Seq. No.
                  uC-zmflmo17256a11b1
Seq. ID
                  BLASTX
Method
                  g1653466
NCBI GI
BLAST score
                  306
                  7.0e-28
E value
Match length
                  61
% identity
                  98
                  (D90913) succinyl-CoA synthetase [Synechocystis sp.]
NCBI Description
                  309392
Seq. No.
                  uC-zmflmo17256b01b1
Seq. ID
                  BLASTN
Method
                  g1653228
NCBI GI
BLAST score
                  384
                  0.0e+00
E value
Match length
                  388
                  75
% identity
                  Synechocystis sp. PCC6803 complete genome, 14/27,
NCBI Description
                  1719644-1848241
                   309393
Seq. No.
                  uC-zmflmo17256b09a1
Seq. ID
Method
                  BLASTX
                   q1652841
NCBI GI
BLAST score
                   687
                   3.0e-75
E value
Match length
                   152
                   99
% identity
                  (D90908) sensory transduction histidine kinase
NCBI Description
                   [Synechocystis sp.]
                   309394
Seq. No.
                   uC-zmflmo17256b10b1
Seq. ID
Method
                   BLASTN
NCBI GI
                   q1653083
BLAST score
                   495
E value
                   0.0e + 00
Match length
                   516
% identity
                   99
                  Synechocystis sp. PCC6803 complete genome, 13/27,
NCBI Description
                   1576593-1719643
Seq. No.
                   309395
                   uC-zmflmo17256b11b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1652044
```

NCBI GI g1652044
BLAST score 165
E value 2.0e-11
Match length 103

```
% identity
                  (D90902) adenylate cyclase [Synechocystis sp.]
NCBI Description
                  309396
Seq. No.
                  uC-zmflmo17256c01b1
Seq. ID
                  BLASTX
Method
                  g1652057
NCBI GI
BLAST score
                  872
                  3.0e-94
E value
Match length
                  171
                  100
% identity
                  (D90902) hypothetical protein [Synechocystis sp.]
NCBI Description
                  309397
Seq. No.
Seq. ID
                  uC-zmflmo17256c08b1
                  BLASTN
Method
NCBI GI
                   q1652844
BLAST score
                   254
                   1.0e-141
E value
Match length
                   262
% identity
                   99
                   Synechocystis sp. PCC6803 complete genome, 11/27,
NCBI Description
                   1311235-1430418
                   309398
Seq. No.
Seq. ID
                   uC-zmflmo17256c09b1
Method
                   BLASTN
NCBI GI
                   g1652844
BLAST score
                   221
                   1.0e-121
E value
                   385
Match length
                   90
% identity
                   Synechocystis sp. PCC6803 complete genome, 11/27,
NCBI Description
                   1311235-1430418
                   309399
Seq. No.
                   uC-zmflmo17256d02a1
Seq. ID
                   BLASTX
Method
                   g1651730
NCBI GI
BLAST score
                   624
                   3.0e-65
E value
Match length
                   145
                   87
% identity
                  (D90899) ribonuclease E [Synechocystis sp.]
NCBI Description
                   309400
Seq. No.
                   uC-zmflmo17256d02b1
Seq. ID
                   BLASTX
Method
                   g1651730
NCBI GI
BLAST score
                   866
E value
                   2.0e-93
Match length
                   171
                   99
% identity
                   (D90899) ribonuclease E [Synechocystis sp.]
NCBI Description
                   309401
Seq. No.
                   uC-zmflmo17256d07b1
Seq. ID
```

```
Method
                  g1653724
NCBI GI
                   491
BLAST score
                  1.0e-49
E value
                  112
Match length
% identity
                   84
                  (D90916) hypothetical protein [Synechocystis sp.]
NCBI Description
                  309402
Seq. No.
Seq. ID
                  uC-zmflmo17256d08b1
Method
                  BLASTN
NCBI GI
                  g1001291
                  271
BLAST score
                  1.0e-151
E value
                  275
Match length
                   100
% identity
                  Synechocystis sp. PCC6803 complete genome, 25/27,
NCBI Description
                   3138604-3270709
                   309403
Seq. No.
                  uC-zmflmo17256d10b1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g1652360
BLAST score
                   186
E value
                   1.0e-100
Match length
                   430
                   86
% identity
                   Synechocystis sp. PCC6803 complete genome, 7/27,
NCBI Description
                   781449-920915
                   309404
Seq. No.
Seq. ID
                   uC-zmflmo17256d11b1
Method
                   BLASTN
NCBI GI
                   q1653348
BLAST score
                   481
E value
                   0.0e + 00
Match length
                   498
                   99
% identity
                   Synechocystis sp. PCC6803 complete genome, 15/27,
NCBI Description
                   1848242-1991549
                   309405
Seq. No.
Seq. ID
                   uC-zmflmo17256e03b1
                   BLASTX
Method
                   g1652468
NCBI GI
BLAST score
                   451
                   8.0e-45
E value
Match length
                   91
                   96
% identity
                   (D90905) short-chain alcohol dehydrogenase family
NCBI Description
```

[Synechocystis sp.]

Seq. No. 309406

uC-zmflmo17256e07a1 Seq. ID

Method BLASTN NCBI GI g1001484 BLAST score 416

```
0.0e + 00
E value
Match length
                  424
                  100
% identity
                  Synechocystis sp. PCC6803 complete genome, 19/27,
NCBI Description
                  2392729-2538999
                  309407
Seq. No.
                  uC-zmflmo17256e07b1
Seq. ID
                  BLASTN
Method
                   g1001484
NCBI GI
BLAST score
                   58
                   8.0e-24
E value
                   343
Match length
                   83
% identity
                  Synechocystis sp. PCC6803 complete genome, 19/27,
NCBI Description
                   2392729-2538999
                   309408
Seq. No.
                   uC-zmflmo17256e08a1
Seq. ID
                   BLASTN
Method
                   g1651650
NCBI GI
BLAST score
                   226
                   1.0e-124
E value
Match length
                   293
% identity
                   95
NCBI Description Synechocystis sp. PCC6803 complete genome, 1/27, 1-133859
Seq. No.
                   309409
                   uC-zmflmo17256e08b1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g1651650
BLAST score
                   344
                   0.0e + 00
E value
                   484
Match length
                   93
% identity
                  Synechocystis sp. PCC6803 complete genome, 1/27, 1-133859
NCBI Description
                   309410
Seq. No.
                   uC-zmflmo17256e09b1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g1653477
BLAST score
                   177
E value
                   4.0e-95
Match length
                   237
                   94
% identity
                   Synechocystis sp. PCC6803 complete genome, 16/27,
NCBI Description
                   1991550-2137258
```

Seq. ID uC-zmflmo172 Method BLASTX

NCBI GI g1653508 BLAST score 339 E value 9.0e-32 Match length 97 % identity 74

NCBI Description (D90914) hypothetical protein [Synechocystis sp.]

```
309412
Seq. No.
                  uC-zmflmo17256e12b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1653395
BLAST score
                  714
                   5.0e-84
E value
Match length
                   161
                   90
% identity
NCBI Description
                   (D90913) PET112 [Synechocystis sp.]
                   309413
Seq. No.
                   uC-zmflmo17256f01b1
Seq. ID
                   BLASTN
Method
                   g1652618
NCBI GI
BLAST score
                   56
                   5.0e-23
E value
Match length
                   132
% identity
                   Synechocystis sp. PCC6803 complete genome, 9/27,
NCBI Description
                   1056467-1188885
                   309414
Seq. No.
                   uC-zmflmo17256f05a1
Seq. ID
                   BLASTX
Method
                   g1651948
NCBI GI
BLAST score
                   257
                   3.0e-22
E value
                   72
Match length
% identity
                   75
                  (D90901) hypothetical protein [Synechocystis sp.]
NCBI Description
                   309415
Seq. No.
                   uC-zmflmo17256f05b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1652521
BLAST score
                   424
                   1.0e-41
E value
Match length
                   84
                   100
% identity
                   (D90906) hypothetical protein [Synechocystis sp.]
NCBI Description
                   309416
Seq. No.
                   uC-zmflmo17256f09b1
Seq. ID
                   BLASTN
Method
                   g1653348
NCBI GI
BLAST score
                   267
                   1.0e-148
E value
                   279
Match length
                   99
% identity
                   Synechocystis sp. PCC6803 complete genome, 15/27,
NCBI Description
                   1848242-1991549
                   309417
Seq. No.
                   uC-zmflmo17256f12b1
Seq. ID
```

BLASTX

g1653067

Method NCBI GI

```
BLAST score
                   9.0e-56
E value
                   132
Match length
% identity
                   86
NCBI Description
                  (D90910) acetolactate synthase [Synechocystis sp.]
                   309418
Seq. No.
                  uC-zmflmo17256g06b1
Seq. ID
Method
                  BLASTX
                   g1652213
NCBI GI
BLAST score
                   386
                   3.0e-37
E value
                   74
Match length
                   99
% identity
NCBI Description
                  (D90903) hypothetical protein [Synechocystis sp.]
                   309419
Seq. No.
                   uC-zmflmo17256g07b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2440163
BLAST score
                   158
                   1.0e-10
E value
                   87
Match length
                   45
% identity
                  (Y14837) beta-galactosidase [Cloning vector pUC57]
NCBI Description
                   309420
Seq. No.
                   uC-zmflmo17256g08b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2648666
BLAST score
                   165
E value
                   2.0e-11
Match length
                   151
% identity
                   34
                  (AE000973) conserved hypothetical protein [Archaeoglobus
NCBI Description
                   fulgidus]
Seq. No.
                   309421
                   uC-zmflmo17256g09a1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g1001779
BLAST score
                   383
                   0.0e + 00
E value
Match length
                   395
                   99
% identity
                   Synechocystis sp. PCC6803 complete genome, 24/27,
NCBI Description
                   3002966-3138603
Seq. No.
                   309422
Seq. ID
                   uC-zmflmo17256g09b1
Method
                   BLASTN
NCBI GI
                   q1001779
BLAST score
                   476
E value
                   0.0e+00
Match length
                   476
% identity
                   100
```

NCBI Description Synechocystis sp. PCC6803 complete genome, 24/27,



3002966-3138603

```
Seq. No.
                  309423
Seq. ID
                  uC-zmflmo17256g11b1
Method
                  BLASTX
NCBI GI
                  q1709285
BLAST score
                  546
                  5.0e-56
E value
                  106
Match length
                  99
% identity
                  PUTATIVE PYRUVATE-FLAVODOXIN OXIDOREDUCTASE
NCBI Description
                  >gi 1006618_dbj_BAA10774_ (D64005) pyruvate oxidoreductase
                  [Synechocystis sp.]
                  309424
Seq. No.
Seq. ID
                  uC-zmflmo17256g12b1
Method
                  BLASTN
NCBI GI
                  q1001291
                  169
BLAST score
                   5.0e-90
E value
                   169
Match length
% identity
                   100
                  Synechocystis sp. PCC6803 complete genome, 25/27,
NCBI Description
                   3138604-3270709
                   309425
Seq. No.
Seq. ID
                   uC-zmflmo17256h01b1
                   BLASTN
Method
                   q1001612
NCBI GI
BLAST score
                   439
                   0.0e + 00
E value
Match length
                   459
                   99
% identity
                   Synechocystis sp. PCC6803 complete genome, 21/27,
NCBI Description
                   2644795-2755702
Seq. No.
                   309426
                   uC-zmflmo17256h02b1
Seq. ID
                   BLASTX
Method
                   q1653832
NCBI GI
BLAST score
                   543
                   1.0e-55
E value
Match length
                   105
                   100
% identity
                  (D90916) hypothetical protein [Synechocystis sp.]
NCBI Description
                   309427
Seq. No.
                   uC-zmflmo17256h04b1
Seq. ID
                   BLASTX
Method
```

NCBI GI g1653174 BLAST score 469 E value 6.0e-47

Match length 93 % identity 98

NCBI Description (D90911) beta ketoacyl-acyl carrier protein synthase

[Synechocystis sp.]

```
q. No. 30
```

Seq. No. 309428 Seq. ID uC-zmflmo17256h05b1 Method BLASTX

NCBI GI g3024897 BLAST score 403 E value 3.0e-39 Match length 79 % identity 99

NCBI Description HYPOTHETICAL 51.0 KD PROTEIN SLL0154

>gi_1001453_dbj_BAA10078_ (D63999) 35.6 kD protein

[Synechocystis sp.]

Seq. No. 309429

Seq. ID uC-zmflmo17256h06b1

Method BLASTX
NCBI GI g1706406
BLAST score 812
E value 3.0e-87
Match length 166
% identity 95

NCBI Description NADP-SPECIFIC GLUTAMATE DEHYDROGENASE (NADP-GDH)

>gi 1361331 pir S56683 glutamate dehydrogenase (NADP+) (EC

1.4.1.4) - Synechocystis sp >gi_1006603_dbj_BAA10756_ (D64005) glutamate dehydrogenase (NADP+) [Synechocystis sp.] >gi_1006751_emb_CAA54601_ (X77454) glutamate

Sp. 1 >gr_1000/31_emb_cAA34001_ (A//434) gr

dehydrogenase (NADP+) [Synechocystis sp.]

Seq. No. 309430

Seq. ID uC-zmflmo17256h09a1

Method BLASTX
NCBI GI g2498452
BLAST score 648
E value 4.0e-68
Match length 130
% identity 97

NCBI Description HISF PROTEIN (CYCLASE) >gi_1653277_dbj_BAA18192_ (D90912)

cyclase [Synechocystis sp.]

Seq. No. 309431

Seq. ID uC-zmflmo17256h11b1

Method BLASTN
NCBI GI g1653715
BLAST score 321
E value 0.0e+00
Match length 321
% identity 100

NCBI Description Synechocystis sp. PCC6803 complete genome, 26/27,

3270710-3418851

Seq. No. 309432

Seq. ID uC-zmflmo17256h12b1

Method BLASTN
NCBI GI g1652027
BLAST score 271
E value 1.0e-151
Match length 283
% identity 99

NCBI Description Synechocystis sp. PCC6803 complete genome, 4/27, 402290-524345

309433 Seq. No.

uC-zmflmo17257e07b1 Seq. ID

BLASTN Method g22332 NCBI GI 235 BLAST score 1.0e-129 E value 354 Match length 92

NCBI Description Z.mays HRGP gene

309434 Seq. No.

% identity

uC-zmflmo17257f01b1 Seq. ID

BLASTX Method g4585871 NCBI GI BLAST score 396 1.0e-38 E value Match length 96 % identity 73

(AC005850) Unknown protein [Arabidopsis thaliana] NCBI Description

309435 Seq. No.

uC-zmflmo17257f08b1 Seq. ID

Method BLASTX g4185740 NCBI GI 248 BLAST score 1.0e-25 E value 108 Match length 61 % identity

(AF079999) putative glutamate receptor [Arabidopsis NCBI Description

thaliana]

309436 Seq. No.

uC-zmflmo17258b01a1 Seq. ID

BLASTN Method g4160401 NCBI GI 169 BLAST score 3.0e-90 E value Match length 229 93 % identity

NCBI Description Zea mays eIF-5 gene, exons 1-2

309437 Seq. No.

uC-zmflmo17258b07b1 Seq. ID

BLASTX Method g2497540 NCBI GI BLAST score 307 4.0e-28 E value Match length 89 % identity 65

NCBI Description PYRUVATE KINASE, CHLOROPLAST ISOZYME G

309438 Seq. No.

Seq. ID uC-zmflmo17258c04b1

Method BLASTX

```
q4105798
NCBI GI
                  276
BLAST score
E value
                  2.0e-27
Match length
                  95
% identity
                  57
NCBI Description (AF049930) PGP237-11 [Petunia x hybrida]
                  309439
Seq. No.
                  uC-zmflmo17258d01a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g11957
BLAST score
                  201
                  1.0e-109
E value
                  229
Match length
% identity
NCBI Description Rice complete chloroplast genome
Seq. No.
                  309440
Seq. ID
                  uC-zmflmo17258d02b1
Method
                  BLASTX
NCBI GI
                  q4126809
```

BLAST score 328 2.0e-30 E value 80 Match length % identity 46

NCBI Description (AB017042) glyoxalase I [Oryza sativa]

309441 Seq. No. uC-zmflmo17258d04b1 Seq. ID Method BLASTN NCBI GI g22332 BLAST score 259 1.0e-144

E value Match length 350 % identity 93

NCBI Description Z.mays HRGP gene

309442 Seq. No.

uC-zmflmo17258f01b1 Seq. ID

BLASTN Method NCBI GI q3821780 36 ₺ BLAST score 1.0e-10 E value Match length 36 100 % identity

NCBI Description Xenopus laevis cDNA clone 27A6-1

309443 Seq. No.

uC-zmflmo17258g01b1 Seq. ID

BLASTX Method g4512714 NCBI GI BLAST score 194 8.0e-15 E value Match length 60 % identity 63

NCBI Description (AC006569) hypothetical protein [Arabidopsis thaliana]

-



```
Seq. No.
Seq. ID
                  uC-zmflmo17258g02a1
                  BLASTX
Method
                  g4185311
NCBI GI
BLAST score
                  460
E value
                  3.0e-46
                  98
Match length
% identity
NCBI Description (AF090446) polyprotein [Zea mays]
                  309445
Seq. No.
                  uC-zmflmo17258g02b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3645898
BLAST score
                  640
                  4.0e-67
E value
Match length
                  155
                  79
% identity
NCBI Description (U68408) in-frame stop codon; possibly a post-transposition
                  mutation [Zea mays]
                   309446
Seq. No.
                  uC-zmflmo17258g03a1
Seq. ID
                  BLASTX
Method
                  g3894187
NCBI GI
                   268
BLAST score
                   6.0e-24
E value
Match length
                   106
                   56
% identity
NCBI Description (AC005662) hypothetical protein [Arabidopsis thaliana]
                   309447
Seq. No.
                   uC-zmflmo17258g10b1
Seq. ID
                   BLASTX
Method
                   g3004480
NCBI GI
BLAST score
                   185
E value
                   9.0e-14
Match length
                   93
                   37
% identity
                  (AJ228333) reverse transcriptase [Pinus elliottii]
NCBI Description
                   309448
Seq. No.
                   uC-zmflmo17258h11b1
Seq. ID
                   BLASTX
Method
                   q115771
NCBI GI
BLAST score
                   753
                   2.0e-80
E value
Match length
                   146
% identity
                   99
                   CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                   (CAB-1) (LHCP) >gi_82682_pir__S04453 chlorophyll
                   a/b-binding protein precursor - maize
                   >gi_22224_emb_CAA32900_ (X14794) chlorophyll a/b-binding
                   preprotein (AA 1 - 262) [Zea mays]
```

309449

uC-zmflmo17259a05b1

Seq. No.

Seq. ID

```
Method
                  q4490737
NCBI GI
                  213
BLAST score
                  7.0e-17
E value
Match length
                  76
% identity
                  55
NCBI Description (AL035708) putative protein [Arabidopsis thaliana]
                  309450
Seq. No.
Seq. ID
                  uC-zmflmo17259b05b1
Method
                  BLASTX
NCBI GI
                  g3687235
BLAST score
                  377
                  4.0e-36
E value
                  115
Match length
                   68
% identity
                  (AC005169) putative copia-like transposable element
NCBI Description
                   [Arabidopsis thaliana]
                   309451
Seq. No.
                  uC-zmflmo17259b08b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4519936
BLAST score
                  174
                  2.0e-12
E value
                  112
Match length
                   35
% identity
NCBI Description (AB019186) RPR1 [Oryza sativa]
                   309452
Seq. No.
                   uC-zmflmo17259b12b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3851333
BLAST score
                   252
E value
                   2.0e-22
Match length
                   75
% identity
                  (Y09302) putative MADS-domain transcription factor [Zea
NCBI Description
                   mays]
                   309453
Seq. No.
                   uC-zmflmo17259d04b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2760839
BLAST score
                   177
                   2.0e-13
E value
Match length
                   41
% identity
                   85
                   (AC003105) putative receptor kinase [Arabidopsis thaliana]
NCBI Description
                   309454
Seq. No.
                   uC-zmflmo17259e08b1
Seq. ID
Method
                   BLASTX
                   g1652057
NCBI GI
BLAST score
                   319
                   2.0e-29
E value
```

119

Match length

```
% identity
                  (D90902) hypothetical protein [Synechocystis sp.]
NCBI Description
                  309455
Seq. No.
Seq. ID
                  uC-zmflmo17259e09b1
Method
                  BLASTN
                  q4140643
NCBI GI
                  40
BLAST score
                  5.0e-13
E value
                  79
Match length
                  89
% identity
                   Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster,
NCBI Description
                  complete sequence
                   309456
Seq. No.
Seq. ID
                   uC-zmflmo17259g02b1
Method
                   BLASTX
NCBI GI
                   q2130139
                   201
BLAST score
                   6.0e-17
E value
                   82
Match length
                   60
% identity
                   hypothetical protein - maize >gi_949980 emb_CAA61258_
NCBI Description
                   (X88779) orf [Zea mays]
                   309457
Seq. No.
Seq. ID
                   uC-zmflmo17259g03b1
Method
                   BLASTN
                   g22332
NCBI GI
BLAST score
                   146
                   2.0e-76
E value
                   293
Match length
% identity
                   88
                   Z.mays HRGP gene
NCBI Description
                   309458
Seq. No.
Seq. ID
                   uC-zmflmo17259g11b1
Method
                   BLASTX
                   g2827709
NCBI GI
BLAST score
                   188
E value
                   1.0e-14
Match length
                   74
% identity
                   49
                   (AL021684) predicted protein [Arabidopsis thaliana]
NCBI Description
                   309459
Seq. No.
                   uC-zmflmo17260c05a1
Seq. ID
                   BLASTX
Method
                   g3157926
NCBI GI
BLAST score
                   168
```

3.0e-12 E value 70 Match length % identity 49

(AC002131) Strong similarity to extensin-like protein NCBI Description

gb Z34465 from Zea mays. [Arabidopsis thaliana]

Seq. No. 309460

```
uC-zmflmo17261a06b1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g2662309
BLAST score
                  37
E value
                  2.0e-11
Match length
                  57
% identity
                  91
NCBI Description Hordeum vulgare mRNA for bpwl, complete cds
Seq. No.
                  309461
                  uC-zmflmo17261a10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2984709
BLAST score
                  422
E value
                  1.0e-41
Match length
                  88
% identity
                  91
                  (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]
NCBI Description
                  309462
Seq. No.
Seq. ID
                  uC-zmflmo17261b05b1
Method
                  BLASTX
NCBI GI
                   g115786
BLAST score
                   251
E value
                   1.0e-21
Match length
                   100
% identity
                   52
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                   (CAB) (LHCP) >gi_82680_pir__A29119 chlorophyll a/b-binding
                   protein - maize >gi_22357_emb_CAA68451_ (Y00379) LHCP [Zea
                   mays]
                   309463
Seq. No.
                   uC-zmflmo17261b08b1
Seq. ID
                   BLASTN
Method
                   g4007864
NCBI GI
BLAST score
                   35
E value
                   2.0e-10
Match length
                   235
                   79
% identity
NCBI Description Zea mays HRGP gene, AC1503 line
                   309464
Seq. No.
                   uC-zmflmo17261d02b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1527001
BLAST score
                   166
                   9.0e-12
E value
Match length
                   69
% identity
                   48
                  (U55867) Ipomoea nil Pn47p [Ipomoea nil]
NCBI Description
```

Seq. No. 309465

Seq. ID uC-zmflmo17261d07b1

Method BLASTX
NCBI GI g3641252
BLAST score 157

```
6.0e-11
E value
Match length
                  80
% identity
                   (AF053127) leucine-rich receptor-like protein kinase [Malus
NCBI Description
                  domestica]
Seq. No.
                  309466
Seq. ID
                  uC-zmflmo17261d09b1
Method
                  BLASTX 🐬
NCBI GI
                  g3063444
BLAST score
                  202
                  7.0e-16
E value
Match length
                  43
% identity
NCBI Description (AC003981) F22013.5 [Arabidopsis thaliana]
Seq. No.
                   309467
Seq. ID
                  uC-zmflmo17261d12b1
Method
                  BLASTX
NCBI GI
                   q1181673
BLAST score
                   501
E value
                   6.0e-51
Match length
                   107
% identity
                   92
                   (U41652) heat shock protein cognate 70 [Sorghum bicolor]
NCBI Description
Seq. No.
                   309468
Seq. ID
                   uC-zmflmo17261e01b1
Method
                   BLASTX
NCBI GI
                   g4558661
BLAST score
                   252
E value
                   9.0e-22
                   119
Match length
                   54
% identity
                   (AC007063) putative malate oxidoreductase (NAD)
NCBI Description
                   [Arabidopsis thaliana]
                   309469
Seq. No.
                   uC-zmflmo17261e10b1
Seq. ID
Method
                   BLASTX
                   g82698
NCBI GI
BLAST score
                   153
                   2.0e-10
E value
                   50
Match length
                   62
% identity
                   hydroxyproline-rich glycoprotein precursor - maize
NCBI Description
                   >gi_257041_bbs_115226 (S45164) hydroxyproline-rich
                   glycoprotein, HRGP [maize, Peptide, 328 aa] [Zea mays]
                   >gi_4007865_emb_CAA10387_ (AJ131535) Hydroxyproline-rich
```

Seq. No. 309470

Seq. ID uC-zmflmo17261e12b1

Method BLASTX
NCBI GI g2655888
BLAST score 206
E value 1.0e-16

44042

Glycoprotein (HRGP) [Zea mays]

Match length

153.

```
Match length
% identity
                  61
NCBI Description
                  (AL009171) 62D9.a [Drosophila melanogaster]
Seq. No.
                  309471
                  uC-zmflmo17262a07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1076315
BLAST score
                  213
E value
                  4.0e-17
Match length
                  53
% identity
                  79
NCBI Description
                  cytochrome P450 - Arabidopsis thaliana
                  >gi 853719 emb CAA60793 (X87367) CYP90 protein
                  [Arabidopsis thaliana] >gi 871988 emb CAA60794 (X87368)
                  CYP90 protein [Arabidopsis thaliana]
Seq. No.
                  309472
Seq. ID
                  uC-zmflmo17262b09b1
Method
                  BLASTX
NCBI GI
                  g548669
BLAST score
                  169
E value
                  7.0e-12
Match length
                  101
% identity
                  38
NCBI Description
                  DNA REPAIR PROTEIN RAD8 >gi 542223 pir S41478 RAD8 protein

    fission yeast (Schizosaccharomyces pombe)

                  >gi 443973 emb CAA52686 (X74615) rad8 [Schizosaccharomyces
                  pombe]
Seq. No.
                  309473
Seq. ID
                  uC-zmflmo17262d11b1
Method
                  BLASTN
NCBI GI
                  g257040
BLAST score
                  146
E value
                  2.0e-76
Match length
                  358
% identity
                  96
NCBI Description hydroxyproline-rich glycoprotein [maize, Genomic, 1703 nt]
Seq. No.
                  309474
Seq. ID
                  uC-zmflmo17262g03a1
Method
                  BLASTX
NCBI GI
                  g2326231
BLAST score
                  171
E value
                  3.0e-12
Match length
                  35
                  91
% identity
NCBI Description
                  (AF012889) tousled-like kinase 4 [Zea mays]
Seq. No.
                  309475
Seq. ID
                  uC-zmflmo17262g05b1
Method
                  BLASTX
NCBI GI
                  g4581164
BLAST score
                  366
E value
                  8.0e-35
```

Method

NCBI GI

BLASTX

g1362162

```
% identity
                  (AC006220) putative polyprotein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  309476
                  uC-zmflmo17263c05b1
Seg. ID
                  BLASTX
Method
                  g1173555
NCBI GI
                  619
BLAST score
                  1.0e-64
E value
Match length
                  132
% identity
                  84
NCBI Description (U31544) UDP-galactose-4-epimerase [Pisum sativum]
                  309477
Seq. No.
Seq. ID
                  uC-zmflmo17263f04b1
Method
                  BLASTX
NCBI GI
                  g2618699
BLAST score
                  209
E value
                  1.0e-16
Match length
                  107
% identity
                  36
NCBI Description (AC002510) unknown protein [Arabidopsis thaliana]
                  309478
Seq. No.
                  uC-zmflmo17263g12b1
Seq. ID
Method
                  BLASTX
                  g1335862
NCBI GI
BLAST score
                  282
E value
                  5.0e-25
Match length
                  101
% identity
                  89
NCBI Description (U42608) clathrin heavy chain [Glycine max]
                   309479
Seq. No.
                  uC-zmflmo17264a02a2
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2632252
BLAST score
                  176
                   1.0e-12
E value
                  52
Match length
% identity
                   63 -
NCBI Description (Y12464) serine/threonine kinase [Sorghum bicolor]
                   309480
Seq. No.
                   uC-zmflmo17264b04a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2262103
BLAST score
                   381
E value
                   8.0e-37
Match length
                   127
% identity
                   58
                  (AC002343) unknown protein [Arabidopsis thaliana]
NCBI Description
                   309481
Seq. No.
Seq. ID
                   uC-zmflmo17264e01a2
```



```
BLAST score
                  6.0e-21
E value
                  52
Match length
                  81
% identity
                  beta-glucosidase BGQ60 precursor - barley >gi_804656
NCBI Description
                  (L41869) beta-glucosidase [Hordeum vulgare]
                  309482
Seq. No.
                  uC-zmflmo17265a11a2
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3183079
BLAST score
                  295
                  9.0e-27
E value
                  63
Match length
                  92
% identity
                  MALATE DEHYDROGENASE, GLYOXYSOMAL PRECURSOR
NCBI Description
                  >gi_1375075_dbj_BAA12870_ (D85763) glyoxysomal malate
                  dehydrogenase [Oryza sativa]
                  309483
Seq. No.
                  uC-zmflmo17265b01a1
Seq. ID
Method
                  BLASTN
                  q22487
NCBI GI
                  57
BLAST score
                  1.0e-23
E value
                  176
Match length
                  89
% identity
NCBI Description Maize gene for sucrose synthase
                   309484
Seq. No.
                  uC-zmflmo17265b03b1
Seq. ID
                  BLASTX
Method
NCBI GI
                   q553073
BLAST score
                   290
E value
                   1.0e-49
Match length
                   140
                   30
% identity
                  (M94481) reverse transcriptase [Zea mays]
NCBI Description
                   309485
Seq. No.
Seq. ID
                   uC-zmflmo17265b04b1
                   BLASTX
Method
                   g2739168
NCBI GI
                   389
BLAST score
                   1.0e-37
E value
                   142
Match length
% identity
                   (AF032386) aldose-1-epimerase-like protein [Nicotiana
NCBI Description
                   tabacum]
                   309486
Seq. No.
                   uC-zmflmo17265c05b1
```

Seq. ID

Method BLASTX g3355477 NCBI GI 567 BLAST score 2.0e-58 E value 151 Match length

NCBI Description



```
% identity
                  (AC004218) putative P-glycoprotein, pgpl [Arabidopsis
NCBI Description
                  thaliana]
                  309487
Seq. No.
                  uC-zmflmo17265e12b1
Seq. ID
                  BLASTX
Method
                  q4544389
NCBI GI
                  421
BLAST score
                  2.0e-41
E value
                  127
Match length
                   62
% identity
                  (AC007047) putative homeodomain protein [Arabidopsis
NCBI Description
                   thaliana]
                   309488
Seq. No.
Seq. ID
                   uC-zmflmo17265h07b1
Method
                   BLASTX
                   g3738315
NCBI GI
                   355
BLAST score
                   1.0e-33
E value
                   86
Match length
                   77
% identity
                  (AC005170) unknown protein [Arabidopsis thaliana]
NCBI Description
                   309489
Seq. No.
Seq. ID
                   uC-zmflmo17266a10b1
                   BLASTN
Method
                   g2062691
NCBI GI
BLAST score
                   34
                   2.0e-09
E value
Match length
                   34
% identity
                   100
                   Human sodium phosphate transporter (NPT4) mRNA, complete
NCBI Description
                   309490
Seq. No.
                   uC-zmflmo17266b05b1
Seq. ID
                   BLASTX
Method
                   g3335376
NCBI GI
BLAST score
                   354
                   1.0e-33
E value
Match length
                   89
                   70
% identity
                   (AC003028) putative ammonium transporter [Arabidopsis
NCBI Description
                   thaliana]
                   309491
Seq. No.
                   uC-zmflmo17266b11b1
Seq. ID
                   BLASTX
Method
                   g3600032
NCBI GI
                   154
BLAST score
                   4.0e-10
E value
Match length
                   45
                   64
 % identity
                   (AF080119) contains similarity to tropomyosin (Pfam:
```

44046

Tropomyosin.hmm, score: 14.57) and ATP synthase (Pfam:



ATP-synt_B.hmm, score: 10.89) [Arabidopsis thaliana]

```
Seq. No.
                   309492
Seq. ID
                   uC-zmflmo17266c01b1
                   BLASTN
Method
NCBI GI
                   q3511235
BLAST score
                   41
                   1.0e-13
E value
Match length
                   69
                   90
% identity
                   Zea mays starch branching enzyme IIb (ae) gene, complete
NCBI Description
                   309493
Seq. No.
Seq. ID
                   uC-zmflmo17266c06b1
Method
                   BLASTX
NCBI GI
                   g2648023
BLAST score
                   190
E value
                   3.0e-14
Match length
                   70
% identity
                   (Z97184) BING4 [Homo sapiens]
NCBI Description
                   309494
Seq. No.
                   uC-zmflmo17266c07b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3560533
BLAST score
                   359
E value
                   1.0e-38
Match length
                   113
% identity
                   73
                   (AF042333) 24-methylene lophenol C24(1)methyltransferase
NCBI Description
                   [Oryza sativa]
                   309495
Seq. No.
                   uC-zmflmo17266c08b1
Seq. ID
Method
                   BLASTX
                   g2244993
NCBI GI
BLAST score
                   411
                   4.0e-40
E value
                   156
Match length
                   51
% identity
                   (Z97341) similarity to AMP-activated protein kinase beta
NCBI Description
                   [Arabidopsis thaliana]
                   309496
Seq. No.
                   uC-zmflmo17266e12b1
Seq. ID
                   BLASTX
Method
                   g3176660
NCBI GI
                   471
BLAST score
                   3.0e-47
E value
Match length
                   165
% identity
                   55
                   (AC004393) Similar to ERECTA receptor protein kinase
NCBI Description
                   gb_U47029 from A. thaliana. [Arabidopsis thaliana]
                   309497
Seq. No.
```

44047

Res 1

```
Seq. ID uC-zmflmo17266f02a1 Method BLASTN NCBI GI g22467 BLAST score 54
```

% identity 88
NCBI Description Maize external transcribed spacer DNA upstream of 18S rRNA

gene

102

6.0e-22

Seq. No. 309498
Seq. ID uC-zmflmo17266f06b1
Method BLASTX
NCBI GI g66009

NCBI GI g66009
BLAST score 215
E value 2.0e-17
Match length 101
% identity 51

E value Match length

NCBI Description glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) C,

cytosolic - maize >gi_22238_emb_CAA30151_ (X07156) GADPH

(AA 1-337) [Zea mays]

Seq. No. 309499

Seq. ID uC-zmflmo17266f08b1

Method BLASTX
NCBI GI g1710008
BLAST score 205
E value 6.0e-16
Match length 38
% identity 95

NCBI Description GTP-BINDING NUCLEAR PROTEIN RAN1B >gi_1370205_emb_CAA98188_

(Z73960) RAN1B [Lotus japonicus]

Seq. No. 309500

Seq. ID uC-zmflmo17266f11b1

Method BLASTN
NCBI GI g1212993
BLAST score 71
E value 1.0e-31
Match length 127

NCBI Description H.vulgare mRNA for coproporphyrinogen oxidase

Seq. No. 309501

% identity

Seq. ID uC-zmflmo17266g04b1

Method BLASTX
NCBI GI g4467107
BLAST score 176
E value 1.0e-12
Match length 163
% identity 28

NCBI Description (AL035538) putative protein [Arabidopsis thaliana]

Seq. No. 309502

Seq. ID uC-zmflmo17266g06b1

Method BLASTX NCBI GI g2224931

```
BLAST score
                  1.0e-58
E value
Match length
                  157
% identity
                  74
                  (AF004215) ethylene-insensitive3-like3 [Arabidopsis
NCBI Description
                  thaliana]
                  309503
Seq. No.
                  uC-zmflmo17267a02a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g733455
BLAST score
                  57
E value
                  9.0e-24
Match length
                  57
                  100
% identity
                  Zea mays chlorophyll a/b-binding apoprotein CP26 (Lhcb5-2)
NCBI Description
                  mRNA, complete cds
                  309504
Seq. No.
Seq. ID
                  uC-zmflmo17267b03b1
Method
                  BLASTX
NCBI GI
                  q2668742
BLAST score
                   367
                   3.0e-35
E value
                   86
Match length
% identity
                   (AF034945) glycine-rich RNA binding protein [Zea mays]
NCBI Description
Seq. No.
                   309505
                   uC-zmflmo17267c05b1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g257040
BLAST score
                   106
                   5.0e-53
E value
                   130
Match length
                   96
% identity
                  hydroxyproline-rich glycoprotein [maize, Genomic, 1703 nt]
NCBI Description
                   309506
Seq. No.
                   uC-zmflmo17267e05a1
Seq. ID
                   BLASTX
Method
                   g3645899
NCBI GI
BLAST score
                   362
                   1.0e-34
E value
                   82
Match length
                   87
% identity
                   (U68408) 5' end not determined experimentally [Zea mays]
NCBI Description
                   309507
Seq. No.
```

Seq. ID uC-zmflmo17267e05b1

Method BLASTN
NCBI GI g507844
BLAST score 101
E value 2.0e-49
Match length 153
% identity 58

NCBI Description Zea mays A188 retrotransposon gag gene, complete cds



```
309508
Seq. No.
                  uC-zmflmo17267g02b1
Seq. ID
                  BLASTN
Method
                  g257040
NCBI GI
                  66
BLAST score
                  1.0e-28
E value
Match length
                  74
% identity
NCBI Description hydroxyproline-rich glycoprotein [maize, Genomic, 1703 nt]
                  309509
Seq. No.
                  uC-zmflmo17267g09b1
Seq. ID
Method
                  BLASTN
                  g168654
NCBI GI
                  57
BLAST score
                  3.0e-23
E value
                  177
Match length
                  83
% identity
                  Zea mays ADP glucose pyrophosphorylase (shrunken-2) gene,
NCBI Description
                  complete cds
                  309510
Seq. No.
                  uC-zmflmo17267h05b1
Seq. ID
Method
                  BLASTX
                  q82698
NCBI GI
                  140
BLAST score
                  7.0e-09
E value
                  66
Match length
                   42
% identity
                  hydroxyproline-rich glycoprotein precursor - maize
NCBI Description
                  >gi 257041 bbs_115226 (S45164) hydroxyproline-rich
                  glycoprotein, HRGP [maize, Peptide, 328 aa] [Zea mays]
                  >gi 4007865_emb_CAA10387 (AJ131535) Hydroxyproline-rich
                  Glycoprotein (HRGP) [Zea mays]
                   309511
Seq. No.
                  uC-zmflmo17268a08b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3650036
BLAST score
                   195
                   6.0e-15
E value
                   62
Match length
% identity
                  (AC005396) putative transposase [Arabidopsis thaliana]
NCBI Description
                   309512
Seq. No.
Seq. ID
                   uC-zmflmo17268c02b1
Method
                   BLASTX
NCBI GI
                   g3924612
                   357
BLAST score
                   7.0e-34
E value
                   123
Match length
% identity
                   (AF069442) mitochondrial elongation factor Tu [Arabidopsis
NCBI Description
```

elongation factor Tu [Arabidopsis thaliana]
44050

thaliana] >gi_4263511_gb_AAD15337_ (AC004044) mitochondrial

```
309513
Seq. No.
                  uC-zmflmo17268d03b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1332579
BLAST score
                  519
                  9.0e-66
E value
                  137
Match length
% identity
NCBI Description (X98063) polyubiquitin [Pinus sylvestris]
                  309514
Seq. No.
Seq. ID
                  uC-zmflmo17268d06b1
                  BLASTN
Method
NCBI GI
                  g22332
BLAST score
                  306
                  1.0e-172
E value
                  361
Match length
                   96
% identity
NCBI Description Z.mays HRGP gene
                   309515
Seq. No.
Seq. ID
                   uC-zmflmo17268e01b1
                   BLASTX
Method
                   q1943751
NCBI GI
                                                Ť,
                   255
BLAST score
                   5.0e-22
E value
                   123
Match length
                   45
% identity
                   (U93845) Arabidopsis thaliana ER-type calcium pump
NCBI Description
                   protein, complete sequence >gi_2078292 (U96455) ER-type
                   Ca2+-pumping ATPase; ECA1p [Arabidopsis thaliana]
                   309516
Seq. No.
                   uC-zmflmo17268f07b1
Seq. ID
                   BLASTN
Method
                   g309556
NCBI GI
BLAST score
                   44
                   7.0e-16
E value
                   68
Match length
                   91
% identity
                   Corn nuclear-encoded mitochondrial chaperonin 60 (cpn60I)
NCBI Description
                   gene, complete cds
                   309517
Seq. No.
                   uC-zmflmo17268f08b1
Seq. ID
```

Method BLASTN
NCBI GI g257040
BLAST score 101
E value 1.0e-49
Match length 165
% identity 90

NCBI Description hydroxyproline-rich glycoprotein [maize, Genomic, 1703 nt]

Seq. No. 309518

Seq. ID uC-zmflmo17268g10b1

Method BLASTX

Method

NCBI GI

BLASTX

g1519251

```
g82040
NCBI GI
                  257
BLAST score
E value
                  3.0e-22
Match length
                  120
% identity
                  ubiquitin precursor - flax (fragment) >gi 168304 (M57895)
NCBI Description
                  ubiquitin [Linum usitatissimum]
Seq. No.
                  309519
Seq. ID
                  uC-zmflmo17268h02a1
Method
                  BLASTN
NCBI GI
                  g22378
BLAST score
                  40
E value
                  3.0e-13
Match length
                  100
% identity
                  86
NCBI Description Z.mays gene for nucleic acid binding protein
Seq. No.
                  309520
Seq. ID
                  uC-zmflmo17268h09a1
Method
                  BLASTN
NCBI GI
                  q1185553
BLAST score
                  44
E value
                  1.0e-15
Match length
                  76
% identity
                  89
                  Zea mays glyceraldehyde-3-phosphate dehydrogenase (gpc2)
NCBI Description
                  gene, complete cds
                  309521
Seq. No.
                  uC-zmflmo17269a05b1
Seq. ID
Method
                  BLASTX
                  g1718097
NCBI GI
BLAST score
                  183
                  2.0e-13
E value
Match length
                  68
% identity
                  47
                  VACUOLAR ATP SYNTHASE SUBUNIT AC39 (V-ATPASE AC39 SUBUNIT)
NCBI Description
                   (41 KD ACCESSORY PROTEIN) (DVA41) >gi_626048_pir__A55016
                  lysosomal membrane protein DVA41 - slime mold
                   (Dictyostelium discoideum) >gi 532733 (U13150) vacuolar
                  ATPase subunit DVA41 [Dictyostelium discoideum]
                  309522
Seq. No.
                  uC-zmflmo17269d08b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1519251
BLAST score
                  217
                  1.0e-17
E value
Match length
                  83
% identity
                  61
NCBI Description (U65957) GF14-c protein [Oryza sativa]
                  309523
Seq. No.
                  uC-zmflmo17269d09b1
Seq. ID
```

```
BLAST score
                  9.0e-19
E value
Match length
                  72
% identity
                  81
                  (U65957) GF14-c protein [Oryza sativa]
NCBI Description
                  309524
Seq. No.
                  uC-zmflmo17269e06b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g135417
BLAST score
                  166
E value
                   9.0e-12
Match length
                   60
                   60
% identity
                  TUBULIN ALPHA-3 CHAIN >gi_100946_pir__JN0105 tubulin
NCBI Description
                   alpha-3 chain - maize >gi_22150_emb CAA44861 (X63176)
                  Alpha-tubulin #3 [Zea mays] >gi_485377 (M60171) alpha-3
                   tubulin [Zea mays]
Seq. No.
                   309525
Seq. ID
                  uC-zmflmo17269f10b1
Method
                  BLASTX
NCBI GI
                   g3702333
BLAST score
                   294
E value
                   2.0e-26
Match length
                   65
% identity
                   78
                   (AC005397) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   309526
                   uC-zmflmo17269g08a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2809246
BLAST score
                   247
                   1.0e-21
E value
Match length
                   66
% identity
                   65
                   (AC002560) F2401.15 [Arabidopsis thaliana]
NCBI Description
                   309527
Seq. No.
                   uC-zmflmo17269g09b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3759184
BLAST score
                   165
                   2.0e-11
E value
                   75
Match length
% identity
                   49
                   (AB018441) phi-1 [Nicotiana tabacum]
NCBI Description
                   309528
Seq. No.
```

uC-zmflmo17269g10a1 Seq. ID

Method BLASTX g2289002 NCBI GI BLAST score 139 E value 1.0e-08 Match length 30 % identity 80

NCBI GI

BLAST score



```
(AC002335) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  309529
                  uC-zmflmo17269g12b1
Seq. ID
                  BLASTX
Method
                  g4097573
NCBI GI
                  163
BLAST score
                  3.0e-11
E value
                  73
Match length
                  47
% identity
NCBI Description (U64917) GMFP7 [Glycine max]
                  309530
Seq. No.
Seq. ID
                  uC-zmflmo17269h03b1
Method
                  BLASTX
                  g4115377
NCBI GI
                  207
BLAST score
                  1.0e-16
E value
Match length
                  95
% identity
                  61
                  (AC005967) unknown protein [Arabidopsis thaliana]
NCBI Description
                  309531
Seq. No.
                  uC-zmflmo17269h11b1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g312180
BLAST score
                  54
                  2.0e-21
E value
Match length
                  90
% identity
                  90
NCBI Description Z.mays GapC4 gene
                  309532
Seq. No.
                  uC-zmflmo17270a04b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3983665
BLAST score
                  242
E value
                  1.0e-20
                  95
Match length
                  60
% identity
NCBI Description (AB011271) importin-beta2 [Oryza sativa]
                  309533
Seq. No.
                  uC-zmflmo17270b01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4336747
BLAST score
                   751
                  5.0e-80
E value
Match length
                  168
% identity
NCBI Description (AF104924) unconventional myosin heavy chain [Zea mays]
                   309534
Seq. No.
Seq. ID
                   uC-zmflmo17270b11b1
Method
                  BLASTX
```

g2760324

```
3.0e-15
E value
Match length
                  66
% identity
NCBI Description
                  (AC002130) F1N21.9 [Arabidopsis thaliana]
Seq. No.
                  309535
                  uC-zmflmo17270f09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1351014
BLAST score
                  191
E value
                  2.0e-14
Match length
                  104
                  43
% identity
                  40S RIBOSOMAL PROTEIN S8 >gi 968902 dbj BAA07207 (D38010)
NCBI Description
                  ribosomal protein S8 [Oryza sativa]
Seq. No.
                  309536
Seq. ID
                  uC-zmflmo17270g04b1
Method
                  BLASTX
NCBI GI
                  a4493972
BLAST score
                  184
E value
                  5.0e-15
                  73
Match length
% identity
                   62
                  (AL034559) predicted using hexExon; MAL3P7.12 (PFC0915w),
NCBI Description
                  ATP-dependent RNA Helicase, len: 434 aa; Similarity to
                  ATP-dependent RNA helicase. A.thaliana ATP-dependent RNA
                  helicase (TR:080838) BLAST Score: 1552, sum P(1) = 1.5e
Seq. No.
                   309537
Seq. ID
                   uC-zmflmo17270g12b1
Method
                  BLASTX
NCBI GI
                   q2668742
BLAST score
                   354
                   1.0e-33
E value
Match length
                   86
% identity
                   81
                  (AF034945) glycine-rich RNA binding protein [Zea mays]
NCBI Description
                   309538
Seq. No.
                   uC-zmflmo17270h09b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q283045
BLAST score
                   256
                   3.0e-22
E value
                  98
Match length
                   54
% identity
                  hydroxyproline-rich glycoprotein - maize
NCBI Description
                   >gi_22333_emb_CAA44844_ (X63134) hydroxyproline-rich
                   glycoprotein [Zea mays] >gi_228936_prf__1814452A Hyp-rich
                   glycoprotein [Zea mays]
Seq. No.
                   309539
                   uC-zmflmo17271a04b1
Seq. ID
Method
                   BLASTX
```

44055

g4204287

467

NCBI GI BLAST score

```
E value 2.0e-56
Match length 154
% identity 70
NCBI Description (AC003027
```

NCBI Description (AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No. 309540

Seq. ID uC-zmflmo17271a06b1

Method BLASTX
NCBI GI g2499535
BLAST score 158
E value 8.0e-13
Match length 75
% identity 67

NCBI Description 2-OXOGLUTARATE/MALATE TRANSLOCATOR PRECURSOR >gi 595681

(U13238) 2-oxoglutarate/malate translocator [Spinacia

oleracea]

Seq. No. 309541

Seq. ID uC-zmflmo17271c02b1

Method BLASTX
NCBI GI g2129613
BLAST score 198
E value 2.0e-15
Match length 108
% identity 38

NCBI Description homeotic protein BEL1 - Arabidopsis thaliana >gi_1122533

(U39944) BELL1 [Arabidopsis thaliana]

Seq. No. 309542

Seq. ID uC-zmflmo17271g12a1

Method BLASTX
NCBI GI g4191744
BLAST score 247
E value 3.0e-21
Match length 49
% identity 90

NCBI Description (L81172) importin alpha homolog [Arabidopsis thaliana]

Seq. No. 309543

Seq. ID uC-zmflmo17272a02a1

Method BLASTN
NCBI GI g257040
BLAST score 54
E value 4.0e-22
Match length 82
% identity 91

NCBI Description hydroxyproline-rich glycoprotein [maize, Genomic, 1703 nt]

Seq. No. 309544

Seq. ID uC-zmflmo17272e12a1

Method BLASTX
NCBI GI g3860319
BLAST score 158
E value 1.0e-10
Match length 81
% identity 47



```
(AJ012686) nucleolar protein [Cicer arietinum]
NCBI Description
                  309545
Seq. No.
                  uC-zmflmo17272f02a1
Seq. ID
                  BLASTN
Method
                  g22153
NCBI GI
BLAST score
                  41
                  4.0e-14
E value
                  57
Match length
                  93
% identity
NCBI Description Z.mays (B37) mRNA for alpha-tubulin
                  309546
Seq. No.
                  uC-zmflmo17272f06a1
Seq. ID
Method
                  BLASTN
                   g22157
NCBI GI
                   99
BLAST score
                   2.0e-48
E value
                   217
Match length
                   96
% identity
NCBI Description Z.mays mRNA for alpha-tubulin
                   309547
Seq. No.
                   uC-zmflmo17273a03b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4210712
BLAST score
                   219
E value
                   7.0e-18
Match length
                   68
                   56
% identity
                  (AJ006870) purple acid phosphatase [Ipomoea batatas]
NCBI Description
                   309548
Seq. No.
                   uC-zmflmo17273a09b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4263050
BLAST score
                   252
                   1.0e-21
E value
                   144
Match length
                   42
% identity
                  (AC005142) putative nodulin [Arabidopsis thaliana]
NCBI Description
                   309549
Seq. No.
                   uC-zmflmo17273a12b1
Seq. ID
                   BLASTX
Method
                   g3377836
NCBI GI
```

BLAST score 234 2.0e-19 E value 140 Match length % identity 41

(AF075598) contains similarity to reverse transcriptases NCBI Description

[Arabidopsis thaliana]

309550 Seq. No.

uC-zmflmo17273b06b1 Seq. ID

Method BLASTN NCBI GI g257040



```
BLAST score
                  2.0e-24
E value
Match length
                  71
                  96
% identity
NCBI Description hydroxyproline-rich glycoprotein [maize, Genomic, 1703 nt]
                  309551
Seq. No.
                  uC-zmflmo17273b12b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3924612
BLAST score
                  471
                  3.0e-47
E value
                  144
Match length
                  67
% identity
                  (AF069442) mitochondrial elongation factor Tu [Arabidopsis
NCBI Description
                  thaliana] >gi 4263511 gb AAD15337 (AC004044) mitochondrial
                  elongation factor Tu [Arabidopsis thaliana]
                  309552
Seq. No.
Seq. ID
                  uC-zmflmo17273c03b1
Method
                  BLASTX
NCBI GI
                  q4584356
BLAST score
                  392
                   3.0e-42
E value
                  132
Match length
                   67
% identity
                  (AC006420) putative replication protein A [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   309553
                   uC-zmflmo17273d08b1
Seq. ID
Method
                   BLASTN
                   g1657762
NCBI GI
BLAST score
                   211
                   1.0e-115
E value
                   338
Match length
% identity
                   91
                   Zea mays retrotransposon Huck-2 5' LTR and primer binding
NCBI Description
                   site DNA sequence
                   309554
Seq. No.
                   uC-zmflmo17273e05a1
Seq. ID
                   BLASTN
Method
                   g4140643
NCBI GI
                   83
BLAST score
                   6.0e-39
E value
Match length
                   175
% identity
                   87
                   Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster,
NCBI Description
                   complete sequence
                   309555
Seq. No.
```

Seq. ID uC-zmflmo17273f04b1

Method BLASTX
NCBI GI g2980798
BLAST score 479
E value 4.0e-48

```
165
Match length
% identity
                   55
NCBI Description
                   (AL022197) putative protein [Arabidopsis thaliana]
Seq. No.
                   309556
                   uC-zmflmo17273g12b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2832641
BLAST score
                   249
                   3.0e-21
E value
Match length
                   74
                   62
% identity
                   (AL021710) glycolate oxidase - like protein [Arabidopsis
NCBI Description
                   thaliana]
                   309557
Seq. No.
                   uC-zmflmo17274d02a1
Seq. ID
                   BLASTN
Method
                   g602252
NCBI GI
BLAST score
                   105
E value
                   4.0e-52
Match length
                   245
% identity
                   86
NCBI Description
                   Zea mays enolase (eno2) mRNA, complete cds
Seq. No.
                   309558
Seq. ID
                   uC-zmflmo17275d11a1
                   BLASTN
Method
                   q19054
NCBI GI
BLAST score
                   44
                   1.0e-15
E value
```

Match length 52 96 % identity

NCBI Description H.vulgare myb2 mRNA

309559

Seq. No. uC-zmflmo17275e01a1 Seq. ID Method BLASTX NCBI GI g122090 BLAST score 205 E value 3.0e-16 Match length 49 90 % identity

NCBI Description

HISTONE H3 >gi_81287_pir__S00940 histone H3 - Volvox carteri >gi_2119017_pir__S59581 histone H3 (clone CH-II) - Chlamydomonas reinhardtii >gi_21985_emb_CAA30035_(X06963) put. histone H3 [Volvox carteri] >gi_21988_emb_CAA30037_ (X06964) put. histone H3 [Volvox carteri] $\overline{>}$ gi_ $\overline{5}$ 71470 (U16724) histone H3 [Chlamydomonas reinhardtii] >gi_571475

(U16725) histone H3 [Chlamydomonas reinhardtii]

309560 Seq. No.

uC-zmflmo17277a05b1 Seq. ID

Method BLASTX g2668742 NCBI GI BLAST score 181 E value 3.0e-13



Match length 66 % identity

(AF034945) glycine-rich RNA binding protein [Zea mays] NCBI Description

Seq. No.

309561

Seq. ID

uC-zmflmo17277b02a1

Method

BLASTN

NCBI GI

g2738749

BLAST score

41

E value

5.0e-14

Match length

135

% identity

84 NCBI Description Zea mays ATP sulfurylase mRNA, complete cds

Seq. No.

309562

Seq. ID

uC-zmflmo17277b02b1

Method

BLASTX

NCBI GI

g2738750

BLAST score E value

280 4.0e-25

Match length

97 57

% identity

NCBI Description (AF016305) ATP sulfurylase [Zea mays]

Seq. No.

309563

Seq. ID

uC-zmflmo17277b04b1

Method

BLASTX g2702376

NCBI GI

265

BLAST score

5.0e-23

E value Match length

% identity

78 69

NCBI Description

(AF038605) Similar to acyl-CoA dehydrogenase; coded for by

C. elegans cDNA yk58h2.3; coded for by C. elegans cDNA yk466c12.3; coded for by C. elegans cDNA yk258d6.3; coded

for by C. elegans cDNA yk158e10.3; coded for by C. elegans cDNA yk427... >gi_4455127_gb_AAD21088_ (AF127558)

isovaleryl-CoA dehydrogenase precursor [Caenorhabditis

elegans]

Seq. No.

309564

Seq. ID

uC-zmflmo17277b08b1

Method NCBI GI BLASTN g559535

BLAST score

291

E value

1.0e-163

Match length

358 96

% identity

NCBI Description Z.mays mRNA for metallothionein

Seq. No.

309565

Seq. ID

uC-zmflmo17277b12b1

Method

BLASTN

NCBI GI

g257040

BLAST score

50

E value

4.0e-19

Match length

82

44060

* . .



```
% identity
NCBI Description hydroxyproline-rich glycoprotein [maize, Genomic, 1703 nt]
                  309566
Seq. No.
Seq. ID
                  uC-zmflmo17277c02a1
Method
                  BLASTN
                  q397395
NCBI GI
BLAST score
                  79
                  2.0e-36
E value
Match length
                  283
% identity
                  81
NCBI Description Z.mays MNB1b mRNA for DNA-binding protein
                  309567
Seq. No.
                  uC-zmflmo17277c05b1
Seq. ID
Method
                  BLASTX
                  q3695403
NCBI GI
BLAST score
                  294
                  2.0e-26
E value
                  142
Match length
% identity
                  46
                  (AF096373) contains similarity to the pfkB family of
NCBI Description
                  carbohydrate kinases (Pfam: PF00294, E=1.6e-75)
                   [Arabidopsis thaliana] >gi 4538955 emb CAB39779.1
                   (AL049488) fructokinase-like protein [Arabidopsis thaliana]
Seq. No.
                  309568
                  uC-zmflmo17277e06b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2997589
BLAST score
                  450
E value
                  7.0e-45
Match length
                  135
% identity
                  71
                  (AF020813) glucose-6-phosphate/phosphate-translocator
NCBI Description
                  precursor [Zea mays]
                   309569
Seq. No.
                  uC-zmflmo17277f09b1
Seq. ID
                  BLASTN
Method
NCBI GI
                   q21622
                   46
BLAST score
                   1.0e-16
E value
                  105
Match length
                   86
% identity
                  S. vulgare mRNA for glycine-rich RNA-binding protein (clone
NCBI Description
                   S1)
                   309570
Seq. No.
                   uC-zmflmo17277g02b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g431162
```

Method BLASTX
NCBI GI g431162
BLAST score 233
E value 3.0e-19
Match length 72
% identity 67

NCBI Description (D21822) ORF [Lilium longiflorum]



```
309571
Seq. No.
                  uC-zmflmo17277h01b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3142300
                  258
BLAST score
                  3.0e-22
E value
                  119
Match length
% identity
                  (AC002411) Contains similarity to pre-mRNA processing
NCBI Description
                  protein PRP39 gb_L29224 from S. cerevisiae. ESTs gb_R64908
                  and gb T88158, gb N38703 and gb AA651043 come from this
                  gene. [Arabidopsis thaliana]
Seq. No.
                  309572
                  uC-zmflmo17277h04a1
Seq. ID
```

Method BLASTN NCBI GI q3694806 BLAST score 72 E value 1.0e-32 Match length 148 % identity 87

Zea mays alanine aminotransferase (alt) gene, complete cds NCBI Description

Seq. No. Seq. ID uC-zmflmo17277h08b1 Method BLASTX NCBI GI g113003 BLAST score 255 E value 3.0e-22 Match length 82 % identity

AUXIN-BINDING PROTEIN 1 PRECURSOR (ABP) (ERABP1) NCBI Description

> >gi 100853 pir S16262 auxin-binding protein precursor maize >gi 22107 emb CAA34376 (X16309) auxin-binding protein (AA 1-201) [Zea mays] >gi 22109_emb_CAA34375 (X16308) precursor polypeptide (AA -38 to 163) [Zea mays] >gi_22175_emb_CAA40061_ (X56737) auxin-binding protein [Zea

mays]

309573

Seq. No. 309574

uC-zmflmo17278a04b1 Seq. ID

Method BLASTX q548770 NCBI GI BLAST score 205 1.0e-18 E value 93 Match length % identity 56

60S RIBOSOMAL PROTEIN L3 >gi_481228_pir__S38359 ribosomal NCBI Description

protein L3 - rice >gi_303853_dbj_BAA02155_ (D12630)

ribosomal protein L3 [Oryza sativa]

309575 Seq. No.

uC-zmflmo17278a05b1 Seq. ID

Method BLASTX NCBI GI g3062801 BLAST score 181



```
1.0e-13
E value
Match length
                  83
% identity
                  48
NCBI Description
                  (AB012873) arginine decarboxylase [Nicotiana sylvestris]
                  309576
Seq. No.
                  uC-zmflmo17278a06b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3337361
BLAST score
                  203
                  3.0e-16
E value
Match length
                  54
% identity
                  67
                  (AC004481) ankyrin-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  309577
                  uC-zmflmo17278c12b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4325354
BLAST score
                  338
E value
                  1.0e-31
Match length
                  133
% identity
                  49
NCBI Description
                  (AF128395) contains similarity to retrovirus-related
                  polyproteins and to CCHC zinc finger protein (Pfam:
                  PF00098, Score=16.3, E=0.051, E= 1) [Arabidopsis thaliana]
Seq. No.
                  309578
                  uC-zmflmo17278d03b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4557078
BLAST score
                  187
                  5.0e-14
E value
Match length
                  133
% identity
                  32
NCBI Description
                  (AC007045) putative Tall-1 pol polyprotein, 5' partial
                   [Arabidopsis thaliana]
                  309579
Seq. No.
                  uC-zmflmo17278d04b1
Seq. ID
Method
                  BLASTX
                  g3063466
NCBI GI
BLAST score
                  176
E value
                  8.0e-13
Match length
                  84
% identity
                  39
NCBI Description
                  (AC003981) F22013.28 [Arabidopsis thaliana]
                  309580
Seq. No.
Seq. ID
                  uC-zmflmo17278e06b1
Method
                  BLASTN
NCBI GI
                  g454880
BLAST score
                  46
                  1.0e-16
E value
Match length
                  92
% identity
                  88
```

44063

NCBI Description Rice mRNA for WSI724 protein induced by water stress,



```
complete cds
Seq. No.
                   309581
Seq. ID
                   uC-zmflmo17278e07b1
Method
                   BLASTX
NCBI GI
                   q3882309
BLAST score
                   205
E value
                   4.0e-16
Match length
                   75
% identity
                   44
NCBI Description (AB018337) KIAA0794 protein [Homo sapiens]
                   309582
Seq. No.
                   uC-zmflmo17278f05b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q417154
BLAST score
                   142
E value
                   9.0e-09
Match length
                   46
```

% identity 59
NCBI Description HEAT SHOCK PROTEIN 82 >gi 100685 pir S25541 heat shock

protein 82 - rice (strain Taichung Native One)

>gi 20256 emb CAA77978 (Z11920) heat shock protein 82

(HSP82) [Oryza sativa]

Seq. No. 309583

Seq. ID uC-zmflmo17278h12b1

Method BLASTX
NCBI GI g1550660
BLAST score 263
E value 7.0e-23
Match length 107
% identity 49

NCBI Description (Z80226) ptrBa [Mycobacterium tuberculosis]

Seq. No. 309584

Seq. ID uC-zmflmo17279f12a1

Method BLASTN
NCBI GI g984713
BLAST score 199
E value 1.0e-108
Match length 227
% identity 97

NCBI Description Z.mays MRFV3 mRNA

Seq. No. 309585

Seq. ID uC-zmflmo17280a02b1

Method BLASTN
NCBI GI g22493
BLAST score 100
E value 4.0e-49
Match length 260
% identity 85

NCBI Description Z.mays transposable element Bg sequence

Seq. No. 309586

Seq. ID uC-zmflmo17280a03b1

```
ethod BL
```

```
Method BLASTX
NCBI GI g2286200
BLAST score 329
E value 1.0e-51
Match length 136
% identity 73
```

NCBI Description (AF010578) polynucleotide phosphorylase [Pisum sativum]

```
Seq. No. 309587
```

Seq. ID uC-zmflmo17280a04b1

Method BLASTX
NCBI GI g4097573
BLAST score 141
E value 7.0e-09
Match length 73
% identity 45

NCBI Description (U64917) GMFP7 [Glycine max]

```
Seq. No. 309588
```

Seq. ID uC-zmflmo17280a06b1

Method BLASTN
NCBI GI g939784
BLAST score 42
E value 2.0e-14
Match length 78
% identity 88

NCBI Description Zea mays MADS-box protein (ZAP1) mRNA, complete cds

Seq. No. 309589

Seq. ID uC-zmflmo17280a10b1

Method BLASTX
NCBI GI g112994
BLAST score 170
E value 2.0e-12
Match length 46
% identity 80

NCBI Description - GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN

>gi_82685_pir__S04536 embryonic abundant protein,
glycine-rich - maize >gi 22313 emb CAA31077 (X12564)

ABA-inducible gene protein [Zea mays]

>gi_226091_prf__1410284A abscisic acid inducible gene [Zea

mays]

Seq. No. 309590

Seq. ID uC-zmflmo17280b02b1

Method BLASTX
NCBI GI g2497748
BLAST score 165
E value 2.0e-11
Match length 72
% identity 46

NCBI Description NONSPECIFIC LIPID-TRANSFER PROTEIN 4 PRECURSOR (LTP 4)

>gi 902058 (U29176) lipid transfer protein precursor [Oryza

sativa]

Seq. No. 309591

Seq. ID uC-zmflmo17280b12b1



Method BLASTX
NCBI GI g2961284
BLAST score 244
E value 9.0e-21
Match length 101
% identity 50

NCBI Description (Y16848) cinnamyl alcohol dehydrogenase-like protein,

subunit a [Arabidopsis thaliana] >gi_4467103_emb_CAB37537_ (AL035538) cinnamyl alcohol dehydrogenase-like protein,

LCADa [Arabidopsis thaliana]

Seq. No. 309592

Seq. ID uC-zmflmo17280c05b1

Method BLASTX
NCBI GI g4204265
BLAST score 288
E value 7.0e-26
Match length 122
% identity 51

NCBI Description (AC005223) 45643 [Arabidopsis thaliana]

Seq. No. 309593

Seq. ID uC-zmflmo17280c06b1

Method BLASTX
NCBI GI g131388
BLAST score 258
E value 1.0e-22
Match length 92
% identity 65

NCBI Description OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD

SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD

THYLAKOID MEMBRANE PROTEIN) >gi 100831 pir S16260

photosystem II oxygen-evolving complex protein 1 - common wheat x Sanduri wheat >gi_21844_emb_CAA40670_ (X57408) 33kDa oxygen evolving protein of photosystem II [Triticum

aestivum]

Seq. No. 309594

Seq. ID uC-zmflmo17280c08b1

Method BLASTX
NCBI GI g2911042
BLAST score 453
E value 3.0e-45
Match length 126
% identity 76

NCBI Description (AL021961) Phosphoglycerate dehydrogenase - like protein

[Arabidopsis thaliana]

Seq. No. 309595

Seq. ID uC-zmflmo17280c11b1

Method BLASTX
NCBI GI g3738295
BLAST score 264
E value 5.0e-23
Match length 66
% identity 76

NCBI Description (AC005309) unknown protein [Arabidopsis thaliana]

Match length

NCBI Description

% identity

76

61

```
309596
Seq. No.
Seq. ID
                  uC-zmflmo17280d02b1
Method
                  BLASTX
NCBI GI
                  g1345588
BLAST score
                  441
                  7.0e-44
E value
                  102
Match length
% identity
                  89
                  14-3-3-LIKE PROTEIN GF14-12 >qi 998432 bbs 164524
NCBI Description
                  GF14-12=GRF2 product/14-3-3 protein homolog [Zea mays,
                  XL80, Peptide, 261 aa]
                  309597
Seq. No.
                  uC-zmflmo17280e03b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g123549
BLAST score
                  261
E value
                  7.0e-23
Match length
                  78
                  72
% identity
NCBI Description
                  17.5 KD CLASS II HEAT SHOCK PROTEIN >gi 100885 pir S14998
                  heat shock protein, 18K - maize >gi 22339 emb CAA38013
                  (X54076) 18kDa heat shock protein [Zea mays]
                  309598
Seq. No.
Seq. ID
                  uC-zmflmo17280e05a1
                  BLASTX
Method
NCBI GI
                  q4185311
BLAST score
                  242
E value
                  8.0e-21
Match length
                  85
% identity
NCBI Description
                  (AF090446) polyprotein [Zea mays]
Seq. No.
                  309599
Seq. ID
                  uC-zmflmo17280e06b1
Method
                  BLASTX
NCBI GI
                  g1170937
BLAST score
                  463
E value
                  1.0e-46
Match length
                  102
% identity
                  88
NCBI Description
                  S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
                  ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                  >gi 450549 emb CAA81481 (Z26867) S-adenosyl methionine
                  synthetase [Oryza sativa]
Seq. No.
                  309600
Seq. ID
                  uC-zmflmo17280e09b1
Method
                  BLASTX
NCBI GI
                  g3046693
BLAST score
                  225
E value
                  1.0e-18
```

44067

(AL022140) receptor like protein (fragment) [Arabidopsis



thaliana]

Seq. No. 309601 Seq. ID uC-zmflmo17280f01b1 Method BLASTX NCBI GI q3413716 BLAST score 269 E value 1.0e-23 Match length 125 % identity 52

NCBI Description (AC004747) unknown protein [Arabidopsis thaliana] >gi 3643589 (AC005395) unknown protein [Arabidopsis

thaliana]

Seq. No. 309602

Seq. ID uC-zmflmo17280f06b1

Method BLASTX
NCBI GI g135417
BLAST score 204
E value 1.0e-16
Match length 38
% identity 95

NCBI Description TUBULIN ALPHA-3 CHAIN >gi_100946_pir__JN0105 tubulin alpha-3 chain - maize >gi_22150 emb CAA44861_ (X63176)

Alpha-tubulin #3 [Zea mays] >gi_485377 (M60171) alpha-3

tubulin [Zea mays]

Seq. No. 309603

Seq. ID uC-zmflmo17280f09b1

Method BLASTX
NCBI GI g3135265
BLAST score 222
E value 3.0e-18
Match length 100
% identity 46

NCBI Description (AC003058) unknown protein [Arabidopsis thaliana]

Seq. No. 309604

Seq. ID uC-zmflmo17280g10b1

Method BLASTX
NCBI GI g4539463
BLAST score 339
E value 7.0e-32
Match length 117
% identity 58

NCBI Description (AL049500) putative protein [Arabidopsis thaliana]

Seq. No. 309605

Seq. ID uC-zmflmo17280h12b1

Method BLASTN
NCBI GI g22332
BLAST score 168
E value 1.0e-89
Match length 243
% identity 93

NCBI Description Z.mays HRGP gene

```
Jo. 30
```

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309606
Seq. No.
                  uC-zmflmo17281b11b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4200338
BLAST score
                  300
E value
                  3.0e-27
Match length
                  116
                  57
% identity
                  (Y17277) P69C protein [Lycopersicon esculentum]
NCBI Description
Seq. No.
                  309607
                  uC-zmflmo17281e06b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2289002
BLAST score
                  236
E value
                  2.0e-20
Match length
                  101
% identity
                  (AC002335) unknown protein [Arabidopsis thaliana]
NCBI Description
                  309608
Seq. No.
Seq. ID
                  uC-zmflmo17281f11b1
Method
                  BLASTN
NCBI GI
                  q4105718
BLAST score
                  37
E value
                  3.0e-11
Match length
                  81
                  88
% identity
                  Zea mays cell wall invertase Incw2 gene, complete cds
NCBI Description
                  309609
Seq. No.
                  uC-zmflmo17282c08b1
Seq. ID
                  BLASTX
Method
                  q3445397
NCBI GI
BLAST score
                  219
                  9.0e-18
E value
Match length
                  106
                  42
% identity
                  (AJ010166) S-domain receptor-like protein kinase [Zea mays]
NCBI Description
                  309610
Seq. No.
                  uC-zmflmo17282e09b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g132147
                  299
BLAST score
                  4.0e-27
E value
Match length
                  59
                  98
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT) >gi_68089_pir__RKZMS
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor - maize >gi_22474_emb_CAA29784_
                                                             (X06535)
                  ribulose-1,5-bisphosphate carboxylase (RuBPC) precursor
                   [Zea mays] >gi_217964_dbj_BAA00120_ (D00170) ribulose
                  1,5-bisphosphate carboxylase small subunit [Zea mays]
                  >gi_359512_prf__1312317A ribulosebisphosphate carboxylase
```

[Zea mays]



```
309611
Seq. No.
Seq. ID
                   uC-zmflmo17282e12b1
Method
                   BLASTX
NCBI GI
                   g3914019
BLAST score
                   395
                   2.0e-38
E value
Match length
                   81
% identity
NCBI Description
```

S-ADENOSYLMETHIONINE SYNTHETASE (METHIONINE

ADENOSYLTRANSFERASE) (ADOMET SYNTHETASE) >gi 2305014

(AF004317) S-adenosyl-L-methionine synthetase homolog [Musa

acuminata]

309612 Seq. No. Seq. ID uC-zmflmo17282f10b1 Method BLASTN NCBI GI g5579440 193 BLAST score 1.0e-104 E value

325 Match length % identity 97

Zea mays histone acetyltransferase HAT B mRNA, complete cds NCBI Description

309613 Seq. No.

uC-zmflmo17282g01b1 Seq. ID

Method BLASTX NCBI GI q1488297 BLAST score 254 E value 8.0e-22 Match length 74 % identity 68

(U63530) osRAD23 [Oryza sativa] NCBI Description

Seq. No. 309614

uC-zmflmo17283a03b1 Seq. ID

Method BLASTX g4325282 NCBI GI BLAST score 236 8.0e-20 E value Match length 94

% identity 52

(AF123310) NAC domain protein NAM [Arabidopsis thaliana] NCBI Description >gi 4325286 gb AAD17314 (AF123311) NAC domain protein NAM

[Arabidopsis thaliana]

Seq. No. 309615

uC-zmflmo17283b01b1 Seq. ID

BLASTX Method NCBI GI g2369766 BLAST score 189 E value 3.0e-14 114 Match length % identity 44

(AJ001304) hypothetical protein [Citrus x paradisi] NCBI Description

Seq: No. 309616



```
uC-zmflmo17283b10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2341027
BLAST score
                  191
E value
                  1.0e-14
Match length
                  89
% identity
                  (AC000104) EST gb_T21788 comes from this gene. [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  309617
Seq. ID
                  uC-zmflmo17283c12b1
Method
                  BLASTX
NCBI GI
                  q4204300
BLAST score
                  166
E value
                  1.0e-11
Match length
                  56
% identity
                  62
NCBI Description
                  (AC003027) Unknown protein [Arabidopsis thaliana]
Seq. No.
                  309618
Seq. ID
                  uC-zmflmo17283e02b1
Method
                  BLASTX
NCBI GI
                  q1076316
BLAST score
                  234
E value
                  1.0e-19
Match length
                  101
                  45
% identity
NCBI Description
                  drought-induced protein Di19 - Arabidopsis thaliana
                  >gi 469110 emb CAA55321 (X78584) Di19 [Arabidopsis
                  thaliana]
Seq. No.
                  309619
                  uC-zmflmo17283g12b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g20193
BLAST score
                  50
                  4.0e-19
E value
Match length
                  94
                  88
% identity
NCBI Description O.sativa mRNA for cdc2+/CDC28-related protein kinase
                  309620
Seq. No.
                  uC-zmflmo17285a06b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3046815
BLAST score
                  197
                  6.0e-27
E value
Match length
                  81
                  77
% identity
NCBI Description
                  (AL021687) cytochrome P450 [Arabidopsis thaliana]
```

Seq. No. 309621

Seq. ID uC-zmflmo17285c06b1

Method BLASTX NCBI GI g2213538 BLAST score 185

BLAST score

E value

369

3.0e-35



```
7.0e-14
E value
Match length
                  57
% identity
                  60
NCBI Description
                  (X98740) DNA-binding protein PD2 [Pisum sativum]
                  309622
Seq. No.
                  uC-zmflmo17285c08b1
Seq. ID
                  BLASTN
Method
                  q3821780
NCBI GI
BLAST score
                  36
                  9.0e-11
E value
Match length
                  36
                  100
% identity
                  Xenopus laevis cDNA clone 27A6-1
NCBI Description
Seq. No.
                  309623
                  uC-zmflmo17285e02b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g112994
BLAST score
                  349
E value
                  4.0e-33
Match length
                  89
% identity
                  81
NCBI Description
                  GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN
                  >gi 82685 pir S04536 embryonic abundant protein,
                  glycine-rich - maize >gi 22313 emb CAA31077 (X12564)
                  ABA-inducible gene protein [Zea mays]
                  >gi 226091 prf 1410284A abscisic acid inducible gene [Zea
                  mays]
Seq. No.
                  309624
Seq. ID
                  uC-zmflmo17285g02b1
Method
                  BLASTX
                  g2664210
NCBI GI
BLAST score
                  320
E value
                  1.0e-29
Match length
                  67
                  88
% identity
                  (AJ222644) asparaginyl-tRNA synthetase [Arabidopsis
NCBI Description
                  thaliana]
                  309625
Seq. No.
                  uC-zmflmo17286b04b1
Seq. ID
Method
                  BLASTX
                  g4586117
NCBI GI
BLAST score
                  240
                  4.0e-20
E value
                  73
Match length
                  63
% identity
NCBI Description
                  (AL049638) putative protein [Arabidopsis thaliana]
Seq. No.
                  309626
                  uC-zmflmo17286b06b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q606811
```

```
Match length 84 84 8 identity 44 NCBI Description (U08401) carbonic anhydrase [Zea mays] Seq. No. 309627
```

Seq. ID uC-zmflmo17286d02b1
Method BLASTX
NCBI GI g1351989
BLAST score 198
E value 3.0e-15
Match length 81
% identity 52

NCBI Description ASPARAGINE SYNTHETASE (GLUTAMINE-HYDROLYZING) (GLUTAMINE-DEPENDENT ASPARAGINE SYNTHETASE)

>gi 984262 emb_CAA58052_ (X82849) asparragine synthetase

[Zea mays]

Seq. No. 309628

Seq. ID uC-zmflmo17286e08b1

Method BLASTX
NCBI GI g4406773
BLAST score 418
E value 5.0e-41
Match length 142
% identity 33

NCBI Description (AC006836) putative cell division control protein 48

[Arabidopsis thaliana]

 Seq. No.
 309629

 Seq. ID
 uC-zmflmo17286e11b1

 Method
 BLASTX

 NCBI GI
 g3915463

 BLAST score
 162

 E value
 4.0e-11

E value 4.0e-Match length 76 % identity 49

NCBI Description HYPOTHETICAL 33.1 KD PROTEIN SLR1592

>gi 1652063 dbj BAA16988 (D90902) hypothetical protein

[Synechocystis sp.]

Seq. No. 309630

Seq. ID uC-zmflmo17286g09b1

Method BLASTX
NCBI GI g3157936
BLAST score 309
E value 2.0e-28
Match length 111
% identity 55

NCBI Description (AC002131) Contains similarity to NFATc3 gb_U28807 from Mus

musculus. [Arabidopsis thaliana]

Seq. No. 309631

Seq. ID uC-zmflmo17286h02a1

Method BLASTX
NCBI GI g1063400
BLAST score 301
E value 2.0e-27



```
Match length
                  80
% identity
                  (X92888) glycolate oxidase [Lycopersicon esculentum]
NCBI Description
                  309632
Seq. No.
                  uC-zmflmo17286h05b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2244753
                  385
BLAST score
                  3.0e-37
E value
                  115
Match length
                  58
% identity
                  (Z97335) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  309633
Seq. No.
Seq. ID
                  uC-zmflmo17287c10b1
Method
                  BLASTX
NCBI GI
                  g4651204
BLAST score
                  229
E value
                  8.0e-19
Match length
                  86
% identity
                   44
                  (AB026262) ring finger protein [Cicer arietinum]
NCBI Description
Seq. No.
                  309634
                  uC-zmflmo17287d02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2160175
BLAST score
                  177
                   6.0e-26
E value
                  86
Match length
                   74
% identity
                   (AC000132) Strong similarity to Dianthus cysteine
NCBI Description
                  proteinase (gb U17135). [Arabidopsis thaliana]
                   309635
Seq. No.
                  uC-zmflmo17288a10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3776573
BLAST score
                   317
E value
                   3.0e-29
Match length
                  133
% identity
                   47
NCBI Description
                   (AC005388) Similar to nodulins and lipase homolog F14J9.5
                   qi 3482914 from Arabidopsis thaliana BAC gb AC003970.
                   Alternate first exon from 72258 to 72509. [Arabidopsis
                   thalianal
Seq. No.
                   309636
Seq. ID
                   uC-zmflmo17288f08b1
Method
                   BLASTX
NCBI GI
                   q4239845
```

BLAST score 391 E value 8.0e-38 Match length 86 % identity

(AB015855) transcription factor TEIL [Nicotiana tabacum] NCBI Description

NCBI Description



```
309637
Seq. No.
Seq. ID
                  uC-zmflmo17288h11b1
Method
                  BLASTX
NCBI GI
                  g2984709
BLAST score
                   471
                   3.0e-47
E value
                  89
Match length
% identity
                  100
                  (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]
NCBI Description
Seq. No.
                  309638
                  uC-zmflmo17289b12b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g116054
BLAST score
                   233
E value
                   2.0e-19
Match length
                   53
% identity
                   89
                  CALCIUM-DEPENDENT PROTEIN KINASE SK5 (CDPK)
NCBI Description
                   >gi_280393_pir__A43713 calcium-dependent protein kinase (EC
                   2.7.1.-) - soybean >gi 169931 (M64987) Glycine max calcium
                   dependent protein kinase mRNA. [Glycine max]
                   309639
Seq. No.
                   uC-zmflmo17289d12b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4056503
BLAST score
                   147
E value
                   2.0e-09
Match length
                   36
% identity
                  (AC005896) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   309640
                   uC-zmflmo17289f07b1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2832242
BLAST score
                   113
E value
                   1.0e-56
Match length
                   418
% identity
                   43
NCBI Description
                  Zea mays 22-kDa alpha zein gene cluster, complete sequence
                   309641
Seq. No.
                   uC-zmflmo17289f08a1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g135535
BLAST score
                   153
E value
                   2.0e-18
                   74
Match length
                   72
% identity
                   T-COMPLEX PROTEIN 1, ALPHA SUBUNIT (TCP-1-ALPHA)
```

44075

thaliana] >gi 2326265 dbj BAA21772 (D11352) CCT

(CCT-ALPHA) >gi_322602_pir__JN0448 t-complex polypeptide Tcp-1 - Arabidopsis thaliana >gi_217871_dbj_BAA01955 (D11351) t-complex polypeptide 1 homologue [Arabidopsis

NCBI Description



alpha/TCP-1 [Arabidopsis thaliana]

```
Seq. No.
                  309642
Seq. ID
                  uC-zmflmo17289g06b1
Method
                  BLASTX
NCBI GI
                   g123613
BLAST score
                   671
E value
                   9.0e-71
Match length
                  139
% identity
                   95
NCBI Description
                  HEAT SHOCK COGNATE 70 KD PROTEIN 1 >qi 100222 pir S14949
                  heat shock cognate protein 70 - tomato
                   >gi 19256 emb CAA37970 (X54029) heat shock protein cognate
                   70 [Lycopersicon esculentum]
Seq. No.
                   309643
Seq. ID
                  uC-zmflmo17289g08b1
Method
                  BLASTX
NCBI GI
                   g2244780
BLAST score
                  222
E value
                   4.0e-18
Match length
                   80
% identity
NCBI Description
                  (Z97335) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   309644
                  uC-zmflmo17289g11b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q733454
BLAST score
                   322
E value
                   7.0e-30
Match length
                   57
% identity
                   100
NCBI Description
                  (U23188) chlorophyll a/b-binding apoprotein CP26 precursor
                   [Zea mays]
                   309645
Seq. No.
                   uC-zmflmo17290b02b1
Seq. ID
Method
                  BLASTX
                   g2146746
NCBI GI
BLAST score
                   164
E value
                   6.0e-20
Match length
                   98
                   61
% identity
NCBI Description
                  protein kinase (EC 2.7.1.-) - Arabidopsis thaliana
                  >gi_166819 (L05562) protein kinase [Arabidopsis thaliana]
                   309646
Seq. No.
Seq. ID
                  uC-zmflmo17290b05b1
Method
                  BLASTX
NCBI GI
                   q3201618
BLAST score
                   732
E value
                   8.0e-78
Match length
                  156
% identity
                   82
```

(AC004669) Sop2p-like protein [Arabidopsis thaliana]

309647 Seq. No. uC-zmflmo17290c03b1 Seq. ID Method BLASTX NCBI GI g115771 BLAST score 550 E value 2.0e-56 Match length 122 % identity 89 CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR NCBI Description (CAB-1) (LHCP) >gi_82682 pir S04453 chlorophyll a/b-binding protein precursor - maize >gi 22224 emb CAA32900 (X14794) chlorophyll a/b-binding preprotein (AA 1 - 262) [Zea mays]

Seq. No. 309648
Seq. ID uC-zmflmo17290c06b1
Method BLASTX

Method BLASTX
NCBI GI g3047123
BLAST score 583
E value 2.0e-60
Match length 140
% identity 73

NCBI Description (AF058919) similar to the family of glycosyl hydrolases

[Arabidopsis thaliana]

Seq. No. 309649

Seq. ID uC-zmflmo17290c10b1 Method BLASTN

 NCBI GI
 g3821780

 BLAST score
 36

 E value
 1.0e-10

 Match length
 48

 % identity
 67

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 309650

Seq. ID uC-zmflmo17290e04b1

Method BLASTX
NCBI GI g112994
BLAST score 395
E value 2.0e-38
Match length 85
% identity 94

NCBI Description GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN

>gi_82685_pir__S04536 embryonic abundant protein,
glycine-rich - maize >gi_22313_emb_CAA31077_ (X12564)

ABA-inducible gene protein [Zea mays]

>gi_226091_prf__1410284A abscisic acid inducible gene [Zea

mays]

Seq. No. 309651

Seq. ID uC-zmflmo17290e07b1

Method BLASTX
NCBI GI g4033469
BLAST score 144
E value 6.0e-09
Match length 36



% identity 69

NCBI Description ARGININE/SERINE-RICH SPLICING FACTOR RSP41

>gi 1707370 emb CAA67799 (X99436) splicing factor

[Arabidopsis thaliana]

Seq. No. 309652

Seq. ID uC-zmflmo17290e10b1

Method BLASTX
NCBI GI g2829688
BLAST score 335
E value 2.0e-31
Match length 85
% identity 84

NCBI Description CYSTEINE SYNTHASE (O-ACETYLSERINE SULFHYDRYLASE)

(O-ACETYLSERINE (THIOL)-LYASE) (CSASE)

>gi_1076798_pir__\$52738 cysteine synthase (EC 4.2.99.8)

precursor - maize >gi_758353_emb_CAA59798_ (X85803)

cysteine synthase [Zea mays]

Seq. No. 309653

Seq. ID uC-zmflmo17290f04b1

Method BLASTX
NCBI GI g2129559
BLAST score 231
E value 2.0e-19
Match length 80
% identity 59

NCBI Description cellulase homolog OR16pep - Arabidopsis thaliana

>gi_1022807 (U37702) cellulase [Arabidopsis thaliana]
>gi_3493633 (AF074092) cellulase [Arabidopsis thaliana]
>gi_3598956 (AF074375) cellulase [Arabidopsis thaliana]
>gi_3978258 (AF073875) endo-1,4-beta-D-glucanase KORRIGAN

[Arabidopsis thaliana]

Seq. No. 309654

Seq. ID uC-zmflmo17290g02b1

Method BLASTN
NCBI GI g432606
BLAST score 59
E value 2.0e-24
Match length 75
% identity 95

NCBI Description ricl=ras-related GTP binding protein possessing GTPase

activity [Oryza sativa=rice, Yamahoushi, callus, mRNA, 955

nt]

Seq. No. 309655

Seq. ID uC-zmflmo17290h05a1

Method BLASTX
NCBI GI g3201612
BLAST score 174
E value 2.0e-12
Match length 123
% identity 33

NCBI Description (AC004669) putative 2A6 protein [Arabidopsis thaliana]

Seq. No. 309656

```
uC-zmflmo17290h05b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1903360
BLAST score
                  161
E value
                   6.0e-11
Match length
                  92
% identity
                   39
                  (ACO00104) Similar to Arabidopsis 2A6 (gb X83096). EST
NCBI Description
                  gb T76913 comes from this gene. [Arabidopsis thaliana]
                  309657
Seq. No.
Seq. ID
                  uC-zmflmo17291g03a1
Method
                  BLASTN
NCBI GI
                   g2605618
BLAST score
                   64
E value
                  2.0e-27
Match length
                   68
                   99
% identity
NCBI Description Oryza sativa mRNA for OSMYB2, complete cds
                   309658
Seq. No.
Seq. ID
                  uC-zmflmo17292b09a1
Method
                  BLASTN
NCBI GI
                   q4160401
BLAST score
                  124
                   2.0e-63
E value
Match length
                  184
% identity
                   92
NCBI Description Zea mays eIF-5 gene, exons 1-2
                   309659
Seq. No.
Seq. ID
                  uC-zmflmo17292b12b1
Method
                  BLASTX
NCBI GI
                   q1176529
BLAST score
                   168
E value
                   1.0e-11
Match length
                   64
% identity
                   48
                  HYPOTHETICAL 100.9 KD PROTEIN C34E10.3 IN CHROMOSOME III
NCBI Description
                   >gi_500726 (U10402) C34E10.3 géne product [Caenorhabditis
                   elegans]
Seq. No.
                   309660
Seq. ID
                   uC-zmflmo17292c07b1
Method
                  BLASTN
NCBI GI
                   q4582786
BLAST score
                   54
E value
                   8.0e-22
Match length
                   78
% identity
                   92
```

NCBI Description Zea mays mRNA for adenosine kinase, putative

Seq. No.

309661

uC-zmflmo17292c10a1 Seq. ID

Method BLASTN NCBI GI q1370602 BLAST score 127

```
5.0e-65
E value
Match length
                  160
% identity
                  95
NCBI Description
                  Z.mays mRNA for annexin p35
                  309662
Seq. No.
                  uC-zmflmo17292e03b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q22091
BLAST score
                  204
E value
                  1.0e-111
Match length
                  454
% identity
NCBI Description Z.diploperennis gene for hydroxyproline-rich glycoprotein
Seq. No.
                  309663
Seq. ID
                  uC-zmflmo17292f07b1
Method
                  BLASTN
NCBI GI
                  g2245648
BLAST score
                  35
E value
                  1.0e-10
Match length
                  39
% identity
                  97
```

NCBI Description Zea mays discolored-1 (mutant allele dsc1-Ref::Mu1) gene,

partial sequence

Seq. No. 309664 Seq. ID uC-zmflmo17292g10b1 Method BLASTX NCBI GI q1709000

BLAST score 147 E value 6.0e-10 Match length 31 % identity 94

NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)

>gi 960357 dbj BAA09895 (D63835) S-adenosylmethionine

synthetase [Hordeum vulgare]

Seq. No. 309665

Seq. ID uC-zmflmo17292h10b1

Method BLASTX NCBI GI q4263519 BLAST score 159 1.0e-10 E value Match length 41 % identity 76

(AC004044) small nuclear riboprotein Sm-D1 [Arabidopsis NCBI Description

thaliana]

Seq. No. 309666

Seq. ID uC-zmflmo17293d03b1

Method BLASTN g3821780 NCBI GI BLAST score 35 E value 5.0e-10 35 Match length



% identity 100

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 309667

Seq. ID uC-zmflmo17293e01b1

Method BLASTN
NCBI GI g22332
BLAST score 307
E value 1.0e-172
Match length 472

% identity 92

NCBI Description Z.mays HRGP gene

Seq. No. 309668

Seq. ID uC-zmflmo17293g01b1

Method BLASTN
NCBI GI g1899026
BLAST score 48
E value 4.0e-18
Match length 48
% identity 100

NCBI Description Zea mays superoxide dismutase 4A (sod4A) gene, complete cds

Seq. No. 309669

Seq. ID uC-zmflmo17293g05b1

Method BLASTX
NCBI GI g4580455
BLAST score 269
E value 6.0e-24
Match length 85
% identity 61

NCBI Description (AC006081) unknown protein [Arabidopsis thaliana]

Seq. No. 309670

Seq. ID uC-zmflmo17294b04b1

Method BLASTX
NCBI GI g1143705
BLAST score 291
E value 3.0e-26
Match length 99
% identity 64

NCBI Description (X89760) Hox2a [Zea mays]

Seq. No. 309671

Seq. ID uC-zmflmo17294e11b1

Method BLASTX
NCBI GI g4220527
BLAST score 553
E value 8.0e-57
Match length 161
% identity 64

NCBI Description (AL035356) putative protein [Arabidopsis thaliana]

Seq. No. 309672

Seq. ID uC-zmflmo17294f06b1

Method BLASTN NCBI GI g257040

BLAST score

% identity

E value Match length 251 2.0e-21

74

59

```
BLAST score
E value
                  2.0e-12
                  50
Match length
                  94
% identity
NCBI Description
                  hydroxyproline-rich glycoprotein [maize, Genomic, 1703 nt]
                  309673
Seq. No.
Seq. ID
                  uC-zmflmo17294f09b1
Method
                  BLASTX
NCBI GI
                  q1709000
BLAST score
                   570
                  8.0e-59
E value
Match length
                  115
                   93
% identity
NCBI Description
                  S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
                  ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                  >gi_960357_dbj_BAA09895_ (D63835) S-adenosylmethionine
                   synthetase [Hordeum vulgare]
                   309674
Seq. No.
                  uC-zmflmo17294h06b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4454032
BLAST score
                  229
E value
                   8.0e-19
Match length
                  78
% identity
                   59
                  (AL035394) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   309675
Seq. ID
                  uC-zmflmo17295a11b1
Method
                  BLASTX
NCBI GI
                   g3056586
BLAST score
                   408
E value
                   8.0e-45
Match length
                   160
% identity
NCBI Description
                  (AC004255) T1F9.7 [Arabidopsis thaliana]
Seq. No.
                   309676
Seq. ID
                   uC-zmflmo17295b09b1
Method
                   BLASTX
NCBI GI
                   g2250699
BLAST score
                   448
E value
                   2.0e-44
Match length
                   154
% identity
                   50
NCBI Description
                  (AB001517) PWP2 protein [Homo sapiens]
                   309677
Seq. No.
                   uC-zmflmo17295d09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3193293
```



(AF069298) contains a short region of similarity to another NCBI Description Arabidopsis hypothetical protein F19K23.8 (GB:AC000375)

[Arabidopsis thaliana]

Seq. No. 309678

uC-zmflmo17295e02b1 Seq. ID

BLASTX Method q1402881 NCBI GI BLAST score 178 8.0e-13 E value 139 Match length % identity 37

(X98130) non-ltr retrotransposon reverse transcriptase-like NCBI Description

protein [Arabidopsis thaliana]

309679 Seq. No.

uC-zmflmo17295f03b1 Seq. ID

BLASTX Method q4165323 NCBI GI BLAST score 424 E value 9.0e-42 130 Match length % identity 61

(AB022442) p-type H+-ATPase [Vicia faba] NCBI Description

Seq. No. 309680

uC-zmflmo17295g05b1 Seq. ID

Method BLASTX NCBI GI g2493494 201 BLAST score 9.0e-16 E value 94 Match length 48 % identity

SERINE CARBOXYPEPTIDASE II-2 PRECURSOR (CP-MII.2) NCBI Description

>gi 619351 bbs 153537 CP-MII.2=serine carboxypeptidase

[Hordeum vulgare=barley, cv. Alexis, aleurone, Peptide, 436

aa]

Seq. No. 309681

uC-zmflmo17295g12b1 Seq. ID

BLASTX Method g2522210 NCBI GI 149 BLAST score 2.0e-09 E value 48 Match length 54 % identity

(AF023132) choline monooxygenase [Beta vulgaris] NCBI Description

Seq. No.

309682

uC-zmflmo17295h02b1 Seq. ID

Method BLASTX NCBI GI q135411 568 BLAST score E value 1.0e-58 Match length 109 95 % identity

NCBI Description TUBULIN ALPHA-2 CHAIN >gi_82732 pir__S15772 tubulin alpha-2



chain - maize >gi_22148_emb_CAA33733_ (X15704)
alpha2-tubulin [Zea mays]

Seq. No. 309683

Seq. ID uC-zmflmo17297a03b1

Method BLASTX
NCBI GI g3341688
BLAST score 339
E value 1.0e-31
Match length 139
% identity 50

NCBI Description (AC003672) putative casein kinase II beta subunit

[Arabidopsis thaliana]

Seq. No. 309684

Seq. ID uC-zmflmo17297a06b1

Method BLASTN
NCBI GI g22091
BLAST score 79
E value 2.0e-36
Match length 132
% identity 28

NCBI Description Z.diploperennis gene for hydroxyproline-rich glycoprotein

Seq. No. 309685

Seq. ID uC-zmflmo17297a11b1

Method BLASTN
NCBI GI g22332
BLAST score 369
E value 0.0e+00
Match length 481
% identity 94

NCBI Description Z.mays HRGP gene

Seq. No. 309686

Seq. ID uC-zmflmo17297a12b1

Method BLASTN
NCBI GI g4007864
BLAST score 79
E value 2.0e-36
Match length 144
% identity 56

NCBI Description Zea mays HRGP gene, AC1503 line

Seq. No. 309687

Seq. ID uC-zmflmo17297c12b1

Method BLASTX
NCBI GI g2618721
BLAST score 457
E value 2.0e-45
Match length 152
% identity 60

NCBI Description (U49072) IAA16 [Arabidopsis thaliana]

Seq. No. 309688

Seq. ID uC-zmflmo17297d01b1

Method BLASTN



```
NCBI GI
                   g3511235
BLAST score
                   40
                   6.0e-13
E value
Match length
                   64
% identity
                   91
```

NCBI Description Zea mays starch branching enzyme IIb (ae) gene, complete

309689 Seq. No.

uC-zmflmo17297e06b1 Seq. ID

Method BLASTX NCBI GI g4001720 BLAST score 146 E value 5.0e-09 Match length 48 % identity 56

NCBI Description (AB015894) neural specific sr protein NSSR 1 [Mus musculus]

Seq. No.

309690

uC-zmflmo17297e08b1 Seq. ID

Method BLASTX NCBI GI g417103 BLAST score 627 E value 2.0e-65 Match length 126 % identity 99

HISTONE H3.2, MINOR >gi 282871 pir S24346 histone NCBI Description

H3.3-like protein - Arabidopsis thaliana

>gi_16324_emb_CAA42957 (X60429) histone H3.3 like protein [Arabidopsis thaliana] >qi 404825 emb CAA42958 (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi 488563 (U09458) histone H3.2 [Medicago sativa] >gi 488567 (U09460) histone H3.2 [Medicago sativa] >qi 488569 (U09461) histone H3.2 [Medicago sativa] >gi 488575 (U09464) histone H3.2

[Medicago sativa] >gi 488577 (U09465) histone H3.2 [Medicago sativa] >gi 510911 emb CAA56153 (X79714) histone H3 [Lolium temulentum] >gi 1435157 emb CAA58445 (X83422)

histone H3 variant H3.3 [Lycopersicon esculentum] >gi_2558944 (AF024716) histone 3 [Gossypium hirsutum] >gi_3273350_dbj_BAA31218_ (AB015760) histone H3 [Nicotiana tabacum] >gi 3885890 (AFO93633) histone H3 [Oryza sativa] >gi 4038469 gb AAC97380 (AF109910) histone H3 [Porteresia coarctata] >gi 4490754 emb CAB38916.1 (AL035708) histone H3.3 [Arabidopsis thaliana] >gi 4490755 emb CAB38917.1

(AL035708) Histon H3 [Arabidopsis thaliana]

309691 Seq. No.

uC-zmflmo17297f06b1 Seq. ID

Method BLASTX NCBI GI g2832643 BLAST score 170 E value 6.0e-12 Match length 81 % identity 43

NCBI Description (AL021710) hypothetical protein [Arabidopsis thaliana]

Seq. No. 309692 . .

```
Seq. ID
                  uC-zmflmo17297h01b1
Method
                  BLASTX
NCBI GI
                  g2984709
BLAST score
                  451
E value
                  6.0e-45
Match length
                  89
% identity
                  96
NCBI Description (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]
Seq. No.
                  309693
Seq. ID
                  uC-zmflmo17297h09b1
Method
                  BLASTX
NCBI GI
                  q3914935
BLAST score
                  376
E value
                  2.0e-40
Match length
                  137
% identity
                  63
NCBI Description 40S RIBOSOMAL PROTEIN SA (P40) >gi 3204099 emb CAA07226
                  (AJ006759) ribosome-associated protein p40 [Cicer
                  arietinum]
Seq. No.
                  309694
Seq. ID
                  uC-zmflmo17299d04b1
Method
                  BLASTX
NCBI GI
                  q3402692
BLAST score
                  196
E value
                  2.0e-15
Match length
                  53
                  79
% identity
NCBI Description
                  (AC004697) putative
                  CDP-diacylglycerol--glycerol-3-phosphate
                  3-phosphatidyltransferase [Arabidopsis thaliana]
Seq. No.
                  309695
Seq. ID
                  uC-zmflmo17300a05a1
Method
                  BLASTN
NCBI GI
                  g483489
BLAST score
                  165
E value
                  5.0e-88
Match length
                  207
% identity
                  96
NCBI Description Z.mays IBP1 mRNA for initiator-binding protein
                  309696
Seq. No.
Seq. ID
                  uC-zmflmo17300a07b1
Method
                  BLASTX
NCBI GI
                  q481477
BLAST score
                  720
E value
                  2.0e-76
Match length
                  144
% identity
                  18
NCBI Description
                  ubiquitin precursor - rice >gi 416038 emb CAA53665
```

(X76064) polyubiquitin [Oryza sativa] >gi_1574944 (U37687) polyubiquitin [Oryza sativa]

Seq. No. 309697

Seq. ID uC-zmflmo17300a10b1



```
Method
                  BLASTX
NCBI GI
                  g2781345
BLAST score
                  196
                  2.0e-15
E value
Match length
                  68
% identity
                  51
NCBI Description (AC003113) F2401.2 [Arabidopsis thaliana]
                  309698
Seq. No.
Seq. ID
                  uC-zmflmo17300b02b1
Method
                  BLASTX
NCBI GI
                  g134597
BLAST score
                  360
                  2.0e-42
E value
                  111
Match length
```

% identity 81 NCBI Description SUPEROXIDE DISMUTASE-4A (CU-ZN) >gi 100926 pir S07007 superoxide dismutase (EC 1.15.1.1) (Cu-Zn) 4, cytosolic -

maize

309699 Seq. No.

Seq. ID uC-zmflmo17300b04b1

Method BLASTX NCBI GI q1084442 BLAST score 323 6.0e-30 E value Match length 72 % identity 79

NCBI Description cellulase (EC 3.2.1.4) - European elder

>gi 575404 emb CAA52343 (X74290) cellulase [Sambucus

nigra]

Seq. No. 309700

Seq. ID uC-zmflmo17300d03b1

Method BLASTX NCBI GI q3169012 BLAST score 499 E value 2.0e-50 Match length 162 % identity 62

NCBI Description (AJ002610) putative calmodulin binding transporter protein

[Hordeum vulgare]

309701 Seq. No.

Seq. ID uC-zmflmo17300d10b1

Method BLASTN NCBI GI q1061307 BLAST score 41 1.0e-13 E value Match length 53 % identity 94

NCBI Description Z.mays Dof3 mRNA

309702 Seq. No.

Seq. ID uC-zmflmo17300e12b1

Method BLASTX NCBI GI g3377802



```
BLAST score
                  3.0e-30
E value
                  148
Match length
                  47
% identity
                 (AF075597) Similar to sucrose synthase; T2H3.8 [Arabidopsis
NCBI Description
                  thaliana]
                  309703
Seq. No.
                  uC-zmflmo17300h05b1
Seq. ID
                  BLASTX
Method
                  g4538624
NCBI GI
BLAST score
                  155
                  3.0e-10
E value
                  79
Match length
% identity
NCBI Description (AJ133502) hypothetical protein [Nicotiana tabacum]
                  309704
Seq. No.
                  uC-zmflmo17301a04b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3914212
BLAST score
                  184
E value
                  1.0e-13
                  134
Match length
                  34
% identity
                  5-OXOPROLINASE (5-OXO-L-PROLINASE) (PYROGLUTAMASE)
NCBI Description
                   (5-OPASE) >gi_1732065 (U70825) 5-oxo-L-prolinase [Rattus
                  norvegicus]
                  309705
Seq. No.
Seq. ID
                  uC-zmflmo17301a07b1
Method
                  BLASTX
NCBI GI
                  q115771
                   798
BLAST score
                   2.0e-85
E value
                   148
Match length
% identity
                   100
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                   (CAB-1) (LHCP) >qi 82682 pir S04453 chlorophyll
                   a/b-binding protein precursor - maize
                   >gi_22224_emb_CAA32900_ (X14794) chlorophyll a/b-binding
                   preprotein (AA 1 - 262) [Zea mays]
Seq. No.
                   309706
                   uC-zmflmo17301a10b1
Seq. ID
Method
                   BLASTX
                   g1890575
NCBI GI
BLAST score
                   154
                   2.0e-10
E value
Match length
                   44
% identity
                   64
                  (X93174) xyloglucan endotransglycosylase (XET) [Hordeum
NCBI Description
                   vulgare]
```

Seq. No. 309707

Seq. ID uC-zmflmo17301e11b1

Method BLASTN

```
NCBI GI
                  g22312
BLAST score
                  88
                  7.0e-42
E value
                  187
Match length
                  93
% identity
NCBI Description
                  Maize ABA-inducible gene for glycine-rich protein ( ABA =
                  abscisic acid)
                  309708
Seq. No.
                  uC-zmflmo17301f06b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2668742
                  416
BLAST score
                  8.0e-41
E value
                  85
Match length
                  94
% identity
NCBI Description (AF034945) glycine-rich RNA binding protein [Zea mays]
                  309709
Seq. No.
Seq. ID
                  uC-zmflmo17303a02b1
                  BLASTX
Method
NCBI GI
                  g112994
BLAST score
                  182
                  2.0e-13
E value
                  96
Match length
                  49
% identity
                  GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN
NCBI Description
                  >gi_82685_pir__S04536 embryonic abundant protein,
                  glycine-rich - maize >gi_22313_emb_CAA31077_ (X12564)
                  ABA-inducible gene protein [Zea mays]
                  >gi 226091 prf 1410284A abscisic acid inducible gene [Zea
                  mays]
                  309710
Seq. No.
                  uC-zmflmo17303b05b1
Seq. ID
```

Method BLASTX
NCBI GI g133361
BLAST score 208
E value 1.0e-23
Match length 122
% identity 53

NCBI Description DNA-DIRECTED RNA POLYMERASE III 128 KD POLYPEPTIDE (RNA

POLYMERASE III SUBUNIT 2) >gi_66988_pir__RNFF32

DNA-directed RNA polymerase (EC 2.7.7.6) III second-largest

chain - fruit fly (Drosophila melanogaster)

>gi_10963_emb_CAA41631_ (X58826) RNA polymerase III
second-largest subunit [Drosophila melanogaster]

Seq. No. 309711

Seq. ID uC-zmflmo17303c04b1

Method BLASTX
NCBI GI g4105772
BLAST score 552
E value 1.0e-56
Match length 167
% identity 40

NCBI Description (AF049917) PGP9B [Petunia x hybrida]



```
      Seq. No.
      309712

      Seq. ID
      uC-zmflmo17304c06a1

      Method
      BLASTN

      NCBL CL
      -204844
```

NCBI GI g294844
BLAST score 181
E value 3.0e-97
Match length 327
% identity 89

NCBI Description Saccharum hybrid cultivar H65-7052 membrane protein mRNA,

complete cds

Seq. No. 309713

Seq. ID uC-zmflmo17305c06a1

Method BLASTN
NCBI GI g1532072
BLAST score 115
E value 5.0e-58
Match length 267
% identity 86

NCBI Description Z.mays mRNA for S-adenosylmethionine decarboxylase

Seq. No. 309714

Seq. ID uC-zmflmo17305h05a1

Method BLASTX
NCBI GI g1209756
BLAST score 319
E value 1.0e-29
Match length 81
% identity 70

NCBI Description (U43629) integral membrane protein [Beta vulgaris]

Seq. No. 309715

Seq. ID uC-zmflmo17306a12b1

Method BLASTX
NCBI GI g2130137
BLAST score 545
E value 6.0e-56
Match length 117
% identity 48

NCBI Description homeotic protein Hox2b - maize >gi 1143707 emb CAA61910

(X89761) Hox2b [Zea mays]

Seq. No. 309716

Seq. ID uC-zmflmo17306b02b1

Method BLASTX
NCBI GI g3293031
BLAST score 684
E value 4.0e-72
Match length 169
% identity 76

NCBI Description (AJ007574) amino acid carrier [Ricinus communis]

Seq. No. 309717

Seq. ID uC-zmflmo17306e06a1

Method BLASTX NCBI GI g2262113

```
BLAST score
                  169
E value
                  7.0e-12
Match length
                  48
% identity
NCBI Description
                 (AC002343) unknown protein [Arabidopsis thaliana]
Seq. No.
                  309718
Seq. ID
                  uC-zmflmo17306e06b1
Method
                  BLASTX
NCBI GI
                  g2262113
BLAST score
                  152
E value
                  9.0e-10
Match length
                  44
% identity
                  70
NCBI Description (AC002343) unknown protein [Arabidopsis thaliana]
Seq. No.
                  309719
Seq. ID
                  uC-zmflmo17306e11b1
Method
                  BLASTX
NCBI GI
                  q2749752
BLAST score
                  156
                  3.0e-10
E value
Match length
                  135
% identity
                  39
NCBI Description
                  (AL021086) 1-evidence=predicted by content;
                  1-method=genefinder;084; 1-method score=147.90;
                  1-evidence_end; 2-evidence=predicted by match;
                  2-match accession=SWISS-PROT:P30630;
                  2-match_description=LIN-9 PROTEIN.; 2-match_species
                  309720
Seq. ID
                  uC-zmflmo17306e12b1
Method
                  BLASTX
                  g2191144
```

Seq. No.

NCBI GI BLAST score 146 E value 4.0e-09 Match length 35 % identity 71

NCBI Description (AF007269) A_IG002N01.24 gene product [Arabidopsis

thaliana]

Seq. No. 309721

Seq. ID uC-zmflmo17306f09b1

Method BLASTX NCBI GI q3413712 BLAST score 451 5.0e-45 E value Match length 103 % identity 69

NCBI Description (AC004747) hypothetical protein [Arabidopsis thaliana]

Seq. No. 309722

Seq. ID uC-zmflmo17306h02a1

Method BLASTN NCBI GI g1617470 BLAST score 52 E value 2.0e-20



Match length 92 % identity

NCBI Description Z.diploperennis DNA for Grandel-4 retrotransposon

Seq. No.

309723

Seq. ID

uC-zmflmo17306h02b1

Method NCBI GI BLASTX q1244653

BLAST score E value

376 2.0e-36

94

Match length % identity

79 NCBI Description (U41000) gag gene product [Zea mays]

Seq. No.

309724

Seq. ID Method

uC-zmflmo17306h09a1

NCBI GI

BLASTN g498774 62

BLAST score E value

1.0e-26

Match length % identity

78 95

NCBI Description Z.mays (cv DH5xDH7) hsp70-5 mRNA for heat shock protein

Seq. No.

309725

Seq. ID Method

uC-zmflmo17307a09b1

NCBI GI

BLASTX g4585991 616

BLAST score E value Match length

3.0e-64 153

% identity NCBI Description

69 (AC005287) very similar to mouse Dhm1 and Dhm2 [Arabidopsis

thalianal

Seq. No.

309726

Seq. ID

uC-zmflmo17307c08b1

Method NCBI GI BLAST score BLASTX q4415990 285

E value Match length

8.0e-44 132

% identity

71

NCBI Description (AF059287) beta-tubulin 1 [Eleusine indica]

Seq. No.

309727

Seq. ID

uC-zmflmo17307d04b1

Method NCBI GI BLASTX g3822403

BLAST score E value Match length 183 2.0e-16

% identity

111

NCBI Description

42 (AF087932) hydroperoxide lyase [Arabidopsis thaliana]

Seq. No.

309728

Seq. ID

uC-zmflmo17307e04b1

```
Method
NCBI GI
                  q4539303
BLAST score
                  189
                  4.0e-14
E value
Match length
                  96
% identity
                  48
NCBI Description (AL049480) putative protein [Arabidopsis thaliana]
                  309729
Seq. No.
                  uC-zmflmo17307e09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4572676
BLAST score
                  219
E value
                  7.0e-18
Match length
                  107
                  43
% identity
NCBI Description (AC006954) unknown protein [Arabidopsis thaliana]
Seq. No.
                  309730
Seq. ID
                  uC-zmflmo17307e12b1
Method
                  BLASTX
NCBI GI
                  g3264596
BLAST score
                  247
E value
                  2.0e-29
Match length
                  131
% identity
                  59
NCBI Description (AF057183) putative tonoplast aquaporin [Zea mays]
                  309731
Seq. No.
Seq. ID
                  uC-zmflmo17307q03b1
Method
                  BLASTX
NCBI GI
                  g1773330
BLAST score
                  347
E value
                  9.0e-33
Match length
                  78
% identity
                  87
NCBI Description (U80071) glycolate oxidase [Mesembryanthemum crystallinum]
Seq. No.
                  309732
Seq. ID
                  uC-zmflmo17307q12b1
Method
                  BLASTX
NCBI GI
                  q113460
BLAST score
                  216
E value
                  2.0e-17
Match length
                  120
                  47
% identity
NCBI Description
                  ADP, ATP CARRIER PROTEIN 2 PRECURSOR (ADP/ATP TRANSLOCASE 2)
                   (ADENINE NUCLEOTIDE TRANSLOCATOR 2) (ANT 2)
                  >gi_100851_pir__S16568 ADP,ATP carrier protein precursor -
                  maize >gi_22164_emb_CAA41812_ (X59086) adenine nucleotide
                  translocator [Zea mays]
```

309733 Seq. No.

Seq. ID uC-zmflmo17307h01b1

Method BLASTN NCBI GI g4007864

BLAST score 44



```
2.0e-15
E value
Match length
                  104
% identity
                  86
NCBI Description Zea mays HRGP gene, AC1503 line
                  309734
Seq. No.
                  uC-zmflmo17308a11b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1890575
BLAST score
                  208
E value
                  2.0e-24
Match length
                  85
% identity
                  65
NCBI Description
                  (X93174) xyloglucan endotransglycosylase (XET) [Hordeum
                  vulgare]
                  309735
Seq. No.
Seq. ID
                  uC-zmflmo17308b02b1
Method
                  BLASTX
                  g2980773
NCBI GI
BLAST score
                  231
E value
                  3.0e-19
Match length
                  87
% identity
                  59
NCBI Description (AL022198) putative protein [Arabidopsis thaliana]
                  309736
Seq. No.
Seq. ID
                  uC-zmflmo17308b10b1
Method
                  BLASTX
NCBI GI
                  q3980415
                  170
BLAST score
                  2.0e-12
E value
Match length
                  54
% identity
                  57
                  (AC004561) putative tropinone reductase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  309737
Seq. ID
                  uC-zmflmo17308d02b1
Method
                  BLASTX
NCBI GI
                  q1513144
BLAST score
                  202
E value
                  1.0e-15
Match length
                  146
% identity
                  32
NCBI Description (U65391) PRF [Lycopersicon esculentum]
Seq. No.
                  309738
Seq. ID
                  uC-zmflmo17308e04b1
Method
                  BLASTX
```

NCBI GI g1658313 BLAST score 279 4.0e-25 E value Match length 72 % identity 38

NCBI Description (Y08987) osr40g2 [Oryza sativa]



```
      Seq. No.
      309739

      Seq. ID
      uC-zmflmo17308f01b1

      Method
      BLASTX

      NCBI GI
      g3603456

      BLAST score
      451

      E value
      3.0e-45
```

E value 3.0 Match length 99 % identity 28

NCBI Description (AF088848) polyubiquitin [Capsicum chinense]

Seq. No. 309740

Seq. ID uC-zmflmo17308f02b1

Method BLASTX
NCBI GI g3004552
BLAST score 177
E value 6.0e-13
Match length 103
% identity 40

NCBI Description (AC003673) unknown protein [Arabidopsis thaliana]

Seq. No. 309741

Seq. ID uC-zmflmo17309a05b1

Method BLASTX
NCBI GI g112994
BLAST score 333
E value 3.0e-31
Match length 86
% identity 81

NCBI Description GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN

>gi_82685_pir__S04536 embryonic abundant protein,
glycine-rich - maize >gi 22313 emb CAA31077 (X12564)

ABA-inducible gene protein [Zea mays]

>gi 226091 prf 1410284A abscisic acid inducible gene [Zea

mays]

Seq. No. 309742

Seq. ID uC-zmflmo17309a06b1

Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 1.0e-10
Match length 36
% identity 100

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 309743

Seq. ID uC-zmflmo17309a08b1

Method BLASTX
NCBI GI g396384
BLAST score 176
E value 1.0e-12
Match length 70
% identity 50

NCBI Description (U00006) No definition line found [Escherichia coli]

Seq. No. 309744

Seq. ID uC-zmflmo17309b01b1

```
Method BLASTX
NCBI GI g4038352
BLAST score 147
E value 2.0e-09
```

% identity 42
NCBI Description (AF098951) breast cancer resistance protein [Homo sapiens]

Ĭ -

Seq. No. 309745

Match length

Seq. ID uC-zmflmo17309b10b1

93

Method BLASTX
NCBI GI g1332579
BLAST score 357
E value 1.0e-55
Match length 124
% identity 9

NCBI Description (X98063) polyubiquitin [Pinus sylvestris]

Seq. No. 309746

Seq. ID uC-zmflmo17309f10b1

Method BLASTN
NCBI GI g22332
BLAST score 292
E value 1.0e-163
Match length 412
% identity 93

NCBI Description Z.mays HRGP gene

Seq. No. 309747

Seq. ID uC-zmflmo17309h06b1

Method BLASTX
NCBI GI g2944417
BLAST score 263
E value 6.0e-25
Match length 108
% identity 61

NCBI Description (AF049881) peroxidase FLXPER4 [Linum usitatissimum]

Seq. No. 309748

Seq. ID uC-zmflmo17309h08b1

Method BLASTX
NCBI GI g4468979
BLAST score 172
E value 2.0e-12
Match length 51
% identity 59

NCBI Description (AL035605) putative protein [Arabidopsis thaliana]

Seq. No. 309749

Seq. ID uC-zmflmo17310d06a1

Method BLASTX
NCBI GI g2570515
BLAST score 167
E value 1.0e-11
Match length 71
% identity 45

NCBI Description (AF022740) glycolate oxidase [Oryza sativa]

BLAST score

403

```
Seq. No.
                  309750
Seq. ID
                  uC-zmflmo17310h06a1
Method
                  BLASTX
NCBI GI
                  g4415937
BLAST score
                  378
E value
                  2.0e-41
Match length
                  122
% identity
                   65
NCBI Description (AC006418) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  309751
Seq. ID
                  uC-zmflmo17310h06b1
Method
                  BLASTX
NCBI GI
                  g4415937
BLAST score
                  195
E value
                  8.0e-15
Match length
                  129
% identity
                  39
NCBI Description (AC006418) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  309752
Seq. ID
                  uC-zmflmo17310h07a1
Method
                  BLASTX
NCBI GI
                  g2499134
BLAST score
                  350
E value
                  3.0e-33
Match length
                  77
% identity
                  79
                  XAP-5 PROTEIN >gi_1203974 (L44140) XAP-5 gene product [Homo
NCBI Description
                  sapiens]
Seq. No.
                  309753
Seq. ID
                  uC-zmflmo17310h07b1
Method
                  BLASTX
NCBI GI
                  g2335055
BLAST score
                  143
                  2.0e-13
E value
Match length
                  85
% identity
NCBI Description
                  (AD001530) putative [Homo sapiens]
Seq. No.
                  309754
Seq. ID
                  uC-zmflmo17311h06a1
Method
                  BLASTX
NCBI GI
                  g1914683
BLAST score
                  166
E value
                  1.0e-11
Match length
                  37
% identity
                  84
                  (Y12013) RAD23, isoform I [Daucus carota]
NCBI Description
Seq. No.
                  309755
Seq. ID
                  uC-zmflmo17312c08b1
Method
                  BLASTX
NCBI GI
                  g2529677
```



309757

E value 3.0e-39 Match length 139 % identity 60 NCBI Description (AC002535) kinesin-like protein, heavy chain [Arabidopsis thaliana] Seq. No. 309756 Seq. ID uC-zmflmo17312e09b1 Method BLASTX NCBI GI g4581164 BLAST score 257 E value 4.0e-22 Match length 145 % identity 43 NCBI Description

(AC006220) putative polyprotein [Arabidopsis thaliana]

. بنيد

Seq. ID uC-zmflmo17312h07b1 Method BLASTX NCBI GI g4417288 BLAST score 172 E value 4.0e-12 Match length 101 % identity 70

Seq. No.

NCBI Description (AC007019) unknown protein [Arabidopsis thaliana]

309758 Seq. No. Seq. ID uC-zmflmo17313b03b1 BLASTN

Method NCBI GI g2773153 BLAST score 202 E value 1.0e-109 Match length 278

% identity 93

NCBI Description Oryza sativa abscisic acid- and stress-inducible protein

(Asr1) mRNA, complete cds

309759 Seq. No.

Seq. ID uC-zmflmo17313b06b1

Method BLASTN NCBI GI g3821780 BLAST score 36 E value 1.0e-10 Match length 47 % identity 66

NCBI Description Xenopus laevis cDNA clone 27A6-1

309760 Seq. No.

Seq. ID uC-zmflmo17313b08b1

Method BLASTX NCBI GI g1890575 BLAST score 491 E value 2.0e-53 Match length 160 % identity 67

NCBI Description (X93174) xyloglucan endotransglycosylase (XET) [Hordeum

vulgare]



Seq. No. 309761

Seq. ID uC-zmflmo17313f11b1

Method BLASTX
NCBI GI g3790575
BLAST score 212
E value 8.0e-17
Match length 105
% identity 43

NCBI Description (AF078825) RING-H2 finger protein RHA3b [Arabidopsis

thaliana]

Seq. No. 309762

Seq. ID uC-zmflmo17313g02b1

Method BLASTN
NCBI GI g22332
BLAST score 231
E value 1.0e-127
Match length 354
% identity 91

NCBI Description Z.mays HRGP gene

Seq. No. 309763

Seq. ID uC-zmflmo17313g10b1

Method BLASTX
NCBI GI g3421090
BLAST score 347
E value 9.0e-33
Match length 123
% identity 60

NCBI Description (AF043525) 20S proteasome subunit PAE2 [Arabidopsis

thaliana]

Seq. No. 309764

Seq. ID uC-zmflmo17315a11a1

Method BLASTN
NCBI GI g3004949
BLAST score 35
E value 3.0e-10
Match length 67
% identity 88

NCBI Description Zea mays tonoplast intrinsic protein (ZmTIP1) mRNA,

complete cds

Seq. No. 309765

Seq. ID uC-zmflmo17315h05a1

Method BLASTX
NCBI GI g1314711
BLAST score 473
E value 2.0e-47
Match length 135
% identity 70

NCBI Description (U54615) calcium-dependent protein kinase [Arabidopsis

thaliana] >gi_3068712 (AF049236) calcium dependent protein

kinase [Arabidopsis thaliana]

Seq. No. 309766



```
Seq. ID
                   uC-zmflmo17316c08a1
Method
                  BLASTN
NCBI GI
                   g507844
BLAST score
                   57
                   2.0e-23
E value
Match length
                  205
% identity
                  82
NCBI Description Zea mays A188 retrotransposon gag gene, complete cds
Seq. No.
                  309767
Seq. ID
                  uC-zmflmo17316d02a1
Method
                  BLASTN
NCBI GI
                  g485376
BLAST score
                  103
E value
                  5.0e-51
Match length
                  200
% identity
                  87
NCBI Description Zea mays alpha-3-tubulin gene, complete cds
Seq. No.
                  309768
Seq. ID
                  uC-zmflmo17317b03a1
Method
                  BLASTX
NCBI GI
                  g3204108
BLAST score
                  171
E value
                  3.0e-12
Match length
                  43
% identity
                  79
NCBI Description
                  (AJ006764) putative deoxycytidylate deaminase [Cicer
                  arietinum]
Seq. No.
                  309769
Seq. ID
                  uC-zmflmo17317b06a1
Method
                  BLASTX
NCBI GI
                  q4314400
BLAST score
                  313
E value
                  8.0e-29
Match length
                  105
% identity
                  60
NCBI Description
                  (AC006232) putative selenium-binding protein [Arabidopsis
                  thaliana]
Seq. No.
                  309770
Seq. ID
                  uC-zmflmo17317c04a1
                  BLASTX
Method
NCBI GI
                  g2130141
BLAST score
                  174
E value
                  1.0e-12
Match length
                  51
% identity
                  59
NCBI Description
                  mudrA protein - maize transposon MuDR >gi_540581 (M76978)
                  mudrA [Zea mays] >gi_595816 (U14597) mudrA gene product
                  [Zea mays]
```

Seq. No.

309771

Seq. ID

uC-zmflmo17317g06a1

Method

BLASTN

NCBI GI

g3925238



BLAST score 46 E value 1.0e-16 Match length 133 % identity 84

NCBI Description Zea mays 6-phosphogluconate dehydrogenase isoenzyme A gene,

partial cds

Seq. No. 309772

Seq. ID uC-zmflmo17318g02a1

Method BLASTX
NCBI GI g1711355
BLAST score 314
E value 6.0e-29
Match length 94
% identity 63

NCBI Description SHORT-CHAIN TYPE DEHYDROGENASE/REDUCTASE

>gi_421786_pir__S34678 short-chain alcohol dehydrogenase Norway spruce >gi_395223_emb_CAA52213_ (X74115) short-chain

alcohol dehydrogenase [Picea abies]

Seq. No. 309773

Seq. ID uC-zmflmo17319b08a1

Method BLASTN
NCBI GI g601870
BLAST score 45
E value 5.0e-16
Match length 57
% identity 95

NCBI Description Oryza sativa manganese superoxide dismutase (rmsod2) mRNA,

complete cds

Seq. No. 309774

Seq. ID uC-zmflmo17319b09a1

Method BLASTX
NCBI GI g4091080
BLAST score 262
E value 7.0e-23
Match length 44
% identity 95

NCBI Description (AF045571) nucleic acid binding protein [Oryza sativa]

Seq. No. 309775

Seq. ID uC-zmflmo17319c04a1

Method BLASTN
NCBI GI 94185305
BLAST score 110
E value 5.0e-55
Match length 202
% identity 45

NCBI Description Zea mays cosmid IV.1E1 22-kDa alpha zein protein 21

(sz22-21) gene, complete cds; retrotransposon Opie-2 gag protein, polyprotein, and copia protein genes, complete

cds; and unknown genes

Seq. No. 309776

Seq. ID uC-zmflmo17320c05b1

Method BLASTN

```
NCBI GI g3821780
BLAST score 35
E value 4.0e-10
Match length 35
% identity 100
NCBI Description Xenopus laevis cDNA clone 27A6-1
```

 Seq. No.
 309777

 Seq. ID
 uC-zmflmo17320c07a1

 Method
 BLASTN

 NCBI GI
 g1657766

 BLAST score
 230

 E value
 1.0e-126

Match length 428 % identity 66

NCBI Description Zea mays retrotransposon Opie-2 5' LTR, primer binding site, gag gene, pol gene, complete cds, polypurine tract

and 3' LTR

Method BLASTX
NCBI GI g2688822
BLAST score 222
E value 4.0e-18
Match length 71
% identity 55

NCBI Description (U93272) pyrophosphate-dependent phosphofructo-1-kinase

[Prunus armeniaca]

Seq. No. 309779

Seq. ID uC-zmflmo17320e04b1

Method BLASTN
NCBI GI g3869066
BLAST score 34
E value 2.0e-09
Match length 62
% identity 89

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MBM17, complete sequence [Arabidopsis thaliana]

Seq. No. 309780

Seq. ID uC-zmflmo17320f04b1

Method BLASTX
NCBI GI g2565436
BLAST score 318
E value 3.0e-29
Match length 117
% identity 59

NCBI Description (AF028842) DegP protease precursor [Arabidopsis thaliana]

Seq. No. 309781

Seq. ID uC-zmflmo17320f07b1

Method BLASTX NCBI GI g625509 BLAST score 537 E value 5.0e-55



```
Match length 145 % identity 22
```

NCBI Description ubiquitin precursor - Arabidopsis thaliana (fragment)

Seq. No. 309782

Seq. ID uC-zmflmo17320g06b1

Method BLASTX
NCBI GI 94406781
BLAST score 327
E value 2.0e-30
Match length 121
% identity 59

NCBI Description (AC006532) putative Na+/H+ antiporter [Arabidopsis

thaliana]

Seq. No. 309783

Seq. ID uC-zmflmo17320g09b1

Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 1.0e-10
Match length 47
% identity 66

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 309784

Seq. ID uC-zmflmo17320g11a1

Method BLASTX
NCBI GI g2645999
BLAST score 194
E value 4.0e-15
Match length 42
% identity 86

NCBI Description (AF034631) chlorophyll a/b binding protein of LHCII type I

precursor [Panax ginseng]

Seq. No. 309785

Seq. ID uC-zmflmo17321c03b1

Method BLASTX
NCBI GI g2182029
BLAST score 175
E value 7.0e-13
Match length 71
% identity 59

NCBI Description (Y13437) shaggy-like kinase etha (OSKetha) [Oryza sativa]

Seq. No. 309786

Seq. ID uC-zmflmo17321c11a1

Method BLASTX
NCBI GI g3033397
BLAST score 208
E value 1.0e-21
Match length 61
% identity 92

NCBI Description (AC004238) unknown protein [Arabidopsis thaliana]

Seq. No. 309787



Seq. ID uC-zmflmo17321d12b1 Method BLASTN NCBI GI g3821780 BLAST score 36 E value 1.0e-10 Match length 36 100 % identity NCBI Description Xenopus laevis cDNA clone 27A6-1 309788 Seq. No. Seq. ID uC-zmflmo17322a06a1 Method BLASTX NCBI GI g4454471 BLAST score 167 E value 4.0e-12 Match length 39 % identity 77 NCBI Description (AC006234) putative G protein coupled receptor [Arabidopsis thaliana] 309789 Seq. No. Seq. ID uC-zmflmo17322b10b1 Method BLASTX g2393775 NCBI GI BLAST score 313 E value 1.0e-28 Match length 60 % identity 85 NCBI Description (U82230) prolamin box binding factor [Zea mays] Seq. No. 309790 Seq. ID uC-zmflmo17322c01b1 Method BLASTN NCBI GI g3821780 BLAST score 37 E value 3.0e-11 Match length 37 % identity 100 NCBI Description Xenopus laevis cDNA clone 27A6-1 Seq. No. 309791 Seq. ID uC-zmflmo17322c05a1 Method BLASTN NCBI GI q22091 BLAST score 216 E value 1.0e-118 Match length 265 % identity 96 NCBI Description Z.diploperennis gene for hydroxyproline-rich glycoprotein 309792 Seq. No. uC-zmflmo17322c05b1

Seq. ID

Method BLASTN NCBI GI g22332 BLAST score 81 E value 1.0e-37 Match length 332

% identity 85
NCBI Description Z.mays HRGP gene

Seq. No. 309793
Seq. ID uC-zmflmo17322d02b1
Method BLASTX
NCBI GI g3242708
RLAST score 408

NCBI GI g3242708
BLAST score 408
E value 8.0e-40
Match length 166
% identity 51

NCBI Description (AC003040) putative serine/threonine protein kinase

[Arabidopsis thaliana]

Seq. No. 309794

Seq. ID uC-zmflmo17322d11b1

Method BLASTX
NCBI GI g1781299
BLAST score 263
E value 9.0e-23
Match length 82
% identity 61

NCBI Description (Y09506) transformer-SR ribonucleoprotein [Nicotiana

tabacum]

Seq. No. 309795

Seq. ID uC-zmflmo17322e10b1

Method BLASTX
NCBI GI g1706256
BLAST score 159
E value 1.0e-10
Match length 50
% identity 60

NCBI Description PEPTIDYL-PROLYL CIS-TRANS ISOMERASE 10 (PPIASE) (ROTAMASE)

(CYCLOPHILIN-10) >gi 733577 (U23453) similar to

peptidyl-prolyl cis-trans isomerase (PPIASE) (CYCLOPHILIN) [Caenorhabditis elegans] >gi 1155225 (U34954) cyclophilin

isoform 10 [Caenorhabditis elegans]

Seq. No. 309796

Seq. ID uC-zmflmo17322f03b1

Method BLASTX
NCBI GI g4432857
BLAST score 145
E value 5.0e-09
Match length 105
% identity 30

NCBI Description (AC006300) hypothetical protein [Arabidopsis thaliana]

Seq. No. 309797

Seq. ID uC-zmflmo17322g02b1

Method BLASTX
NCBI GI g419789
BLAST score 304
E value 1.0e-27
Match length 96
% identity 59



```
NCBI Description hypothetical protein - potato
```

Seq. No. 309798

Seq. ID uC-zmflmo17322g11a1

Method BLASTN
NCBI GI g602605
BLAST score 45
E value 1.0e-16
Match length 137
% identity 82

NCBI Description Zea mays tandem genes for alpha1-tubulin and alpha2-tubulin

Seq. No. 309799

Seq. ID uC-zmflmo17322h02b1

Method BLASTX
NCBI GI g2286153
BLAST score 171
E value 3.0e-12
Match length 49
% identity 71

NCBI Description (AF007581) cytoplasmic malate dehydrogenase [Zea mays]

Seq. No. 309800

Seq. ID uC-zmflmo17323e04a1

Method BLASTX
NCBI GI g3451078
BLAST score 158
E value 1.0e-10
Match length 128
% identity 32

NCBI Description (AL031326) putative protein [Arabidopsis thaliana]

Seq. No. 309801

Seq. ID uC-zmflmo17324a07a1

Method BLASTX
NCBI GI g3378134
BLAST score 206
E value 2.0e-16
Match length 109
% identity 43

NCBI Description (AF071503) brahma associated protein 60 kDa [Drosophila

melanogaster]

Seq. No. 309802

Seq. ID uC-zmflmo17324q11a1

Method BLASTX
NCBI GI g2832700
BLAST score 186
E value 5.0e-14
Match length 60
% identity 62

NCBI Description (AL021713) unknown protein [Arabidopsis thaliana]

Seq. No. 309803

Seq. ID uC-zmflmo17326g04a1

Method BLASTN NCBI GI g2341060

NCBI GI

E value

BLAST score

```
BLAST score
E value
                   4.0e-31
Match length
                   280
% identity
                   82
NCBI Description
                  Zea mays translational initiation factor eIF-4A (tif-4A3)
                  mRNA, complete cds
Seq. No.
                   309804
Seq. ID
                  uC-zmflmo17327a01a1
Method
                  BLASTX
NCBI GI
                  g4432835
BLAST score
                   201
E value
                   9.0e-16
Match length
                   64
% identity
NCBI Description (AC006283) unknown protein [Arabidopsis thaliana]
Seq. No.
                  309805
Seq. ID
                  uC-zmflmo17327a11b1
Method
                  BLASTX
NCBI GI
                  g2559012
BLAST score
                  540
E value
                   2.0e-55
Match length
                  144
% identity
                   76
NCBI Description
                   (AF026293) chaperonin containing t-complex polypeptide 1,
                  beta subunit; CCT-beta [Homo sapiens] >gi 4090929
                   (AF026166) chaperonin-containing TCP-1 beta subunit homolog
                   [Homo sapiens]
Seq. No.
                  309806
Seq. ID
                  uC-zmflmo17327b08b1
Method
                  BLASTX
NCBI GI
                  g3335359
BLAST score
                  406
                  1.0e-39
E value
                  125
Match length
% identity
                  62
NCBI Description (AC003028) unknown protein [Arabidopsis thaliana]
Seq. No.
                  309807
Seq. ID
                  uC-zmflmo17327h07b1
Method
                  BLASTX
NCBI GI
                  g4432821
BLAST score
                  443
E value
                  4.0e-44
Match length
                  120
% identity
NCBI Description
                   (AC006593) putative transmembrane protein [Arabidopsis
                  thaliana]
Seq. No.
                  309808
Seq. ID
                  uC-zmflmo17328a04a1
Method
                  BLASTN
```

44107

q3695004

9.0e-16



Match length 130 % identity 82

NCBI Description Zea mays pyruvate dehydrogenase kinase isoform 2 mRNA, nuclear gene encoding mitochondrial protein, complete cds

309809 Seq. No.

Seq. ID uC-zmflmo17328b04a1

Method BLASTN NCBI GI q3694806 BLAST score 120 E value 4.0e-61 Match length 224 % identity 89

NCBI Description Zea mays alanine aminotransferase (alt) gene, complete cds

Seq. No.

309810

Seq. ID uC-zmflmo17328g01a1 Method BLASTN NCBI GI q507844 BLAST score 35 E value 3.0e-10 Match length 47

% identity 94

NCBI Description Zea mays A188 retrotransposon gag gene, complete cds

309811 Seq. No.

Seq. ID uC-zmflmo17329e02a1

Method BLASTX NCBI GI g421843 BLAST score 190 E value 2.0e-14 Match length 65 % identity 55

NCBI Description protein kinase (EC 2.7.1.37) 5 - Arabidopsis thaliana

>gi 217861 dbj BAA01715 (D10909) serine/threonine protein

kinase [Arabidopsis thaliana]

Seq. No. -309812

Seq. ID uC-zmflmo17330a02a1

Method BLASTN NCBI GI g22091 BLAST score 275 E value 1.0e-153 Match length 351 % identity 95

NCBI Description Z.diploperennis gene for hydroxyproline-rich glycoprotein

Seq. No. 309813

uC-zmflmo17330a12b1 Seq. ID

Method BLASTX NCBI GI g82080 BLAST score 267 E value 2.0e-23 Match length 70 % identity 74

NCBI Description chlorophyll a/b-binding protein type III precursor - tomato

>gi 226872_prf 1609235A chlorophyll a/b binding protein



[Lycopersicon esculentum]

Seq. No. 309814
Seq. ID uC-zmflmo17330b10b1
Method BLASTX
NCBI GI g3421104
BLAST score 494
E value 7.0e-50
Match length 108

% identity 83
NCBI Description (AF043531) 20S proteasome beta subunit PBB2 [Arabidopsis

thaliana]

Seq. No. 309815

Seq. ID uC-zmflmo17330d04b1

Method BLASTN
NCBI GI g2668741
BLAST score 43
E value 5.0e-15
Match length 63
% identity 92

NCBI Description Zea mays glycine-rich RNA binding protein (GRP) mRNA,

complete cds

Seq. No. 309816

Seq. ID uC-zmflmo17330f10b1

Method BLASTX
NCBI GI g112994
BLAST score 209
E value 2.0e-20
Match length 90
% identity 72

NCBI Description GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN

>gi_82685_pir__S04536 embryonic abundant protein,
glycine-rich - maize >gi_22313_emb_CAA31077_ (X12564)

ABA-inducible gene protein [Zea mays]

>gi_226091_prf__1410284A abscisic acid inducible gene [Zea

mays]

Seq. No. 309817

Seq. ID uC-zmflmo17330g02b1

Method BLASTX
NCBI GI g1209703
BLAST score 208
E value 2.0e-16
Match length 137
% identity 36

NCBI Description (U40489) maize gl1 homolog [Arabidopsis thaliana]

Seq. No. 309818

Seq. ID uC-zmflmo17330h10b1

Method BLASTX
NCBI GI g4165488
BLAST score 271
E value 2.0e-37
Match length 120
% identity 71





NCBI Description (AJ132399) alpha-tubulin 3 [Hordeum vulgare]

Seq. No. 309819

Seq. ID uC-zmflmo17333c04b1

Method BLASTX
NCBI GI g3355486
BLAST score 245
E value 1.0e-20
Match length 100
% identity 51

NCBI Description (AC004218) unknown protein [Arabidopsis thaliana]

Seq. No. 309820

Seq. ID uC-zmflmo17333c08b1

Method BLASTX
NCBI GI g2496897
BLAST score 164
E value 3.0e-11
Match length 107
% identity 40

NCBI Description HYPOTHETICAL 45.1 KD PROTEIN C16C10.6 IN CHROMOSOME III

>gi_3874384_emb_CAA86744_ (Z46787) cDNA EST EMBL:T01156
comes from this gene; cDNA EST EMBL:C08256 comes from this
gene; cDNA EST EMBL:C09941 comes from this gene; cDNA EST
yk340a10.3 comes from this gene; cDNA EST yk340a10.5 comes

from this gene [Caeno

Seq. No. 309821

Seq. ID uC-zmflmo17333d10b1

Method BLASTX
NCBI GI g2583129
BLAST score 491
E value 2.0e-71
Match length 164
% identity 82

NCBI Description (AC002387) putative methionine aminopeptidase [Arabidopsis

thaliana]

Seq. No. 309822

Seq. ID uC-zmflmo17333h01b1

Method BLASTX
NCBI GI g3024122
BLAST score 492
E value 9.0e-50
Match length 98
% identity 96

NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE

ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2) >gi_1778821 (U82833) S-adenosyl-L-methionine synthetase [Oryza sativa]

Seq. No. 309823

Seq. ID uC-zmflmo17333h02b1

Method BLASTX
NCBI GI g3281870
BLAST score 144
E value 7.0e-09
Match length 112



% identity 34 NCBI Description (AL031004) putative protein [Arabidopsis thaliana]

Seq. No. 309824

Seq. ID uC-zmflmo17334b09b1

Method BLASTX
NCBI GI g4539660
BLAST score 400
E value 2.0e-39
Match length 85
% identity 85

NCBI Description (AF061282) polyprotein [Sorghum bicolor]

Seq. No. 309825

Seq. ID uC-zmflmo17334c03b1

Method BLASTX
NCBI GI g1519253
BLAST score 322
E value 4.0e-30
Match length 69
% identity 94

NCBI Description (U65958) GF14-d protein [Oryza sativa]

Seq. No. 309826

Seq. ID uC-zmflmo17334c05a1

Method BLASTN
NCBI GI g577818
BLAST score 41
E value 9.0e-14
Match length 97
% identity 87

NCBI Description Z.mays gene for H2B histone (gH2B4)

Seq. No. 309827

Seq. ID uC-zmflmo17334e01b1

Method BLASTX
NCBI GI g282994
BLAST score 428
E value 2.0e-42
Match length 84
% identity 90

NCBI Description Sipl protein - barley >gi 167100 (M77475) seed imbibition

protein [Hordeum vulgare]

Seq. No. 309828

Seq. ID uC-zmflmo17334f11b1

Method BLASTX
NCBI GI g4455225
BLAST score 225
E value 9.0e-19
Match length 58
% identity 66

NCBI Description (AL035440) putative protein [Arabidopsis thaliana]

Seq. No. 309829

Seq. ID uC-zmflmo17334g01b1

Method BLASTN

327

```
NCBI GI
                   g1652725
BLAST score
                   177
E value
                   6.0e-95
Match length
                   241
% identity
                   94
NCBI Description
                  Synechocystis sp. PCC6803 complete genome, 10/27,
                   1188886-1311234
                   309830
Seq. No.
Seq. ID
                   uC-zmflmo17334g08b1
Method
                   BLASTN
NCBI GI
                   q2370460
BLAST score
                   72
E value
                   1.0e-32
Match length
                   144
% identity
                   88
NCBI Description Sorghum bicolor mRNA for putative glycoprotein
Seq. No.
                   309831
Seq. ID
                   uC-zmflmo17334h10b1
Method
                   BLASTX
NCBI GI
                   q3860321
BLAST score
                   146
E value
                   5.0e-09
Match length
                   43
% identity
                   63
NCBI Description (AJ012687) beta-galactosidase [Cicer arietinum]
Seq. No.
                   309832
Seq. ID
                   uC-zmflmo17335a07b1
Method
                   BLASTX
NCBI GI
                   g2244852
BLAST score
                   168
E value
                   1.0e-11
Match length
                  70
% identity
                   46
                  (Z97337) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   309833
Seq. No.
Seq. ID
                   uC-zmflmo17335b07b1
Method
                  BLASTX
NCBI GI
                   g861170
BLAST score
                   711
E value
                  2.0e-75
Match length
                  145
% identity
                  98
NCBI Description (X03697) heat shock protein 70 [Zea mays]
                   309834
Seq. No.
Seq. ID
                  uC-zmflmo17335b09a1
Method
                  BLASTN
NCBI GI
                  g4140643
BLAST score
                  146
E value
                  2.0e-76
Match length
                  342
```

44112

NCBI Description Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster,

89

% identity



complete sequence

```
Seq. No.
                  309835
Seq. ID
                  uC-zmflmo17335b09b1
Method
                  BLASTN
NCBI GI
                  q4140643
BLAST score
                  145
E value
                  1.0e-75
Match length
                  444
% identity
                  87
                  Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster,
NCBI Description
                  complete sequence
Seq. No.
                  309836
Seq. ID
                  uC-zmflmo17335c12a1
Method
                  BLASTN
NCBI GI
                  g2655290
BLAST score
                  48
E value
                  6.0e-18
Match length
                  104
% identity
                  87
NCBI Description
                  Oryza sativa germin-like protein 4 (GER4) mRNA, complete
                  309837
Seq. No.
Seq. ID
                  uC-zmflmo17335d03b1
Method
                  BLASTN
NCBI GI
                  g257040
BLAST score
                  116
E value
                  2.0e-58
Match length
                  293
% identity
                  95
NCBI Description hydroxyproline-rich glycoprotein [maize, Genomic, 1703 nt]
Seq. No.
                  309838
Seq. ID
                  uC-zmflmo17335e03b1
Method
                  BLASTX
NCBI GI
                  g3600059
BLAST score
                  307
E value
                  5.0e-28
Match length
                  155
% identity
                  41
                  (AF080120) contains similarity to WB domains, G-beta
NCBI Description
                  repeats (Pfam: G-beta.hmm, score: 14.83 and 23.03)
                  [Arabidopsis thaliana]
Seq. No.
                  309839
Seq. ID
                  uC-zmflmo17335f04a1
Method
                  BLASTN
NCBI GI
                  g1638870
BLAST score
                  250
E value
                  1.0e-138
Match length
                  250
% identity
                  100
```

Seq. No. 309840

NCBI Description Maize mRNA for dihydrodipicolinate synthase (EC 4.2.1.52)



uC-zmflmo17335h08b1 Seq. ID Method BLASTX NCBI GI g2244785 BLAST score 271 E value 4.0e-24 Match length 86 % identity NCBI Description (Z97335) hypothetical protein [Arabidopsis thaliana] Seq. No. 309841 Seq. ID uC-zmflmo17336a05b1 Method BLASTX NCBI GI g4218014 BLAST score 196 E value 5.0e-15 Match length 100 % identity 48 NCBI Description (AC006135) putative spliceosomal protein (RNA binding protein) [Arabidopsis thaliana] Seq. No. 309842 Seq. ID uC-zmflmo17336b11b1 Method BLASTX NCBI GI g399853 BLAST score 374 E value 8.0e-36 Match length 77 % identity 99 NCBI Description HISTONE H2B.1 >gi 283041 pir S28048 histone H2B - maize >gi 22323 emb CAA40564 (X57312) H2B histone [Zea mays] Seq. No. 309843 uC-zmflmo17336e03b1 Seq. ID Method BLASTX NCBI GI g4263790 BLAST score 500 E value 1.0e-50 Match length 149 % identity 66 NCBI Description (AC006068) putative ch-TOG protein [Arabidopsis thaliana] 309844 Seq. No. Seq. ID uC-zmflmo17336f10a1 Method BLASTN NCBI GI g2340107 BLAST score 104 E value 1.0e-51 Match length 204 % identity 88 NCBI Description Zea mays starch branching enzyme IIa (Sbe2a) mRNA, partial cds

309845 Seq. No.

uC-zmflmo17336g01b1 Seq. ID

Method BLASTX NCBI GI g2104446 BLAST score 402



```
E value
                  4.0e-39
Match length
                  158
% identity
                  54
NCBI Description
                  (Z95396) WD-repeat protein [Schizosaccharomyces pombe]
Seq. No.
                  309846
Seq. ID
                  uC-zmflmo17336h05b1
Method
                  BLASTX
```

NCBI GI q3738298 BLAST score 158

E value 1.0e-10 Match length 89 % identity 37

NCBI Description (AC005309) unknown protein [Arabidopsis thaliana] >gi_4249394 (AC006072) unknown protein [Arabidopsis

thaliana]

Seq. No. 309847

Seq. ID uC-zmflmo17336h11b1

Method BLASTX NCBI GI q135398 BLAST score 143 E value 2.0e-09 Match length 57 % identity

NCBI Description TUBULIN ALPHA-1 CHAIN >gi_82731_pir_S15773 tubulin alpha-1

chain - maize >gi 22147 emb CAA33734 (X15704)

alphal-tubulin [Zea mays]

Seq. No. 309848

Seq. ID uC-zmflmo17337b09a1

Method BLASTN NCBI GI g498774 BLAST score 144 E value 2.0e-75 Match length 266 % identity 89

NCBI Description Z.mays (cv DH5xDH7) hsp70-5 mRNA for heat shock protein

Seq. No. 309849

Seq. ID uC-zmflmo17337d05a1

Method BLASTN NCBI GI g717080 BLAST score 40 E value 3.0e-13 Match length 156 % identity 87

NCBI Description Zea mays glyceraldehyde-3-phosphate dehydrogenase (GapC4)

gene, promoter region

Seq. No. 309850

uC-zmflmo17337e06a1 Seq. ID

Method BLASTX NCBI GI g134018 BLAST score 243 E value 8.0e-21 Match length 68

% identity NCBI Description CHLOROPLAST 30S RIBOSOMAL PROTEIN S8 >gi_70915_pir__R3ZMBC ribosomal protein S8 - maize chloroplast >gi_12454_emb CAA29913 (X06734) ribosomal protein S8 (AA $1-1\overline{3}6$) [Zea mays] >gi 902257 emb CAA60321 (X86563) ribosomal protein S8 [Zea mays] 309851 Seq. No. Seq. ID uC-zmflmo17337e12a1 Method BLASTX g4580389 NCBI GI BLAST score 184 E value 1.0e-13 Match length 48 % identity 73 NCBI Description (AC007171) unknown protein [Arabidopsis thaliana]

Seq. No. 309852 Seq. ID uC-zmflmo17338a07b1 Method BLASTX g3885334

NCBI GI BLAST score 182 E value 1.0e-13 Match length 74 % identity 58

NCBI Description (AC005623) putative argonaute protein [Arabidopsis

thaliana]

309853 Seq. No.

Seq. ID uC-zmflmo17338d12b1

Method BLASTX NCBI GI g320583 BLAST score 476 E value 4.0e-48 Match length 104 % identity 87

NCBI Description H+-transporting ATPase (EC 3.6.1.35) LHA2 - tomato

(fragment)

Seq. No. 309854

uC-zmflmo17339c03a1 Seq. ID

Method BLASTN NCBI GI g4154280 BLAST score 113 E value 7.0e-57 Match length 168 % identity 92

NCBI Description Zea mays C13 endopeptidase NP1 precursor, mRNA, complete

Seq. No. 309855

Seq. ID uC-zmflmo17339e05b1

Method BLASTX NCBI GI g1708863 BLAST score 147 E value 3.0e-09 Match length 79



% identity

NCBI Description ACYL-[ACYL-CARRIER-PROTEIN] -- UDP-N-ACETYLGLUCOSAMINE

O-ACYLTRANSFERASE (UDP-N-ACETYLGLUCOSAMINE ACYLTRANSFERASE)

>gi 1262294 (U51683) LpxA [Brucella abortus]

Seq. No. 309856

Seq. ID uC-zmflmo17339e08b1

Method BLASTX g3746060 NCBI GI BLAST score 195 E value 5.0e-15 Match length 43 % identity 81

NCBI Description (AC005311) unknown protein [Arabidopsis thaliana]

Seq. No.

309857 uC-zmflmo17339f01b1

Seq. ID Method BLASTN NCBI GI q1707641 BLAST score 39 E value 2.0e-12

Match length 59 % identity 92

NCBI Description O.sativa mRNA for leucine rich repeat receptor-like kinase

309858 Seq. No.

Seq. ID uC-zmflmo17339f03b1

Method BLASTX NCBI GI g2344889 BLAST score 151 E value 9.0e-10 Match length 149 % identity 23

NCBI Description (AC002388) unknown protein [Arabidopsis thaliana]

Seq. No. 309859

Seq. ID uC-zmflmo17339f04b1

Method BLASTX NCBI GI g3927831 BLAST score 182 2.0e-13 E value Match length 55 % identity 62

NCBI Description (AC005727) similar to mouse ankyrin 3 [Arabidopsis

thaliana]

Seq. No. 309860

Seq. ID uC-zmflmo17339g05b1

Method BLASTX NCBI GI g3445208 BLAST score 201 E value 1.0e-15 Match length 58 % identity 60

NCBI Description (AC004786) putative amino-acid acetyltransferase

[Arabidopsis thaliana]



```
309861
Seq. No.
Seq. ID
                  uC-zmflmo17339g12b1
Method
                  BLASTX
NCBI GI
                  g3075398
BLAST score
                  164
                  2.0e-11
E value
Match length
                  60
% identity
                  57
NCBI Description (AC004484) unknown protein [Arabidopsis thaliana]
                  309862
Seq. No.
Seq. ID
                  uC-zmflmo17339h11b1
Method
                  BLASTX
NCBI GI
                  q99898
BLAST score
                  613
E value
                  6.0e-64
Match length
                  145
% identity
                  83
NCBI Description DNA-directed RNA polymerase (EC 2.7.7.6) largest chain
                  (isoform B1) - soybean (fragment)
Seq. No.
                  309863
Seq. ID
                uC-zmflmo17340a12b1
Method
                  BLASTX
                  g3024657
NCBI GI
BLAST score
                  318
E value
                  3.0e-29
Match length
                  75
% identity
                  83
NCBI Description
                  PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)
                  >gi 2668740 (AF034944) translation initiation factor; GOS2
                  [Zea mays]
Seq. No.
                  309864
Seq. ID
                  uC-zmflmo17340b09b1
Method
                  BLASTX
NCBI GI
                  q4206306
BLAST score
                  338
E value
                  4.0e-49
Match length
                  162
% identity
                  67
NCBI Description (AF049110) prpol [Zea mays]
Seq. No.
                  309865
Seq. ID
                  uC-zmflmo17340c04b1
Method
                  BLASTX
NCBI GI
                  q4206306
BLAST score
                  361
E value
                  2.0e-34
Match length
                  114
% identity
                  66
NCBI Description (AF049110) prpol [Zea mays]
```

Seq. No. 309866

Seq. ID uC-zmflmo17340c10b1

Method BLASTX NCBI GI g1076509



BLAST score 171 E value 5.0e-12 Match length 97 % identity 39

NCBI Description chloroplast RNA binding protein - kidney bean

>gi 558629 emb CAA57551 (X82030) chloroplast RNA binding

protein [Phaseolus vulgaris]

Seq. No. 309867

Seq. ID uC-zmflmo17340e04b1

Method BLASTN
NCBI GI g22294
BLAST score 117
E value 6.0e-59
Match length 193
% identity 91

NCBI Description Maize Gpa1 gene for glyceraldehyde-3-phosphate

dehydrogenase subunit A >gi_168478_gb_M18976_MZEG3PD Zea mays chloroplast glyceraldehyde-3-phosphate dehydrogenase

gene, complete cds, clone lambda-gapA1

Seq. No. 309868

Seq. ID uC-zmflmo17340g01b1

Method BLASTX
NCBI GI g1346107
BLAST score 522
E value 4.0e-53
Match length 116
% identity 86

NCBI Description GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT >gi 557696

(U12233) GTP binding protein beta subunit [Zea mays]

Seq. No. 309869

Seq. ID uC-zmflmo17340g06b1

Method BLASTX
NCBI GI g3004565
BLAST score 279
E value 1.0e-24
Match length 79
% identity 61

NCBI Description (AC003673) putative protein kinase [Arabidopsis thaliana]

Seq. No. 309870

Seq. ID uC-zmflmo17341a07a1

Method BLASTX
NCBI GI g2809385
BLAST score 249
E value 3.0e-21
Match length 61
% identity 74

NCBI Description (AF024634) NADPH cytochrome P450 reductase [Petroselinum

crispum]

Seq. No. 309871

Seq. ID uC-zmflmo17341a10a1

Method BLASTX NCBI GI 92735008

E value

Match length

% identity

6.0e-18

82



```
BLAST score
E value
                  9.0e-30
Match length
                  75
% identity
                  88
NCBI Description
                  (U81960) kinase associated protein phosphatase [Zea mays]
                  309872
Seq. No.
                  uC-zmflmo17341e05b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3080740
BLAST score
                  442
E value
                  7.0e-44
Match length
                  133
% identity
                  61
NCBI Description
                  (U77366) pasticcino 1-D [Arabidopsis thaliana]
Seq. No.
                  309873
Seq. ID
                  uC-zmflmo17341e10a1
Method
                  BLASTN
NCBI GI
                  q22342
BLAST score
                  45
E value
                  2.0e-16
Match length
                  85
% identity
                  88
NCBI Description
                  Maize gene for heat shock protein 70 exon 2 and 3'-UT
                  (hsp70; clone pMON 9502)
Seq. No.
                  309874
Seq. ID
                  uC-zmflmo17341e12b1
Method
                  BLASTX
NCBI GI
                  g4539348
BLAST score
                  213
                  5.0e-17
E value
Match length
                  93
% identity
                  51
NCBI Description
                  (AL035539) putative pollen allergen [Arabidopsis thaliana]
                  309875
Seq. No.
Seq. ID
                  uC-zmflmo17341g12b1
Method
                  BLASTX
NCBI GI
                  g82426
BLAST score
                  623
E value
                  4.0e-65
Match length
                  131
% identity
                  45
NCBI Description
                  ubiquitin precursor - barley (fragment)
                  >gi 755763 emb CAA27751 (X04133) ubiquitin polyprecursor
                  (171 aa) [Hordeum vulgare]
Seq. No.
                  309876
Seq. ID
                  uC-zmflmo17341h02b1
Method
                  BLASTX
NCBI GI
                  g1352186
BLAST score
                  217
```



NCBI Description ALLENE OXIDE SYNTHASE PRECURSOR (HYDROPEROXIDE DEHYDRASE) (CYTOCHROME P450 74) >gi 404866 (U00428) allene oxide

synthase [Linum usitatissimum]

Seq. No. 309877

Seq. ID uC-zmflmo17341h11a1

Method BLASTN
NCBI GI g22312
BLAST score 70
E value 1.0e-31
Match length 125
% identity 87

NCBI Description Maize ABA-inducible gene for glycine-rich protein (ABA =

abscisic acid)

Seq. No. 309878

Seq. ID uC-zmflmo17342a03b1

Method BLASTX
NCBI GI g2501296
BLAST score 186
E value 7.0e-14
Match length 84
% identity 46

NCBI Description DNA GYRASE SUBUNIT B >gi_1652801_dbj_BAA17720_ (D90908) DNA

gyrase B subunit [Synechocystis sp.]

Seq. No. 309879

Seq. ID uC-zmflmo17342a09b1

Method BLASTX
NCBI GI g2564237
BLAST score 191
E value 2.0e-14
Match length 99
% identity 47

NCBI Description (Y10112) omega-6 desaturase [Gossypium hirsutum]

Seq. No. 309880

Seq. ID uC-zmflmo17342b03b1

Method BLASTN
NCBI GI g575730
BLAST score 41
E value 1.0e-13
Match length 65
% identity 91

NCBI Description Z.mays mRNA for transmembrane protein

Seq. No. 309881

Seq. ID uC-zmflmo17342b06b1

Method BLASTX
NCBI GI g4539452
BLAST score 179
E value 4.0e-13
Match length 57
% identity 68

NCBI Description (AL049500) putative phosphoribosylanthranilate transferase

[Arabidopsis thaliana]



```
Seq. No.
                   309882
Seq. ID
                   uC-zmflmo17342c03b1
Method
                   BLASTX
NCBI GI
                   g3236253
BLAST score
                   217
E value
                  1.0e-17
Match length
                   80
% identity
                   57
NCBI Description
                  (AC004684) receptor-like protein kinase [Arabidopsis
                  309883
Seq. No.
Seq. ID
                  uC-zmflmo17342c04a1
Method
                  BLASTN
NCBI GI
                  g602605
BLAST score
                  131
                  1.0e-67
E value
Match length
                  247
% identity
                  88
NCBI Description Zea mays tandem genes for alphal-tubulin and alpha2-tubulin
                  309884
Seq. No.
Seq. ID
                  uC-zmflmo17342c10b1
Method
                  BLASTX
NCBI GI
                  g126401
BLAST score
                  262
E value
                  8.0e-23
Match length
                  115
% identity
                  54
NCBI Description
                  LIPOXYGENASE L-2 >gi 100690 pir S23454 lipoxygenase (EC
                  1.13.11.12) L-2 - rice >gi \overline{20267} emb CAA45738 (X64396)
                  lipoxygenase [Oryza sativa]
                  309885
Seq. No.
Seq. ID
                  uC-zmflmo17342d12b1
Method
                  BLASTX
NCBI GI
                  g3913427
BLAST score
                  502
E value
                  5.0e-51
Match length
                  107
% identity
                  88
NCBI Description
                  S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC)
                  (SAMDC) >gi 1532073 emb CAA69075 (Y07767)
                  S-adenosylmethionine decarboxylase [Zea mays]
Seq. No.
                  309886
Seq. ID
                  uC-zmflmo17342e07b1
```

Method BLASTX NCBI GI q2984709 BLAST score 323 E value 5.0e-30 Match length 81 % identity 79

NCBI Description (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]

Seq. No. 309887

Seq. ID uC-zmflmo17342e11b1

Match length

% identity

112

```
Method
                   BLASTX
                 -<u>*</u> g2980806
NCBI GI
BLAST score
                   150
E value
                   4.0e-10
Match length
                   56
                   48
% identity
NCBI Description
                  (AL022197) putative protein [Arabidopsis thaliana]
                   309888
Seq. No.
                   uC-zmflmo17342g01b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4138265
BLAST score
                   143
E value
                   5.0e-09
Match length
                  76
% identity
                   45
NCBI Description
                  (AJ006228) Avr9 elicitor response protein [Nicotiana
                   tabacum]
                   309889
Seq. No.
Seq. ID
                  uC-zmflmo17342g05a1
Method
                  BLASTX
NCBI GI
                  g2292907
BLAST score
                   486
E value
                   6.0e-49
Match length
                  141
% identity
                   38
NCBI Description
                 (Y10099) P-glycoprotein homologue [Hordeum vulgare]
Seq. No.
                   309890
Seq. ID
                  uC-zmflmo17342g10b1
Method
                  BLASTX
                  g4567304
NCBI GI
BLAST score
                  260
E value
                  1.0e-22
Match length
                  88
% identity
                  53
                  (AC005956) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  309891
Seq. ID
                  uC-zmflmo17342h02b1
Method
                  BLASTN
NCBI GI
                  g602605
BLAST score
                  46
                  1.0e-16 125 "
E value
Match length
                  82
% identity
                  89
NCBI Description Zea mays tandem genes for alpha1-tubulin and alpha2-tubulin
Seq. No.
                  309892
                  uC-zmflmo17342h05b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4522012
BLAST score
                  316
E value
                  3.0e-29
```





```
NCBI Description
                  (AC007069) hypothetical protein [Arabidopsis thaliana]
                  309893
Seq. No.
Seq. ID
                  uC-zmflmo17342h10b1
Method
                  BLASTX
NCBI GI
                  g3043428
BLAST score
                  252
E value
                  1.0e-21
Match length
                  96
% identity
                  57
NCBI Description (AJ005346) 40S ribosomal protein S5 [Cicer arietinum]
Seq. No.
                  309894
Seq. ID
                  uC-zmflmo17342h11a1
Method
                  BLASTN
NCBI GI
                  g22243
BLAST score
                  204
E value
                  1.0e-111
Match length
                  450
% identity
                  87
NCBI Description Zea mays Cin1 repeat from Cin1 middle repetitive family
Seq. No.
                  309895
Seq. ID
                  uC-zmflmo17342h12b1
Method
                  BLASTN
NCBI GI
                  g6012171
BLAST score
                  42
E value
                  2.0e-14
Match length
                  78
                  88
% identity
NCBI Description Hordeum vulgare mRNA for vacuolar membrane
                  proton-translocating inorganic pyrophosphat
Seq. No.
                  309896
Seq. ID
                  uC-zmflmo17344c12b1
Method
                  BLASTX
NCBI GI
                  g1002800
BLAST score
                  175
E value
                  1.0e-16
Match length
                  75
% identity
                  64
NCBI Description
                  (U33917) Cpm7 [Craterostigma plantagineum]
Seq. No.
                  309897
Séq. ID
                  uC-zmflmo17344d04a1
Method
                  BLASTN
NCBI GI
                  g3821780
BLAST score
                  36
E value
                  7.0e-11
Match length
                  36
% identity
                  100
NCBI Description Xenopus laevis cDNA clone 27A6-1
```

Seq. No. 309898

Seq. ID uC-zmflmo17354g04a1

Method BLASTN NCBI GI g312178

```
BLAST score
E value
                  1.0e-93
Match length
                  235
                  94
% identity
NCBI Description Z.mays GapC2 gene
Seq. No.
                  309899
Seq. ID
                  uC-zmflmo17355e01a1
Method
                  BLASTN
NCBI GI
                  q22430
BLAST score
                  95
E value
                  3.0e-46
Match length
                  213
% identity
                  88
NCBI Description
                  Maize pseudo-Gpa2 pseudogene for glyceraldehyde-3-phosphate
                  dehydrogenase subunit A
Seq. No.
                  309900
                  uC-zmflmo17356h04a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g468055
BLAST score
                  217
E value
                  1.0e-119
Match length
                  229
% identity
                  99
NCBI Description Zea mays B73 QM protein mRNA, complete cds
                  309901
Seq. No.
                  uC-zmflmo17357f03a1
Seq. ID
Method
                  BLASTX
                  g1346956
NCBI GI
                  173
BLAST score
                  1.0e-12
E value
Match length
                  34
% identity
                  100
NCBI Description
                  RAS-RELATED PROTEIN RAB-2-A >gi 722326 (U22432) GTP binding
                  protein [Zea mays]
                  309902
Seq. No.
Seq. ID
                  uC-zmflmo17359a04a1
Method
                  BLASTX
NCBI GI
                  q533775
BLAST score
                  428
E value
                  2.0e-42
Match length
                  126
% identity
```

NCBI Description (U09989) H(+)-transporting ATPase [Zea mays]

Seq. No. 309903

Seq. ID uC-zmflmo17360h08a1

Method BLASTN NCBI GI q1658192 BLAST score 105 5.0e-52 E value Match length 260 % identity 86

NCBI Description Sorghum bicolor obtusifoliol 14-alpha demethylase CYP51

Seq. ID



(CYP51) mRNA, complete cds

```
309904
Seq. No.
Seq. ID
                  uC-zmflmo17362h03a1
Method
                  BLASTX
NCBI GI
                  q1321627
BLAST score
                  157
E value
                  7.0e-16
Match length
                  57
% identity
                  82
NCBI Description
                  (D83656) thylakoid-bound ascorbate peroxidase [Cucurbita
                  309905
Seq. No.
Seq. ID
                  uC-zmflmo17364d08a1
Method
                  BLASTX
NCBI GI
                  q3080369
BLAST score
                  158
E value
                  8.0e-11
Match length
                  61
% identity
                  56
NCBI Description
                  (AL022580) putative protein [Arabidopsis thaliana]
                  309906
Seq. No.
Seq. ID
                  uC-zmflmo17364h11a1
Method
                  BLASTX
NCBI GI
                  q3096930
BLAST score
                  373
E value
                  5.0e-36
Match length
                  88
% identity
                  81
NCBI Description
                  (AL023094) Homeodomain - like protein [Arabidopsis
                  thaliana]
                  309907
Seq. No.
Seq. ID
                  uC-zmflmo17366b11a1
Method
                  BLASTX
NCBI GI
                  g2935575
BLAST score
                  152
E value
                  5.0e-10
Match length
                  55
% identity
                  73
NCBI Description
                  (AF050181) KNOX class homeodomain protein [Oryza sativa]
                  309908
Seq. No.
                  uC-zmflmo17366e02a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2352794
BLAST score
                  58
E value
                  6.0e-24
Match length
                  134
% identity
                  86
NCBI Description
                  Zea mays retinoblastoma-related protein 1 (RRB1) mRNA,
                  complete cds
Seq. No.
                  309909
```

uC-zmflmo17367a07a1

Method

NCBI GI

BLAST score



```
Method
                   BLASTN
NCBI GI
                   q3821780
BLAST score
                   36
                   6.0e-11
E value
Match length
                   48
% identity
                   67
NCBI Description Xenopus laevis cDNA clone 27A6-1
                  309910
Seq. No.
Seq. ID
                  uC-zmflmo17367g06a1
Method
                  BLASTX
NCBI GI
                   g2465923
BLAST score
                   229
E value
                   3.0e-24
Match length
                  107
% identity
                   61
NCBI Description
                  (AF024648) receptor-like serine/threonine kinase
                   [Arabidopsis thaliana]
Seq. No.
                   309911
Seq. ID
                  uC-zmflmo17368g12a1
Method
                  BLASTX
NCBI GI
                  g542192
BLAST score
                   246
E value
                   4.0e-21
Match length
                   60
                  75
% identity
NCBI Description
                  floral homeotic protein ZAG2 - maize (fragment) >gi 309576
                   (L18925) homologue of Arabidopsis Agamous-like gene [Zea
                  mays]
Seq. No.
                  309912
Seq. ID
                  uC-zmflmo17371g10a1
Method
                  BLASTN
NCBI GI
                  q2668739
BLAST score
                  54
E value
                   4.0e-22
Match length
                  114
% identity
NCBI Description
                  Zea mays translation initiation factor GOS2 (TIF) mRNA,
                  complete cds
Seq. No. Seq. ID
                  309913
                  uC-zmflmo17374h01a1
Method
                  BLASTX
NCBI GI
                  q4416301
BLAST score
                  232
E value
                  2.0e-19
Match length
                  81
% identity
                  59
NCBI Description
                  (AF105716) gag protein [Zea mays]
Seq. No.
                  309914
Seq. ID
```

44127

uC-zmflmo17375c01a1

BLASTN

g22091



E value 1.0e-141
Match length 327
% identity 95
NCBI Description Z.diplope

NCBI Description Z.diploperennis gene for hydroxyproline-rich glycoprotein

Seq. No. Seq. ID 309915 uC-zmflmo17377a07a1

Method BLASTN
NCBI GI g945021
BLAST score 390
E value 0.0e+00
Match length 454
% identity 96

NCBI Description Z.mays DNA for tbp1 gene

Seq. No.

309916

Seq. ID

uC-zmflmo17377c12a1

Method BLASTN
NCBI GI g22292
BLAST score 54
E value 7.0e-22
Match length 110
% identity 87

NCBI Description Z.mays mRNA for glycine-rich protein

Seq. No.

309917

Seq. ID

uC-zmflmo17380f01a1

Method BLASTN
NCBI GI g4336204
BLAST score 96
E value 6.0e-47
Match length 164
% identity 88

NCBI Description Zea mays cytochrome b5 reductase (NFR) mRNA, complete cds

Seq. No.

309918

Seq. ID

uC-zmflmo17391b08a1

Method BLASTN
NCBI GI g2274989
BLAST score 50
E value 3.0e-19
Match length 58
% identity 97

NCBI Description Hordeum vulgare mRNA for expressed sequence tag

Seq. No.

309919

Seq. ID

uC-zmflmo17393d02a1

Method BLASTX
NCBI GI g1237183
BLAST score 230
E value 3.0e-19
Match length 79
% identity 54

NCBI Description (D43773) 4-coumarate:coenzyme A ligase [Nicotiana tabacum]

Seq. No.

309920

Seq. ID

uC-zmflmo17393d09a1



```
Method
                  BLASTN
NCBI GI
                  q168406
BLAST score
                  61
E value
                  1.0e-25
Match length
                  121
% identity
                  88
NCBI Description
                  Z.mays alcohol dehydrogenase (ADH-1 C-m allele) gene,
                  complete cds
                  309921
Seq. No.
Seq. ID
                  uC-zmflmo17393f04a1
Method
                  BLASTN
NCBI GI
                  g4160401
BLAST score
                  62
                  2.0e-26
E value
Match length
                  98
% identity
                  91
NCBI Description Zea mays eIF-5 gene, exons 1-2
Seq. No.
                  309922
Seq. ID
                  uC-zmflmo17393f08a1
Method
                  BLASTX
NCBI GI
                  g4567210
BLAST score
                  242
                  2.0e-20
E value
Match length
                  55
% identity
                  87
NCBI Description (AC007168) unknown protein [Arabidopsis thaliana]
                  309923
Seq. No.
Seq. ID
                  uC-zmflmo17393h02a1
Method
                  BLASTX
NCBI GI
                  g4056490
BLAST score
                  166
E value
                  4.0e-12
Match length
                  53
% identity
                  64
NCBI Description (AC005896) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  309924
Seq. ID
                  uC-zmflmo17394f11a1
Method
                  BLASTX
NCBI GI
                  g1841475
BLAST score
                  404
E value
                  2.0e-39
Match length
                  97
% identity
                  72
NCBI Description (Y11105) Myb26 [Pisum sativum]
                  309925
Seq. No.
Seq. ID
                  uC-zmflmo17395a10a1
Method
                  BLASTX
NCBI GI
                  g3551960
```

BLAST score 149 E value 9.0e-10 Match length 59 % identity 53



NCBI Description (AF082033) senescence-associated protein 15 [Hemerocallis hybrid cultivar]

Ť.::

Seq. No. 309926

Seq. ID uC-zmflmo17395d04a1

Method BLASTX
NCBI GI 94454026
BLAST score 152
E value 5.0e-10
Match length 40
% identity 68

NCBI Description (AL035394) phosphatase like protein [Arabidopsis thaliana]

Seq. No. 309927

Seq. ID uC-zmflmo17395d07a1

Method BLASTX
NCBI GI g4204277
BLAST score 142
E value 9.0e-09
Match length 61
% identity 49

NCBI Description (AC004146) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 309928

Seq. ID uC-zmflmo17396g09a1

Method BLASTX
NCBI GI g3096949
BLAST score 244
E value 1.0e-20
Match length 73
% identity 66

NCBI Description (Y16328) putative cyclic nucleotide-regulated ion channel

[Arabidopsis thaliana] >gi_3894399 (AF067798) cyclic nucleotide-gated cation channel [Arabidopsis thaliana]

Seq. No. 309929

Seq. ID uC-zmflmo17396g10a1

Method BLASTN
NCBI GI g902200
BLAST score 40
E value 2.0e-13
Match length 172
% identity 86

NCBI Description Z.mays complete chloroplast genome

Seq. No. 309930

Seq. ID uC-zmflmo17398b10a1

Method BLASTX
NCBI GI g548669
BLAST score 158
E value 1.0e-10
Match length 84
% identity 39

NCBI Description DNA REPAIR PROTEIN RAD8 >gi 542223 pir S41478 RAD8 protein

- fission yeast (Schizosaccharomyces pombe)

>gi_443973_emb_CAA52686_ (X74615) rad8 [Schizosaccharomyces

pombe]

Method

NCBI GI

BLAST score

BLASTN

81

g257040

```
Seq. No.
                  309931
Seq. ID
                  uC-zmflmo17398d09a1
Method
                  BLASTN
NCBI GI
                  g507844
BLAST score
                  115
                  7.0e-58
E value
Match length
                  251
% identity
                  91
NCBI Description Zea mays A188 retrotransposon gag gene, complete cds
                  309932
Seq. No.
                  uC-zmflmo17398f03a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4151124
BLAST score
                  176
E value
                  2.0e-94
Match length
                  252
% identity
                  92
NCBI Description Zea mays PDI-like protein mRNA, complete cds
                  309933
Seq. No.
Seq. ID
                  uC-zmflmo17398h04a1
Method
                  BLASTN
NCBI GI
                  g3452290
BLAST score
                  65
E value
                  5.0e-28
Match length
                  258
% identity
                  88
NCBI Description Zea mays retrotransposon Huck-1 5' LTR, partial sequence
Seq. No.
                  309934
                  uC-zmflmo17400h10a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2695937
BLAST score
                  141
E value
                  8.0e-09
Match length
                  60
% identity
                  48
NCBI Description (AJ222782) subtilisin-like protease [Hordeum vulgare]
Seq. No.
                  309935
                  uC-zmflmo17404g03a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q3318612
BLAST score
                  141
                  1.0e-73
E value
Match length
                  179
% identity
                  96
NCBI Description Zea mays mRNA for mitochondrial phosphate transporter,
                  complete cds
Seq. No.
                  309936
Seq. ID
                  uC-zmflmo17404h06a1
```



E value 4.0e-38 Match length 144 % identity 90

NCBI Description hydroxyproline-rich glycoprotein [maize, Genomic, 1703 nt]

Seq. No. 309937

Seq. ID uC-zmflmo17404h07a1

Method BLASTN
NCBI GI g3452305
BLAST score 58
E value 6.0e-24
Match length 217
% identity 87

NCBI Description Zea mays retrotransposon Opie-3 3' LTR, partial sequence

Seq. No. 309938

Seq. ID uC-zmflmo17405c02a1

Method BLASTX
NCBI GI g2708743
BLAST score 156
E value 1.0e-10
Match length 67
% identity 37

NCBI Description (AC003952) putative Tal-1-like reverse transcriptase

[Arabidopsis thaliana]

Seq. No. 309939

Seq. ID uC-zmflmo17407b07a1

Method BLASTX
NCBI GI g4586033
BLAST score 143
E value 7.0e-09
Match length 57
% identity 49

NCBI Description (AC007109) unknown protein [Arabidopsis thaliana]

Seq. No. 309940

Seq. ID uC-zmflmo17408d01a1

Method BLASTX
NCBI GI g3874563
BLAST score 181
E value 2.0e-13
Match length 74
% identity 50

NCBI Description (Z81042) similar to Yeast hypothetical protein YEY6 like;

cDNA EST yk206h5.3 comes from this gene; cDNA EST yk206h5.5 comes from this gene; cDNA EST yk303h1.3 comes from this gene; cDNA EST yk303h1.5 comes from this gene; cDNA ... >gi_3924825_emb_CAB05549_ (Z83113) similar to Yeast hypothetical protein YEY6 like; cDNA EST yk206h5.3 comes from this gene; cDNA EST yk206h5.5 comes from this gene; cDNA EST yk303h1.5

comes from this gene; cDNA

Seq. No. 309941

Seq. ID uC-zmflmo17408e08a1

Method BLASTN

```
NCBI GI
                  g22091
BLAST score
                  109
E value
                  1.0e-54
Match length
                  170
% identity
                  91
NCBI Description
                 Z.diploperennis gene for hydroxyproline-rich glycoprotein
                  309942
Seq. No.
                  uC-zmflmo17417d08a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g119286
BLAST score
                  251
E value
                  1.0e-21
Match length
                  63
% identity
                  79
                  LOW MOLECULAR MASS EARLY LIGHT-INDUCIBLE PROTEIN PRECURSOR
NCBI Description
                  (ELIP) (CLONE HV90) >gi 100630 pir S07474 early
                  light-induced protein, low molecular weight, precursor
                  (clone HV90) - barley chloroplast >gi 19033 emb CAA33727
                  (X15692) precursor peptide (AA -38 to 134) [Hordeum
                  vulgare]
                  309943
Seq. No.
Seq. ID
                  uC-zmflmo17419c07a1
Method
                  BLASTN
NCBI GI
                  g22192
BLAST score
                  39
E value
                  7.0e-13
Match length
                  47
% identity
                  96
NCBI Description Z.mays B-I gene for B transcriptional activator
                  309944
Seq. No.
Seq. ID
                  uC-zmflmo17420b05a1
Method
                  BLASTX
NCBI GI
                  g2341032
BLAST score
                  356
E value
                  6.0e-34
Match length
                  73
% identity
                  90
                  (AC000104) EST gb_ATTS0956 comes from this gene.
NCBI Description
                  [Arabidopsis thaliana]
                  309945
Seq. No.
                  uC-zmflmo17420b07a1
                  BLASTX
NCBI GI
                  q3602942
BLAST score
                  171
```

Seq. ID Method

2.0e-12 E value Match length 46 % identity 65

NCBI Description (AF041468) PSII protein W [Guillardia theta]

Seq. No. 309946

Seq. ID uC-zmflmo17421b04a1

Method BLASTN NCBI GI g2632251



```
BLAST score
E value
                  2.0e-10
Match length
                  35
                  100
% identity
NCBI Description
                  S.bicolor DNA for gene encoding putative protein
                  serine/threonine kinase, clone cSNFL1
                  309947
Seq. No.
                  uC-zmflmo17421d05a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g22091
BLAST score
                  204
E value
                  1.0e-111
Match length
                  321
% identity
                  91
NCBI Description Z.diploperennis gene for hydroxyproline-rich glycoprotein
                  309948
Seq. No.
Seq. ID
                  uC-zmflmo17421f09a1
Method
                  BLASTX
NCBI GI
                  g4538939
BLAST score
                  149
E value
                  6.0e-10
Match length
                  51
```

% identity 57
NCBI Description (AL049483) Col-0 casein kinase I-like protein [Arabidopsis

thaliana]

Seq. No. 309949

Seq. ID uC-zmflmo17424b10a1

Method BLASTN
NCBI GI g1220422
BLAST score 47
E value 2.0e-17
Match length 95
% identity 87

NCBI Description Zea mays ubiquitin (MUB14) mRNA, 3' end

Seq. No. 309950

Seq. ID uC-zmflmo17424c10a1

Method BLASTX
NCBI GI g3386567
BLAST score 284
E value 2.0e-25
Match length 70
% identity 89

NCBI Description (AF079589) 1-aminocyclopropane-1-carboxylate oxidase

[Sorghum bicolor]

Seq. No. 309951

Seq. ID uC-zmflmo17424f04a1

Method BLASTX
NCBI GI g3785972
BLAST score 173
E value 2.0e-12
Match length 42
% identity 81



NCBI Description (AC005560) putative auxin transport protein [Arabidopsis thaliana] >gi_4262249_gb_AAD14542_ (AC006200) putative

auxin transport protein [Arabidopsis thaliana]

309952 Seq. No.

uC-zmflmo17424h06a1 Seq. ID

Method BLASTX NCBI GI g3021270 BLAST score 239 E value 5.0e-20 Match length 123 % identity 44

NCBI Description (AL022347) serine/threonine kinase -like protein

[Arabidopsis thaliana]

309953 Seq. No.

Seq. ID uC-zmflmo17425b04a1

Method BLASTX NCBI GI g4091806 BLAST score 158 E value 1.0e-10 Match length 79

% identity 52

NCBI Description (AF052585) CONSTANS-like protein 2 [Malus domestica]

Seq. No. 309954

Seq. ID uC-zmflmo17425e02a1

Method BLASTX NCBI GI g4574406 BLAST score 298 E value 4.0e-27 Match length 105

% identity 52

NCBI Description (AF121139) RIM2 protein [Oryza sativa]

Seq. No. 309955

Seq. ID uC-zmflmo17425h10a1

Method BLASTN NCBI GI g609287 BLAST score 53 E value 6.0e-21 Match length 129 % identity 85

NCBI Description Z.diploperennis Grandel gene

309956 Seq. No.

Seq. ID uC-zmflmo17a02b1

Method BLASTN NCBI GI g257040 BLAST score 193 E value 1.0e-104 Match length 253 % identity

NCBI Description hydroxyproline-rich glycoprotein [maize, Genomic, 1703 nt]

Seq. No. 309957

Seq. ID uC-zmflmo17a10b1



Method BLASTX
NCBI GI g3142300
BLAST score 428
E value 3.0e-42
Match length 147
% identity 56

NCBI Description (AC002411) Contains similarity to pre-mRNA processing

protein PRP39 gb_L29224 from S. cerevisiae. ESTs gb_R64908 and gb_T88158, gb_N38703 and gb_AA651043 come from this

gene. [Arabidopsis thaliana]

Seq. No. 309958

Seq. ID uC-zmflmo17b05b1

Method BLASTX
NCBI GI g3337367
BLAST score 157
E value 2.0e-10
Match length 50
% identity 62

NCBI Description (AC004481) hypothetical protein [Arabidopsis thaliana]

Seq. No. 309959

Seq. ID uC-zmflmo17c08b1

Method BLASTN
NCBI GI g2062705
BLAST score 34
E value 2.0e-09
Match length 34
% identity 100

NCBI Description Human butyrophilin (BTF5) mRNA, complete cds

Seq. No. 309960

Seq. ID uC-zmflmo17e12b1

Method BLASTN
NCBI GI g4140643
BLAST score 156
E value 3.0e-82
Match length 223
% identity 93

NCBI Description Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster,

complete sequence

Seq. No. 309961

Seq. ID uC-zmflmo17g08b1

Method BLASTX
NCBI GI g3805853
BLAST score 183
E value 2.0e-13
Match length 51
% identity 67

NCBI Description (AL031986) putative protein [Arabidopsis thaliana]

Seq. No. 309962

Seq. ID uC-zmroB73001a04b1

Method BLASTX NCBI GI g4239889 BLAST score 299



```
E value 4.0e-27
Match length 84
% identity 73
```

NCBI Description (AB016802) MAP kinase 5 [Zea mays]

Seq. No. 309963

Seq. ID uC-zmroB73001a07b1

Method BLASTX
NCBI GI g4538961
BLAST score 158
E value 3.0e-15
Match length 69
% identity 70

NCBI Description (AL049488) isoleucine-tRNA ligase-like protein [Arabidopsis

thaliana]

Seq. No. 309964

Seq. ID uC-zmroB73001a09b1

Method BLASTX
NCBI GI g1806140
BLAST score 298
E value 3.0e-27
Match length 101
% identity 61

NCBI Description (X97314) cdc2MsC [Medicago sativa]

Seq. No. 309965

Seq. ID uC-zmroB73001b07b1

Method BLASTX
NCBI GI g4006891
BLAST score 234
E value 2.0e-19
Match length 78
% identity 59

MCBI Description (Z99708) putative protein [Arabidopsis thaliana]

Seq. No. 309966

Seq. ID uC-zmroB73001d05b1

Method BLASTX
NCBI GI 9479413
BLAST score 184
E value 8.0e-14
Match length 108
% identity 38

NCBI Description myosin-like protein - Arabidopsis thaliana

Seq. No. 309967

Seq. ID uC-zmroB73001d10b1

Method BLASTX
NCBI GI g4309741
BLAST score 208
E value 2.0e-16
Match length 53
% identity 74

NCBI Description (AC006439) hypothetical protein [Arabidopsis thaliana]

Seq. No. 309968

```
Seq. ID
                  uC-zmroB73001e06b1
Method
                  BLASTX
NCBI GI
                  q2894534
BLAST score
                  159
E value
                  2.0e-15
Match length
                  87
% identity
                  57
NCBI Description
                  (AJ224327) aquaporin [Oryza sativa]
Seq. No.
                  309969
Seq. ID
                  uC-zmroB73001e12b1
Method
                  BLASTX
NCBI GI
                  g1709000
BLAST score
                  397
E value
                  2.0e-38
Match length
                  79
% identity
                  94
NCBI Description
                  S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
                  ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                  >gi_960357_dbj_BAA09895_ (D63835) S-adenosylmethionine
                  synthetase [Hordeum vulgare]
Seq. No.
                  309970
Seq. ID
                  uC-zmroB73001f01b1
Method
                  BLASTX
NCBI GI
                  q167012
BLAST score
                  239
E value
                  4.0e-20
Match length
                  51
% identity
                  84
NCBI Description (J03897) carboxypeptidase I precursor [Hordeum vulgare]
Seq. No.
                  309971
Seq. ID
                  uC-zmroB73001f02b1
Method
                  BLASTX
NCBI GI
                  q1825645
BLAST score
                  295
E value
                  1.0e-26
Match length
                  72
% identity
                  75
NCBI Description
                  (U88173) weak similarity to Arabidopsis thaliana
                  ubiquitin-like protein 8 [Caenorhabditis elegans]
Seq. No.
                  309972
Seq. ID
                  uC-zmroB73001f10b1
```

Method BLASTX NCBI GI g1169014 BLAST score 245 E value 1.0e-20 Match length 73 % identity 63

NCBI Description COATOMER BETA SUBUNIT (BETA-COAT PROTEIN) (BETA-COP)

>gi_472343 (L31852) bcop [Drosophila melanogaster]

309973 Seq. No.

Seq. ID uC-zmroB73001g09b1

Method BLASTX

```
NCBI GI
                  g3269291
BLAST score
                  647
E value
                  7.0e-68
Match length
                  163
% identity
                  72
NCBI Description
                  (AL030978) putative receptor protein kinase [Arabidopsis
                  thaliana]
                  309974
Seq. No.
                  uC-zmroB73001h09b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g311236
BLAST score
                  39
E value
                  2.0e-12
Match length
                  85
% identity
                  87
NCBI Description Z.mays mRNA for ATPase (delta subunit)
                  309975
Seq. No.
Seq. ID
                  uC-zmroB73013a11b1
Method
                  BLASTX
NCBI GI
                  g1019946
BLAST score
                  275
E value
                  2.0e-24
Match length
                  85
% identity
                  65
NCBI Description (U37060) ascorbate peroxidase [Gossypium hirsutum]
                  309976
Seq. No.
Seq. ID
                  uC-zmroB73013b11b1
Method
                  BLASTX
NCBI GI
                  g2924509
BLAST score
                  244
E value
                  1.0e-32
Match length
                  104
% identity
                  65
NCBI Description
                  (AL022023) subtilisin proteinase - like [Arabidopsis
                  thaliana]
Seq. No.
                  309977
Seq. ID
                  uC-zmroB73013c06b1
Method
                  BLASTN
NCBI GI
                  g2950394
BLAST score
                  143
E value
                  1.0e-74
Match length
                  306
                  97
% identity
NCBI Description Zea mays me gene, exons 1 to
Seq. No.
                  309978
Seq. ID
                  uC-zmroB73013d01b1
Method
                  BLASTX
```

NCBI GI g128405 BLAST score 285 E value 2.0e-25 Match length 118 % identity 👺 54



NCBI Description NODULIN 21 (N-21) >gi_99942_pir__S08632 nodulin-21 - soybean >gi_18694_emb_CAA34506_ (X16488) nodulin-21 (AA

1-201) [Glycine max]

Seq. No. 309979

Seq. ID uC-zmroB73013f06b1

Method BLASTX
NCBI GI g3319342
BLAST score 153
E value 7.0e-11
Match length 47
% identity 77

NCBI Description (AF077407) similar to mitochondrial carrier proteins (Pfam:

mit_carr.hmm, score: 79.74 and 42.50) [Arabidopsis

thaliana]

Seq. No. 309980

Seq. ID uC-zmroB73014a02b1

Method BLASTX
NCBI GI g82040
BLAST score 325
E value 2.0e-30
Match length 77
% identity 24

NCBI Description ubiquitin precursor - flax (fragment) >gi 168304 (M57895)

ubiquitin [Linum usitatissimum]

Seq. No. 309981

Seq. ID uC-zmroB73014a03b1

Method BLASTX
NCBI GI g131770
BLAST score 264
E value 3.0e-23
Match length 86
% identity 57

NCBI Description 40S RIBOSOMAL PROTEIN S9 (40S RIBOSOMAL PROTEIN 1024)

(VEGETATIVE SPECIFIC PROTEIN V12) >gi_70880_pir R3D024

ribosomal protein S9.e - slime mold (Dictyostelium discoideum) >gi_7353_emb_CAA29844_ (X06636) rp1024 protein

[Dictyostelium discoideum]

Seq. No. 309982

Seq. ID uC-zmroB73014a05b1

Method BLASTX
NCBI GI g2459432
BLAST score 150
E value 4.0e-10
Match length 47
% identity 55

NCBI Description (AC002332) CONSTANS-like protein [Arabidopsis thaliana]

Seq. No. 309983

Seq. ID uC-zmroB73014a08b1

Method BLASTX
NCBI GI g4506745
BLAST score 198
E value 2.0e-15



```
Match length 89
% identity 51
NCBI Description ri
```

ribosomal protein S9 >gi_1173285_sp_P46781_RS9_HUMAN 40S RIBOSOMAL PROTEIN S9 >gi_1362936_pir__ S55917 ribosomal protein S9 - human >gi_550023 (U14971) ribosomal protein S9 [Homo sapiens] >gi_1096943_prf__2113200F ribosomal protein S9 [Homo sapiens]

Seq. No. 309984

Seq. ID uC-zmroB73014b01b1

Method BLASTX
NCBI GI g1931645
BLAST score 169
E value 7.0e-12
Match length 106
% identity 38

NCBI Description (U95973) Fe(II) transporter isolog [Arabidopsis thaliana]

Seq. No.

309985

Seq. ID uC-zmroB73014b11b1

Method BLASTX
NCBI GI g1703108
BLAST score 289
E value 7.0e-27
Match length 80
% identity 82

NCBI Description ACTIN 2/7 >gi_2129525_pir__S71210 actin 2 - Arabidopsis

thaliana >gi_2129528_pir___\$68107 actin 7 - Arabidopsis thaliana >gi_1049307 (U37281) actin-2 [Arabidopsis thaliana] >gi_1943863 (U27811) actin7 [Arabidopsis

thaliana]

Seq. No. 309986

Seq. ID uC-zmroB73014b12b1

Method BLASTN
NCBI GI g22292
BLAST score 141
E value 1.0e-73
Match length 241
% identity 90

NCBI Description Z.mays mRNA for glycine-rich protein

Seq. No.

309987

Seq. ID uC-zmroB73014c10b1

Method BLASTX
NCBI GI g2739008
BLAST score 302
E value 2.0e-27
Match length 143
% identity 47

NCBI Description (AF022463) CYP78A3p [Glycine max]

Seq. No.

309988

Seq. ID uC-zmroB73014d04b1

Method BLASTX NCBI GI g4335745 BLAST score 194



E value 5.0e-15 Match length 92 % identity 39

NCBI Description (AC006284) putative hydrolase (contains an

esterase/lipase/thioesterase active site serine domain

(prosite: PS50187) [Arabidopsis thaliana]

Seq. No. 309989

Seq. ID uC-zmroB73014d08b1

Method BLASTX NCBI GI g3236247 BLAST score 385 E value 4.0e-37 Match length 150 % identity 49

NCBI Description (AC004684) SCARECROW-like protein [Arabidopsis thaliana]

309990 Seq. No.

Seq. ID uC-zmroB73014e05b1

Method BLASTN NCBI GI g4154280 BLAST score 36 7.0e-11 E value Match length 44 % identity 95

NCBI Description Zea mays C13 endopeptidase NP1 precursor, mRNA, complete

cds

309991 Seq. No.

Seq. ID uC-zmroB73014f07b1

Method BLASTN NCBI GI g3132824 BLAST score 66 1.0e-28 E value Match length 132

% identity 88

NCBI Description Zea mays putative cytosine-5 DNA methyltransferase (ZMET1)

gene, complete cds

Seq. No. 309992

Seq. ID uC-zmroB73014q06b1

Method BLASTX NCBI GI g4582783 BLAST score 308 E value 4.0e-28 Match length 150 % identity 42

NCBI Description (AJ006752) starch synthase, isoform V [Vigna unguiculata]

Seq. No. 309993

Seq. ID uC-zmroB73014h06b1

Method BLASTX NCBI GI g1172809 BLAST score 512 E value 2.0e-53 Match length 130 % identity 83



NCBI Description 60S RIBOSOMAL PROTEIN L10 (QM PROTEIN HOMOLOG) >gi_468056 (U06108) QM protein [Zea mays]

Seq. No. 309994

Seq. ID uC-zmroB73014h11b1

Method BLASTX
NCBI GI g4218120
BLAST score 259
E value 2.0e-22
Match length 98
% identity 50

NCBI Description (AL035353) Proline-rich APG-like protein [Arabidopsis

thaliana]

Seq. No. 309995

Seq. ID uC-zmroB73015b12b1

Method BLASTX
NCBI GI 94415921
BLAST score 145
E value 5.0e-09
Match length 94
% identity 37

NCBI Description (AC006282) putative glucosyl transferase [Arabidopsis

thaliana]

Seq. No. 309996

Seq. ID uC-zmroB73015c06b1

Method BLASTX
NCBI GI g585338
BLAST score 356
E value 7.0e-34
Match length 122
% identity 62

NCBI Description ADENYLATE KINASE B (ATP-AMP TRANSPHOSPHORYLASE)

>gi_391879 dbj BAA01181 (D10335) adenylate kinase-b [Oryza

£ 1

satīva]

Seq. No. 309997

Seq. ID uC-zmroB73015c11b1

Method BLASTX
NCBI GI g4538927
BLAST score 186
E value 7.0e-14
Match length 53
% identity 60

NCBI Description (AL049483) putative peroxidase [Arabidopsis thaliana]

Seq. No. 309998

Seq. ID uC-zmroB73015d02b1

Method BLASTN
NCBI GI g2832242
BLAST score 54
E value 2.0e-21
Match length 179
% identity 90

NCBI Description Zea mays 22-kDa alpha zein gene cluster, complete sequence



```
Seq. No.
Seq. ID
                  uC-zmroB73015d04b1
Method
                  BLASTX
NCBI GI
                  q3335353
BLAST score
                  172
E value
                  2.0e-26
Match length
                  139
% identity
                  42
                  (AC004512) Similar to cytochrome P450 gb_X90458 from A.
NCBI Description
                  thaliana. [Arabidopsis thaliana]
Seq. No.
                  310000
Seq. ID
                  uC-zmroB73015e07b1
Method
                  BLASTN
                  g168423
NCBI GI
BLAST score
                  62
E value
                  2.0e-26
Match length
                  74
% identity
                  97
NCBI Description Zea mays polypeptide chain-binding protein mRNA, 3' end
                  310001
Seq. No.
                  uC-zmroB73015e12b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3641838
BLAST score
                  338
E value
                  1.0e-31
Match length
                  147
% identity
                  50
NCBI Description
                  (AL023094) putative protein (fragment) [Arabidopsis
                  thaliana]
Seq. No.
                  310002
Seq. ID
                  uC-zmroB73015f10b1
Method
                  BLASTX
NCBI GI
                  q3445208
BLAST score
                  187
E value
                  6.0e-14
Match length
                  61
% identity
                  62
NCBI Description
                  (AC004786) putative amino-acid acetyltransferase
                  [Arabidopsis thaliana]
Seq. No.
                  310003
Seq. ID
                  uC-zmroB73015g04b1
Method
                  BLASTX
NCBI GI
                  g2290528
BLAST score
                  221
E value
                  4.0e-18
Match length
                  49
```

% identity

NCBI Description (U94746) ATAN11 [Arabidopsis thaliana]

Seq. No. 310004

Seq. ID uC-zmroB73015g05b1

Method BLASTX NCBI GI g3135543



```
BLAST score
                  1.0e-37
E value
Match length
                  127
% identity
                  69
                  (AF062393) aquaporin [Oryza sativa]
NCBI Description
                  310005
Seq. No.
                  uC-zmroB73015q08b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1483177
BLAST score
                  348
                  9.0e-33
E value
Match length
                  119
% identity
                  61
NCBI Description
                  (D86598) antifreeze-like protein (af70) [Picea abies]
                  310006
Seq. No.
                  uC-zmroB73015h09b1
Seq. ID
                  BLASTN
Method
NCBI GI
                  q2431766
BLAST score
                  46
                  9.0e-17
E value
Match length
                  202
% identity
                  81
                  Zea mays acidic ribosomal protein P3a (rpp3a) mRNA,
NCBI Description
                  complete cds
                  310007
Seq. No.
Seq. ID
                  uC-zmroB73015h12b1
                  BLASTX
Method
NCBI GI
                  g3396079
BLAST score
                  303
                  2.0e-27
E value
Match length
                  159
% identity
                   44
                   (AF080173) inositol 1,3,4-trisphosphate 5/6-kinase
NCBI Description
                   [Arabidopsis thaliana]
                   310008
Seq. No.
                  uC-zmroB73017a10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q4140691
BLAST score
                   202
E value
                  1.0e-15
Match length
                  157
% identity
                   32
                  (AF101972) zeatin O-glucosyltransferase [Phaseolus lunatus]
NCBI Description
Seq. No.
                   310009
                   uC-zmroB73017b02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q100490
```

BLAST score 518 E value 9.0e-53 Match length 108 % identity 25

NCBI Description polyubiquitin - garden snapdragon (fragment)



>gi_16071_emb_CAA48140_ (X67957) ubiquitin [Antirrhinum majus]

Seq. No. 310010

Seq. ID uC-zmroB73017b10b1

Method BLASTX
NCBI GI g1345588
BLAST score 273
E value 5.0e-24
Match length 58

% identity 98
NCBI Description 14-3-3-LIKE PROTEIN GF14-12 >gi 998432_bbs_164524

GF14-12=GRF2 product/14-3-3 protein homolog [Zea mays,

XL80, Peptide, 261 aa]

Seq. No. 310011

Seq. ID uC-zmroB73017c05b1 Method BLASTX

NCBI GI g3036840
BLAST score 245
E value 1.0e-20
Match length 110
% identity 45

NCBI Description (AJ222967) cystinosin [Homo sapiens]

>gi 3036851 emb CAA75882 (Y15924) cystinosin [Homo

sapiens]

Seq. No. 310012

Seq. ID uC-zmroB73017c11b1

Method BLASTX
NCBI GI g3335376
BLAST score 478
E value 5.0e-48
Match length 144
% identity 62

NCBI Description (AC003028) putative ammonium transporter [Arabidopsis

thaliana]

Seq. No. 310013

Seq. ID uC-zmroB73017e01b1

Method BLASTX
NCBI GI g3256035
BLAST score 173
E value 4.0e-19
Match length 81
% identity 65

NCBI Description (Y14274) putative serine/threonine protein kinase [Sorghum

bicolor]

Seq. No. 310014

Seq. ID uC-zmroB73017f11b1

Method BLASTX
NCBI GI 94388820
BLAST score 281
E value 6.0e-25
Match length 63
% identity 78



```
NCBI Description
                   (AC006528) putative myb DNA-binding protein [Arabidopsis
                   thaliana]
 Seq. No.
                   310015
 Seq. ID
                   uC-zmroB73017g05b1
 Method
                   BLASTX
 NCBI GI
                   g1174162
 BLAST score
                   194
 E value
                   9.0e-15
 Match length
                   46
 % identity
                   80
 NCBI Description
                   (U44976) ubiquitin-conjugating enzyme [Arabidopsis
                   thaliana] >gi_3746915 (AF091106) E2
                   ubiquitin-conjugating-like enzyme [Arabidopsis thaliana]
 Seq. No.
                   310016
 Seq. ID
                   uC-zmroB73017g07b1
 Method
                   BLASTX
 NCBI GI
                   q4262241
 BLAST score
                   209
 E value
                   2.0e-16
 Match length
                   143
 % identity
                   41
 NCBI Description (AC006200) unknown protein [Arabidopsis thaliana]
Seq. No.
                 .- 310017
                   uC-zmroB73017h12b1
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   g1491615
 BLAST score
                   272
 E value
                   6.0e-24
 Match length
                   101
                   52
 % identity
 NCBI Description
                   (X99923) male sterility 2-like protein [Arabidopsis
                   thaliana]
 Seq. No.
                   310018
                   uC-zmroB73020b08b1
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   q1857256
 BLAST score
                   257
 E value
                   3.0e-22
 Match length
                   135
 % identity
                   43
 NCBI Description (U75360) MURAZC [Zea mays]
 Seq. No.
                   310019
 Seq. ID
                   uC-zmroB73020d04b1
 Method
                   BLASTX
 NCBI GI
                   q4454017
```

Method BLASTX
NCBI GI 9445401
BLAST score 212
E value 6.0e-17
Match length 108
% identity 45

NCBI Description (AL035396) hypothetical protein [Arabidopsis thaliana]

Seq. No. 310020

44147

and the state of t



Seq. ID uC-zmroB73020d08b1

Method BLASTX
NCBI GI g3024122
BLAST score 663
E value 9.0e-70
Match length 153
% identity 84

NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE

ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2) >gi_1778821 (U82833) S-adenosyl-L-methionine synthetase [Oryza sativa]

Seq. No. 310021

Seq. ID uC-zmroB73020d10b1

Method BLASTX
NCBI GI g1362152
BLAST score 155
E value 3.0e-10
Match length 58
% identity 60

NCBI Description ribosomal protein S6 kinase homolog (clone Aspk11) - oat

>gi_871986_emb_CAA56313 (X79992) putative pp70 ribosomal

protein S6 kinase [Avena sativa]

Seq. No. 310022

Seq. ID uC-zmroB73020d12b1

Method BLASTX
NCBI GI g4204793
BLAST score 358
E value 5.0e-34
Match length 151
% identity 22

NCBI Description (U52079) P-glycoprotein [Solanum tuberosum]

Seq. No. 310023

Seq. ID uC-zmroB73020f09b1

Method BLASTX
NCBI GI g3953481
BLAST score 264
E value 5.0e-23
Match length 138
% identity 46

NCBI Description (AC002328) F2202.26 [Arabidopsis thaliana]

Seq. No. 310024

Seq. ID uC-zmroB73020g07b1

Method BLASTX
NCBI GI g2522534
BLAST score 428
E value 4.0e-42
Match length 159
% identity 55

NCBI Description (AF027302) TNF-alpha stimulated ABC protein [Homo sapiens]

Seq. No. 310025

Seq. ID uC-zmroB73020g11b1

Method BLASTX NCBI GI g2655008

```
BLAST score
E value
                  1.0e-22
Match length
                  80
                  57
% identity
                  (AF017144) (1-4)-beta-mannan endohydrolase [Lycopersicon
NCBI Description
                  esculentum]
                  310026
Seq. No.
                  uC-zmroB73028a02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2351374
BLAST score
                  363
E value
                  1.0e-46
Match length
                  124
% identity
                  79
                  (U54560) putative 26S proteasome subunit athMOV34
NCBI Description
                  [Arabidopsis thaliana]
                  310027
Seq. No.
                  uC-zmroB73028d07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4539301
BLAST score
                  281
                  2.0e-26
E value
Match length
                  97
% identity
                  64
                  (AL049480) putative mitochondrial protein [Arabidopsis
NCBI Description
                  thaliana]
                  310028
Seq. No.
                  uC-zmroB73028d12b1
Seq. ID
Method
                  BLASTX
                  g1702987
NCBI GI
BLAST score
                  220
E value
                  5.0e-18
Match length
                  66
% identity
                  74
NCBI Description
                  14-3-3-LIKE PROTEIN GF14 PHI >gi 1493805 (L09111) GF14
                  protein phi chain [Arabidopsis thaliana] >gi_2232146
                   (AF001414) 14-3-3-like protein GF14 phi [Arabidopsis
                  thaliana]
Seq. No.
                  310029
```

Seq. ID uC-zmroB73028g03b1

Method BLASTX NCBI GI g2244905 BLAST score 266 2.0e-23 E value Match length 71

62 % identity

NCBI Description (Z97339) indole-3-acetate beta-glucosyltransferase

[Arabidopsis thaliana]

Seq. No. 310030

Seq. ID uC-zmroB73028g05b1

Method BLASTX NCBI GI g3402682



BLAST score 308 E value 5.0e-28 Match length 180 % identity 6

NCBI Description (AC004697) unknown protein [Arabidopsis thaliana]

Seq. No.

310031

Seq. ID uC-zmroB73028h04b1

Method BLASTX
NCBI GI g4587550
BLAST score 440
E value 2.0e-43
Match length 157
% identity 61

NCBI Description (AC006577) EST gb_R64848 comes from this gene. [Arabidopsis

thaliana]

Seq. No.

310032

Seq. ID uC-zmroB73028h09b1

Method BLASTX
NCBI GI g3628757
BLAST score 448
E value 2.0e-44
Match length 177
% identity 49

NCBI Description (AF038007) FIC1 [Homo sapiens]

Seq. No. 310033

Seq. ID uC-zmroB73028h11b1

Method BLASTX
NCBI GI g1419758
BLAST score 266
E value 4.0e-23
Match length 156
% identity 44

NCBI Description (X98795) geranylgeranyl pyrophosphate synthase [Sinapis

alba]

Seq. No.

310034

Seq. ID uC-zmroB73030b05b1

Method BLASTX
NCBI GI g4033424
BLAST score 228
E value 4.0e-19
Match length 78
% identity 64

NCBI Description SOLUBLE INORGANIC PYROPHOSPHATASE (PYROPHOSPHATE

PHOSPHO-HYDROLASE) (PPASE) >gi_2668746 (AF034947) inorganic

pyrophosphatase [Zea mays]

Seq. No.

310035

Seq. ID uC-zmroB73030c09b1

Method BLASTX
NCBI GI 94115923
BLAST score 302
E value 2.0e-27
Match length 138



% identity

NCBI Description (AF118222) contains similarity to ubiquitin

carboxyl-terminal hydrolase family 2 (Pfam: PF00443,

score=40.0, E=5.2e-08, N=1) and (Pfam:PF00442, Score=37.9

E=5.3e-10, N=1) [Arabidopsis thaliana]

310036 Seq. No.

Seq. ID uC-zmroB73030e08b1

Method BLASTX NCBI GI q4467125 BLAST score 204 E value 5.0e-16 Match length 50 70 % identity

NCBI Description (AL035538) putative protein [Arabidopsis thaliana]

Seq. No. 310037

Seq. ID uC-zmroB73030f04b1

Method BLASTX NCBI GI g3980416 BLAST score 425 E value 1.0e-41 Match length 138 % identity

(AC004561) putative tropinone reductase [Arabidopsis NCBI Description

thaliana]

Seq. No. 310038

Seq. ID uC-zmroB73030f06b1

Method BLASTX NCBI GI q3063449 BLAST score 563 E value 5.0e-58 Match length 151 % identity 74

(AC003981) F22013.11 [Arabidopsis thaliana] NCBI Description

310039 Seq. No.

Seq. ID uC-zmroB73030f08b1

Method BLASTX NCBI GI g3806098 BLAST score 182 E value 2.0e-13 Match length 129 % identity 33

NCBI Description (AF079100) arginine-tRNA-protein transferase 1; Atelp

[Arabidopsis thaliana]

Seq. No. 310040

Seq. ID uC-zmroB73030h10b1

Method BLASTX g4572673 NCBI GI BLAST score 191 E value 2.0e-14 Match length 100 % identity 43

NCBI Description (AC006954) putative sarcosine oxidase [Arabidopsis



thaliana]

 Seq. No.
 310041

 Seq. ID
 uC-zmroB73070a05b1

 Method
 BLASTN

 NCBI GI
 g2984708

 BLAST score
 45

 E value
 2.0e-16

E value 2.0e Match length 81 % identity 89

NCBI Description Zea mays DnaJ-related protein ZMDJ1 (mdJ1) gene, complete

cds

Seq. No. 310042

Seq. ID uC-zmroB73070b01b1

Method BLASTX
NCBI GI g4522008
BLAST score 248
E value 5.0e-21
Match length 158
% identity 38

NCBI Description (AC007069) hypothetical protein [Arabidopsis thaliana]

Seq. No. 310043

Seq. ID uC-zmroB73070c06b1

Method BLASTX
NCBI GI g1076748
BLAST score 140
E value 4.0e-09
Match length 41
% identity 63

NCBI Description major intrinsic protein - rice >gi_440869_dbj_BAA04257_

(D17443) major intrinsic protein [Oryza sativa]

Seq. No. 310044

Seq. ID uC-zmroB73070d02b1

Method BLASTX
NCBI GI g3928084
BLAST score 178
E value 2.0e-13
Match length 62
% identity 50

NCBI Description (AC005770) retrotransposon-like protein [Arabidopsis

thaliana]

Seq. No. 310045

Seq. ID uC-zmroB73070d08b1

Method BLASTX
NCBI GI g4469014
BLAST score 224
E value 2.0e-18
Match length 68
% identity 62

NCBI Description (AL035602) putative protein [Arabidopsis thaliana]

Seq. No. 310046

Seq. ID uC-zmroB73070d09b1

44152

```
Method
NCBI GI
                  q4469014
BLAST score
                  286
                  2.0e-25
E value
Match length
                  91
                  63
% identity
                  (AL035602) putative protein [Arabidopsis thaliana]
NCBI Description
                  310047
Seq. No.
                  uC-zmroB73070e03b1
Seq. ID
                  BLASTX
Method
                  q1917019
NCBI GI
BLAST score
                  465
E value
                  1.0e-46
Match length
                  89
                  97
% identity
NCBI Description (U92045) ribosomal protein S6 RPS6-1 [Zea mays]
                  310048
Seq. No.
                  uC-zmroB73070h08b1
Seq. ID
                  BLASTX
Method
                  g2150000
NCBI GI
BLAST score
                  212
E value
                  6.0e-17
Match length
                  128
                   41
% identity
NCBI Description (AF000939) aleurone ribonuclease [Hordeum vulgare]
                  310049
Seq. No.
                  uC-zmroB73070h09b1
Seq. ID
                  BLASTX
Method
NCBI GI
                   g4581164
BLAST score
                   311
                   2.0e-28
E value
Match length
                  104
                   56
% identity
                  (AC006220) putative polyprotein [Arabidopsis thaliana]
NCBI Description
                   310050
Seq. No.
Seq. ID
                   uC-zmrob73002a01a1
                   BLASTX
Method
                   q1171579
NCBI GI
BLAST score
                   140
E value
                   1.0e-08
Match length
                   44
                   57
% identity
                  (X95342) cytochrome P450 [Nicotiana tabacum]
NCBI Description
Seq. No.
                   310051
Seq. ID
                   uC-zmrob73002a06a1
Method
                   BLASTX
NCBI GI
                   q1076634
```

Method BLASTX
NCBI GI g1076634
BLAST score 154
E value 2.0e-10
Match length 86
% identity 36

NCBI Description protein-serine/threonine kinase NPK15 - common tobacco



>gi_505146_dbj_BAA06538_ (D31737) protein-serine/threonine kinase [Nicotiana tabacum]

Seq. No. 310052

Seq. ID uC-zmrob73002b01b1

BLASTN Method q20243 NCBI GI BLAST score 50 3.0e-19 E value Match length 110 % identity 86

NCBI Description O.sativa GP28 gene (partial)

310053 Seq. No.

Seq. ID uC-zmrob73002b06b1

Method BLASTX g4038034 NCBI GI BLAST score 146 8.0e-10 E value Match length 35 % identity - 74

NCBI Description (AC005936) unknown protein [Arabidopsis thaliana]

Seq. No. 310054

uC-zmrob73002c04b1 Seq. ID

Method BLASTX g119167 NCBI GI BLAST score 144 E value 4.0e-13 Match length 68 66 % identity

ELONGATION FACTOR 2 (EF-2) >gi_421771_pir__S32819 NCBI Description

translation elongation factor eEF-2 - Chlorella kessleri

>gi_167245 (M68064) elongation factor 2 [Chlorella kessleri] >gi_228693_prf__1808323A elongation factor 2

[Chlorella kessleri]

310055 Seq. No.

uC-zmrob73002c06b1 Seq. ID

Method BLASTX NCBI GI q3212854 BLAST score 317 2.0e-29 E value Match length 106 59 % identity

(AC004005) unknown protein [Arabidopsis thaliana] NCBI Description

310056 Seq. No.

uC-zmrob73002d11b1 Seq. ID

Method BLASTX NCBI GI q4539351 209 BLAST score 6.0e-17 E value Match length 68 59 % identity

NCBI Description (AL035539) putative protein [Arabidopsis thaliana]



Seq. No. 310057

Seq. ID uC-zmrob73002e12b1

Method BLASTX
NCBI GI g1171966
BLAST score 285
E value 2.0e-25
Match length 83
% identity 71

NCBI Description PHOSPHATIDYLINOSITOL 3-KINASE, NODULE ISOFORM (PI3-KINASE)

(PTDINS-3-KINASE) (PI3K) (SPI3K-1) >gi_736337 (L29770)

phosphatidylinositol 3-kinase [Glycine max]

Seq. No. 310058

Seq. ID uC-zmrob73002f02b1

Method BLASTN
NCBI GI g3511235
BLAST score 52
E value 2.0e-20
Match length 108
% identity 89

NCBI Description Zea mays starch branching enzyme IIb (ae) gene, complete

cds

Seq. No. 310059

Seq. ID uC-zmrob73002f11b1

Method BLASTX
NCBI GI g1946372
BLAST score 263
E value 6.0e-23
Match length 72
% identity 72

NCBI Description (U93215) yeast hypothetical protein YDB1 SCHPO isolog

[Arabidopsis thaliana]

Seq. No. 310060

Seq. ID uC-zmrob73002f12b1

Method BLASTX
NCBI GI g2565009
BLAST score 228
E value 7.0e-19
Match length 60
% identity 62

NCBI Description (AC002983) putative zinc finger protein [Arabidopsis

thaliana]

Seq. No. 310061

Seq. ID uC-zmrob73002g01b1

Method BLASTX
NCBI GI g4455015
BLAST score 193
E value 1.0e-14
Match length 89
% identity 45

NCBI Description (AF113131) host cell factor homolog LCP [Homo sapiens]

Seq. No. 310062

Seq. ID uC-zmrob73002g05b1

```
RLASTX
Method
NCBI GI
                  g1706958
                  177
BLAST score
E value
                  8.0e-13
Match length
                  136
                  33
% identity
                  (U58284) cellulose synthase [Gossypium hirsutum]
NCBI Description
                  310063
Seq. No.
                  uC-zmrob73004a01b1
Seq. ID
                  BLASTX
Method
                  g2984709
NCBI GI
BLAST score
                  393
                  3.0e-38
E value
Match length
                  84
% identity
                  90
                  (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]
NCBI Description
                  310064
Seq. No.
                  uC-zmrob73004b01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2662341
BLAST score
                   266
                   2.0e-23
E value
Match length
                  72
% identity
                   74
                   (D63580) EF-1 alpha [Oryza sativa]
NCBI Description
                   >gi 2662345 dbj BAA23659 (D63582) EF-1 alpha [Oryza
                   satīva] >gi_2662347_dbj_BAA23660_ (D63583) EF-1 alpha
                   [Oryza sativa]
                   310065
Seq. No.
                   uC-zmrob73004d01b1
Seq. ID
                   BLASTX
Method
                   g2208944
NCBI GI
BLAST score
                   158
                   8.0e-11
E value
Match length
                   65
% identity
                   54
                  (Y11120) nodulin-35 homologue [Arabidopsis thaliana]
NCBI Description
                   310066
Seq. No.
                   uC-zmrob73004d02b1
Seq. ID
                   BLASTX
Method
                   g1710841
NCBI GI
BLAST score
                   441
                   9.0e-44
E value
                   122
Match length
                   71
% identity
```

NCBI Description ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE

HYDROLASE) (ADOHCYASE) >gi_758247_emb_CAA56278_ (X79905)

S-adenosylhomocysteine hydrolase [Phalaenopsis sp.]

Seq. No. 310067

Seq. ID uC-zmrob73004d06b1

Method BLASTX NCBI GI g1170937



```
BLAST score
                  1.0e-11
E value
Match length
                  52
% identity
                  62
NCBI Description
                  S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
                  ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                  >qi 450549 emb CAA81481 (Z26867) S-adenosyl methionine
                  synthetase [Oryza sativa]
Seq. No.
                  310068
```

uC-zmrob73004d07b1 Seq. ID

310069

Method BLASTX NCBI GI g2760345 BLAST score 150 E value 7.0e-10 Match length 38 % identity 27

(U84967) ubiquitin [Arabidopsis thaliana] NCBI Description

Seq. ID uC-zmrob73004e03b1 Method BLASTX NCBI GI g2914703 BLAST score 158 E value 8.0e-11 Match length 92 % identity

Seq. No.

NCBI Description (AC003974) unknown protein [Arabidopsis thaliana]

310070 Seq. No. uC-zmrob73004g01b1 Seq. ID Method BLASTX q2129550 NCBI GI BLAST score 317 3.0e-29 E value Match length 81 % identity 73

calcium-dependent protein kinase (EC 2.7.1.-) CDPK6 -NCBI Description

Arabidopsis thaliana >gi_2129554_pir__S71901

calcium-dependent protein kinase 6 - Arabidopsis thaliana

>gi 836940 (U20623) calcium-dependent protein kinase

[Arabidopsis thaliana] >gi_836944 (U20625)

calcium-dependent protein kinase [Arabidopsis thaliana] >gi 4454034 emb CAA23031.1 (AL035394) calcium-dependent

protein kinase (CDPK6) [Arabidopsis thaliana]

Seq. No. 310071

uC-zmrob73004g02b1Seq. ID

Method BLASTX g1001311 NCBI GI BLAST score 293 2.0e-26 E value Match length 77 % identity 70

(D64006) hypothetical protein [Synechocystis sp.] NCBI Description

Seq. No. 310072



```
uC-zmrob73004g04b1
Seq. ID
                  BLASTX
Method
                  g3046696
NCBI GI
BLAST score
                  275
E value
                  2.0e-24
Match length
                  131
% identity
                  48
                  (AL022224) CTP synthase like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  310073
                  uC-zmrob73004g05b1
Seq. ID
                  BLASTX
Method
                  g1703200
NCBI GI
BLAST score
                  549
E value
                  7.0e-58
Match length
                  137
% identity
                  80
                  PROTEIN KINASE AFC2 >gi 601789 (U16177) protein kinase
NCBI Description
                  [Arabidopsis thaliana] >gi 642130 dbj BAA08214 (D45353)
                  protein kinase [Arabidopsis thaliana]
                  >gi_4220516_emb_CAA22989_ (AL035356) protein kinase (AFC2)
                   [Arabidopsis thaliana]
                  310074
Seq. No.
                  uC-zmrob73004g09b1
Seq. ID
Method
                  BLASTX
                  g1498386
NCBI GI
BLAST score
                  284
E value
                  2.0e-25
Match length
                  80
                  75
% identity
NCBI Description
                  (U60509) actin [Zea mays]
                  310075
Seq. No.
                  uC-zmrob73004h02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3882355
BLAST score
                  315
                  7.0e-29
E value
Match length
                  127
                  53
% identity
                   (U92460) 12-oxophytodienoate reductase OPR1 [Arabidopsis
NCBI Description
                  thaliana]
                  310076
Seq. No.
                  uC-zmrob73004h07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2232254
BLAST score
                  281
                   3.0e-25
E value
Match length
                   64
```

% identity

(AF005237) old-yellow-enzyme homolog [Catharanthus roseus] NCBI Description

Seq. No.

310077

Seq. ID uC-zmrob73004h09b1

Method BLASŢX

```
g4314365
NCBI GI
                  276
BLAST score
                  2.0e-24
E value
Match length
                  120
% identity
                  51
                   (AC006340) putative copia-like retrotransposon Hopscotch
NCBI Description
                   [Arabidopsis thaliana]
                   310078
Seq. No.
                   uC-zmrob73005b01b1
Seq. ID
                  BLASTX
Method
                   g3367568
NCBI GI
BLAST score
                   400
                   6.0e-39
E value
Match length
                   115
% identity
                   62
                   (AL031135) protein kinase - like protein [Arabidopsis
NCBI Description
                   thaliana]
                   310079
Seq. No.
Seq. ID
                   uC-zmrob73005b04b1
Method
                   BLASTN
NCBI GI
                   g2738749
BLAST score
                   83
                   2.0e-39
E value
Match length
                   99
                   96
% identity
NCBI Description Zea mays ATP sulfurylase mRNA, complete cds
                   310080
Seq. No.
                   uC-zmrob73005c07b1
Seq. ID
Method
                   BLASTX
                   q2492504
NCBI GI
                   271
BLAST score
                   2.0e-24
E value
Match length
                   63
% identity
                   84
                   CELL DIVISION CYCLE PROTEIN 48 HOMOLOG
NCBI Description
                   >gi 1669660_emb_CAA70565_ (Y09396) protein of AAA family
                   [Capsicum annuum]
                   310081
Seq. No.
                   uC-zmrob73005c12b1
Seq. ID
                   BLASTX
Method
                   g1498053
NCBI GI
                   192
BLAST score
                   3.0e-15
E value
                   45
Match length
                   82
% identity
                  (U64436) ribosomal protein S8 [Zea mays]
NCBI Description
Seq. No.
                   310082
                   uC-zmrob73005d05b1
```

Seq. ID

BLASTN Method g1800218 NCBI GI BLAST score 104 E value 9.0e-52

```
Match length
% identity
                   93
                  Sorghum bicolor phytochrome C (PHYC) mRNA, complete cds
NCBI Description
Seq. No.
                  310083
                  uC-zmrob73005e08b1
Seq. ID
                  BLASTX
Method
                  q3451075
NCBI GI
BLAST score
                  149
                   4.0e-10
E value
Match length
                   63
% identity
                   48
                   (AL031326) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   310084
                  uC-zmrob73005f10b1
Seq. ID
Method
                  BLASTN
NCBI GI
                   g3869069
BLAST score
                   46
E value
                   1.0e-16
Match length
                   66
% identity
                   92
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MEB5, complete sequence [Arabidopsis thaliana]
Seq. No.
                   310085
                   uC-zmrob73005g03b1
Seq. ID
Method
                   BLASTX
                   g478753
NCBI GI
BLAST score
                   202
E value
                   3.0e-16
Match length
                   43
                   86
% identity
                  tubulin alpha-4 chain - maize (fragment)
NCBI Description
Seq. No.
                   310086
                   uC-zmrob73005h04b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g113456
BLAST score
                   207
E value
                   2.0e-16
                   54
Match length
                   74
% identity
                  ADP, ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1)
NCBI Description
                   (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1)
                   >gi_22162_emb_CAA40781_ (X57556) adenine nucleotide
                   translocator [Zea mays]
```

Seq. No. 310087

Seq. ID uC-zmrob73006a10b1

Method BLASTX
NCBI GI g128405
BLAST score 192
E value 1.0e-14
Match length 87
% identity 52

NCBI Description NODULIN 21 (N-21) >gi_99942_pir__S08632 nodulin-21 -





```
soybean >gi_18694_emb_CAA34506_ (X16488) nodulin-21 (AA
                  1-201) [Glycine max]
                  310088
Seq. No.
                  uC-zmrob73006b02b1
Seg. ID
                  BLASTX
Method
                  q4586053
NCBI GI
                  467
BLAST score
                  6.0e-47
E value
Match length
                  107
                  70
% identity
                  (AC007020) putative lacasse [Arabidopsis thaliana]
NCBI Description
```

 Seq. No.
 310089

 Seq. ID
 uC-zmrob73006d07a1

Method BLASTN
NCBI GI g168508
BLAST score 42
E value 2.0e-14
Match length 102
% identity 85

NCBI Description Maize oleosin KD18 (KD18; L2) gene, complete cds

Seq. No. 310090

Seq. ID uC-zmrob73006d08b1

Method BLASTX
NCBI GI g3915826
BLAST score 138
E value 7.0e-09
Match length 47
% identity 62

NCBI Description 60S RIBOSOMAL PROTEIN L5

Seq. No. 310091

Seq. ID uC-zmrob73006e02b1

Method BLASTX
NCBI GI 94544436
BLAST score 234
E value 1.0e-19
Match length 131
% identity 44

NCBI Description (AC006592) anthocyanidin-3-glucoside rhamnosyltransferase,

3' partial [Arabidopsis thaliana]

Seq. No. 310092

Seq. ID uC-zmrob73006g03b1

Method BLASTX
NCBI GI g4309738
BLAST score 227
E value 8.0e-19
Match length 85
% identity 49

NCBI Description (AC006439) putative tubby protein [Arabidopsis thaliana]

Seq. No. 310093

Seq. ID uC-zmrob73006h01b1

Method BLASTX

10-

```
g4455360
NCBI GI
                  259
BLAST score
                  2.0e-22
E value
                  135
Match length
% identity
                  (AL035524) putative protein [Arabidopsis thaliana]
NCBI Description
                  310094
Seq. No.
                  uC-zmrob73006h03b1
Seq. ID
Method
                  BLASTX
                  g4519938
NCBI GI
BLAST score
                  424
                  7.0e-42
E value
Match length
                  112
% identity
                  72
                  (AB019240) RPR1h [Oryza sativa]
NCBI Description
                  310095
Seq. No.
                  uC-zmrob73006h12b1
Seq. ID
                  BLASTX
Method
                  g3935152
NCBI GI
                  332
BLAST score
                  4.0e-31
E value
                  107
Match length
                  59
% identity
                  (AC005106) T25N20.16 [Arabidopsis thaliana]
NCBI Description
                  310096
Seq. No.
                  uC-zmrob73011a04b1
Seq. ID
Method
                  BLASTX
                  g3941480
NCBI GI
BLAST score
                   290
                   6.0e-26
E value
                   60
Match length
% identity
                   80
                   (AF062894) putative transcription factor [Arabidopsis
NCBI Description
                   thaliana]
                   310097
Seq. No.
Seq. ID
                   uC-zmrob73011b01b1
                   BLASTX
Method
                   q3047096
NCBI GI
                   428
BLAST score
                   1.0e-55
E value
Match length
                   183
% identity
                   63
                   (AF058826) similar to eukaryotic protein kinase domains
NCBI Description
                   (Pfam: pkinase.hmm, score: 189.74) [Arabidopsis thaliana]
                   310098
Seq. No.
```

Seq. ID uC-zmrob73011b03b1

Method BLASTX
NCBI GI g4514635
BLAST score 331
E value 1.0e-30
Match length 82
% identity 66

44162





```
(AB021175) root cap protein 1 [Zea mays]
NCBI Description
                  310099
Seq. No.
                  uC-zmrob73011e07b1
Seq. ID
                  BLASTX
Method
                  g2583120
NCBI GI
BLAST score
                  314
E value
                  7.0e-29
                  119
Match length
% identity
                  53
                   (AC002387) putative receptor-like protein kinase
NCBI Description
                   [Arabidopsis thaliana]
                  310100
Seq. No.
                  uC-zmrob73011f02b1
Seq. ID
                  BLASTX
Method
                  g4063750
NCBI GI
BLAST score
                  314
                   5.0e-29
E value
                  89
Match length
                   62
% identity
                   (AC005851) putative indole-3-acetate
NCBI Description
                  beta-glucosyltransferase synthetase [Arabidopsis thaliana]
Seq. No.
                   310101
                   uC-zmrob73011g12b1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g218190
BLAST score
                   38
                   9.0e-12
E value
                   50
Match length
                   94
% identity
                   Rice genomic DNA encoding peroxidase component RP-2 and/or
NCBI Description
                   4 >gi 244767 gb S80193 S80193 peroxidase isoform RP-2 or
                   RP-4 [Oryza sativa L.=rice, Genomic, 89 nt]
Seq. No.
                   310102
Seq. ID
                   uC-zmrob73012a01b1
                   BLASTX
Method
                   q417570
NCBI GI
                   377
BLAST score
                   3.0e-36
E value
                   122
Match length
% identity
                   59
                   DIHYDROOROTATE DEHYDROGENASE PRECURSOR (DIHYDROOROTATE
NCBI Description
                   OXIDASE) (DHODEHASE) >gi_478676_pir__S23762 dihydroorotate
                   oxidase (EC 1.3.3.1) - Arabidopsis thaliana
                   >gi 16449 emb CAA44695_ (X62909) dihydroorotate
                   dehydrogenase [Arabidopsis thaliana]
                   310103
Seq. No.
Seq. ID
                   uC-zmrob73012a06b1
```

Method BLASTX
NCBI GI g1944132
BLAST score 359
E value 3.0e-34

88

Match length

44163

```
% identity
                  (AB002560) CUC2 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  310104
                  uC-zmrob73012c09b1
Seq. ID
                  BLASTN
Method
NCBI GI
                  q2832242
BLAST score
                  174
E value
                   4.0e-93
Match length
                   395
% identity
                   87
                  Zea mays 22-kDa alpha zein gene cluster, complete sequence
NCBI Description
                   310105
Seq. No.
Seq. ID
                   uC-zmrob73012c10b1
Method
                   BLASTX
NCBI GI
                   g1109600
BLAST score
                   184
E value
                   9.0e-14
Match length
                   69
                   51
% identity
                   (D16628) ATsEH [Arabidopsis thaliana] >gi 2760840
NCBI Description
                   (AC003105) soluble epoxide hydrolase [Arabidopsis thaliana]
Seq. No.
                   310106
Seq. ID
                   uC-zmrob73012d02b1
Method
                   BLASTX
NCBI GI
                   q4544423
BLAST score
                   150
E value
                   9.0e-10
Match length
                   104
% identity
                   38
                  (AC006955) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   310107
Seq. No.
                   uC-zmrob73012d07b1
Seq. ID
Method
                   BLASTX
                   g4097948
NCBI GI
BLAST score
                   325
                   3.0e - 30
E value
Match length
                   103
% identity
                   62
                  (U72255) beta-1,3-glucanase precursor [Oryza sativa]
NCBI Description
                   310108
Seq. No.
                   uC-zmrob73012e02b1
```

Seq. ID

Method BLASTN g2565304 NCBI GI BLAST score 56 1.0e-22 E value 88 Match length % identity 91

Hordeum sp. x Triticum sp. glycine decarboxylase P subunit NCBI Description

mRNA, complete cds

Seq. No.

310109

Seq. ID

uC-zmrob73012e04b1

```
BLASTX
Method
                  g4586112
NCBI GI
BLAST score
                  275
                  3.0e-24
E value
                  161
Match length
                  44
% identity
NCBI Description (AL049638) putative protein [Arabidopsis thaliana]
                  310110
Seq. No.
                  uC-zmrob73012h01b1
Seq. ID
                  BLASTX
Method
                  g4580394
NCBI GI
                  240
BLAST score
E value
                  2.0e-20
Match length
                  69
                  67
% identity
                  (AC007171) putative fatty acid elongase [Arabidopsis
NCBI Description
                  thaliana]
                  310111
Seq. No.
                  uC-zmrob73016g07a1
Seq. ID
                  BLASTN
Method
                  g1008878
NCBI GI
BLAST score
                  100
                  2.0e-49
E value
                  112
Match length
                   97
% identity
NCBI Description Zea mays RS1 mRNA, complete cds
                   310112
Seq. No.
                   uC-zmrob73019a03b1
Seq. ID
                  BLASTX
Method
                   g3894158
NCBI GI
BLAST score
                   189
                   4.0e-14
E value
Match length
                   143
% identity
                   (AC005312) similar to phloem-specific lectin [Arabidopsis
NCBI Description
                   thaliana]
                   310113
Seq. No.
                   uC-zmrob73019d05b1
Seq. ID
                   BLASTX
Method
                   q3355480
NCBI GI
BLAST score
                   198
                   2.0e-15
E value
Match length
                   122
                   39
% identity
                   (AC004218) Medicago nodulin N21-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   310114
Seq. No.
```

uC-zmrob73019d06b1 Seq. ID

Method BLASTX NCBI GI g124226 BLAST score 274 4.0e-24 E value



```
Match length 49

NCBI Description INITIATION FACTOR 5A-2 (EIF-5A) (EIF-4D)

>gi_100278_pir__S21059 translation initiation factor
eIF-5A.2 - curled-leaved tobacco >gi_19702_emb_CAA45104_
(X63542) eukaryotic initiation factor 5A (2) [Nicotiana plumbaginifolia]

Seq. No. 310115

Seq. ID UC-zmrob73019d08b1
```

Method BLASTX
NCBI GI g3915847
BLAST score 165
E value 2.0e-11
Match length 53
% identity 58

NCBI Description 40S RIBOSOMAL PROTEIN S2 >gi_2335095 (AC002339) putative

40S ribosomal protein S2 [Arabidopsis thaliana]

, and

 Seq. No.
 310116

 Seq. ID
 uC-zmrob73019f08b1

 Method
 BLASTX

 NCBI GI
 g3377820

 BLAST score
 357

 E value
 7.0e-34

E value 7.0e-Match length 98 % identity 71

NCBI Description (AF076275) contains similarity to coatomer zeta chains

[Arabidopsis thaliana]

Seq. No. 310117

Seq. ID uC-zmrob73019f11b1

Method BLASTX
NCBI GI g4467124
BLAST score 234
E value 2.0e-19
Match length 147
% identity 35

NCBI Description (AL035538) hypothetical protein [Arabidopsis thaliana]

Seq. No. 310118

Seq. ID uC-zmrob73019g04b1

Method BLASTX
NCBI GI g2688828
BLAST score 195
E value 1.0e-14
Match length 87
% identity 43

NCBI Description (U97530) ethylene-forming-enzyme-like dioxygenase [Prunus

armeniaca]

Seq. No. 310119

Seq. ID uC-zmrob73019h08b1

Method BLASTX
NCBI GI g4314388
BLAST score 458
E value 1.0e-45

44166

```
Match length
% identity
                  59
                  (AC006232) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  310120
Seq. No.
                  uC-zmrob73022a10a1
Seq. ID
                  BLASTX
Method
                  q3935181
NCBI GI
                  401
BLAST score
                   4.0e-39
E value
Match length
                  91
% identity
                  (AC004557) F17L21.24 [Arabidopsis thaliana]
NCBI Description
                   310121
Seq. No.
Seq. ID
                   uC-zmrob73022e01a1
Method
                   BLASTN
NCBI GI
                   g22237
                   47
BLAST score
                   1.0e-17
E value
                   111
Match length
% identity
                   86
                  Maize mRNA for cytosolic GAPDH (GapC)
NCBI Description
                   glyceraldehyde-3-phosphate dehydrogenase
                   310122
Seq. No.
Seq. ID
                   uC-zmrob73022e02a1
                   BLASTX
Method
                   q4210504
NCBI GI
BLAST score
                   428
                   3.0e-42
E value
                   140
Match length
% identity
                   58
                   (AC002392) putative cadmium-transporting ATPase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   310123
                   uC-zmrob73022h10a1
Seq. ID
Method
                   BLASTX
                   g3096910
NCBI GI
BLAST score
                   150
                   1.0e-09
E value
Match length
                   74
                   41
% identity
                   (AJ005813) neoxanthin cleavage enzyme [Arabidopsis
NCBI Description
                   thaliana]
                   310124
Seq. No.
                   uC-zmrob73033b08b1
Seq. ID
                   BLASTX
Method
                   g1082403
NCBI GI
BLAST score
                   325
                   4.0e-30
E value
Match length
                   133
                   47
% identity
                   glutamine--phenylpyruvate transaminase (EC 2.6.1.64) -
NCBI Description
```

human >gi_2146953_pir__S69001 glutamine--phenylpyruvate



aminotransferase (EC 2.6.1.64) - human >gi 758591 emb CAA57702 (X82224) glutamine--phenylpyruvate

aminotransferase [Homo sapiens] 310125 Seq. No. uC-zmrob73033b09b1 Seq. ID BLASTX Method NCBI GI g3641661 561 BLAST score 8.0e-58 E value 124 Match length 88 % identity NCBI Description (AB008519) high affinity nitrate transporter [Oryza sativa] 310126 Seq. No. uC-zmrob73033c06b1 Seq. ID BLASTX Method NCBI GI g3549681 321 BLAST score 1.0e-29 E value Match length 136 % identity 48 (AL031394) male sterility 2-like protein [Arabidopsis NCBI Description thaliana] 310127 Seq. No. Seq. ID uC-zmrob73033d08b1 BLASTX Method NCBI GI g3738339 151 BLAST score 8.0e-10 E value Match length 37 % identity

(AC005170) putative kinase [Arabidopsis thaliana] NCBI Description

Seq. No. Seq. ID uC-zmrob73033d11b1 Method BLASTX q399900 NCBI GI BLAST score 264 5.0e-23 E value

Match length 91 % identity 58 HOMEOBOX-LEUCINE ZIPPER PROTEIN HAT5 (HD-ZIP PROTEIN 5) NCBI Description

(HD-ZIP PROTEIN ATHB-1) >qi 99659 pir S16325 homeotic

protein Athb-1 - Arabidopsis thaliana

>gi 16329 emb CAA41625 (X58821) Athb-1 protein

[Arabidopsis thaliana]

Seq. No. 310129

uC-zmrob73033e10b1 Seq. ID

310128

Method BLASTX NCBI GI g4538961 BLAST score 467 8.0e-47 E value 119 Match length % identity 68

44168



```
(AL049488) isoleucine-tRNA ligase-like protein [Arabidopsis
NCBI Description
                  thaliana]
                   310130
Seq. No.
                  uC-zmrob73034c02a1
Seq. ID
Method
                  BLASTX
                   g483412
NCBI GI
                   220
BLAST score
                   8.0e-18
E value
Match length
                   54
% identity
                   (L01497) calmodulin-binding protein [Zea mays]
NCBI Description
                   310131
Seq. No.
Seq. ID
                   uC-zmrob73036b02b1
Method
                   BLASTX
NCBI GI
                   q425194
BLAST score
                   399
                   9.0e-44
E value
                   108
Match length
                   87
% identity
                   (L26243) heat shock protein [Spinacia oleracea] >gi_2660772
NCBI Description
                   (AF034618) cytosolic heat shock 70 protein [Spinacia
                   oleracea]
                   310132
Seq. No.
                   uC-zmrob73036b07b1
Seq. ID
                   BLASTX
Method
                   g537437
NCBI GI
BLAST score
                   171
                   3.0e-12
E value
                   50
Match length
% identity
                   (U12637) cysteine proteinase [Hemerocallis hybrid cultivar]
NCBI Description
                   310133
Seq. No.
                   uC-zmrob73036d03b1
 Seq. ID
                   BLASTX
Method
                   g2564066
NCBI GI
                   210
BLAST score
                   7.0e-17
 E value
                   54
 Match length
                   69
 % identity
                   (D45900) LEDI-3 protein [Lithospermum erythrorhizon]
 NCBI Description
                   310134
 Seq. No.
                   uC-zmrob73036f02b1
 Seq. ID
                   BLASTX
 Method
                   q135060
 NCBI GI
```

405 BLAST score 1.0e-39 E value Match length 120 % identity 70

SUCROSE SYNTHASE 1 (SUCROSE-UDP GLUCOSYLTRANSFERASE 1) NCBI Description (SHRUNKEN-1) >gi_66570_pir__YUZMS sucrose synthase (EC 2.4.1.13) - maize >gi_22486_emb_CAA26247_ (X02400) sucrose

synthase [Zea mays] $> \overline{gi}_224\overline{88} = \overline{mb}_CAA262\overline{29}$ (X02382)

Seq. ID



sucrose synthase [Zea mays]

```
310135
Seq. No.
                  uC-zmrob73036f03b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3617741
                  154
BLAST score
                  1.0e-10
E value
                  43
Match length
% identity
                   (AC005687) L3 cytoplasmic ribosomal protein [Arabidopsis
NCBI Description
                  thaliana]
                   310136
Seq. No.
                  uC-zmrob73037a05a1
Seq. ID
                  BLASTX
Method
NCBI GI
                   g82700
BLAST score
                   200
                   7.0e-16
E value
                   90
Match length
                   59
% identity
NCBI Description hypothetical protein 2 - maize transposon Mu1
                   310137
Seq. No.
Seq. ID
                   uC-zmrob73039c03a1
                   BLASTX
Method
NCBI GI
                   g2944178
                   257
BLAST score
                   8.0e-33
E value
Match length
                   139
% identity
                   (AF007778) trehalose-6-phosphate phosphatase [Arabidopsis
NCBI Description
                   thaliana]
                   310138
Seq. No.
                   uC-zmrob73039d12a1
Seq. ID
Method
                   BLASTX
                   g2244981
NCBI GI
BLAST score
                   165
                   2.0e-11
E value
Match length
                   87
                   40
% identity
                   (Z97340) similarity to proline-rich protein APG -
NCBI Description
                   Arabidopsis [Arabidopsis thaliana]
                   310139
Seq. No.
                   uC-zmrob73039g03a1
Seq. ID
Method
                   BLASTX
                   g4490735
NCBI GI
                   142
BLAST score
                   7.0e-09
E value
                   81
Match length
% identity
                   35
                   (AL035708) putative protein [Arabidopsis thaliana]
NCBI Description
                   310140
Seq. No.
```

uC-zmrob73044b04a1



```
Method
                  BLASTN
NCBI GI
                  q168606
BLAST score
                  126
E value
                  8.0e-65
Match length
                  185
% identity
                  91
                  Zea mays mitochondrial Rieske Fe-S protein mRNA, complete
NCBI Description
                  310141
Seq. No.
                  uC-zmrob73044d01a1
Seq. ID
                  BLASTN
Method
NCBI GI
                  q22192
BLAST score
                  36
                  7.0e-11
E value
                  52
Match length
```

% identity 92 NCBI Description Z.mays B-I gene for B transcriptional activator

310142 Seq. No. Seq. ID uC-zmrob73044f04a1

Method BLASTN NCBI GI g1895083 BLAST score 111 1.0e-55 E value Match length 220 % identity 87

NCBI Description Zea mays golgi associated protein se-wap41 mRNA, complete

310143 Seq. No.

uC-zmrob73045b10a1 Seq. ID

Method BLASTX NCBI GI g4378066 BLAST score 286 E value 1.0e-25 Match length 105 % identity 50

NCBI Description (AF098806) polyprotein [Sorghum bicolor]

310144 Seq. No.

Seq. ID uC-zmrob73049d08a1

Method BLASTN NCBI GI g22272 BLAST score 53 E value 3.0e-21Match length 188 % identity 88

NCBI Description Maize mRNA for enolase (2-phospho-D-glycerate hydrolase)

310145 Seq. No.

Seq. ID uC-zmrob73049g04a1

Method BLASTX NCBI GI q4056437 BLAST score 356 E value 4.0e-34 Match length 96



```
% identity
                  (AC005990) Strong similarity to PFAM PF_00069 Eukaryotic
NCBI Description
                  protein kinase domain. [Arabidopsis thaliana]
                  310146
Seq. No.
Seq. ID
                  uC-zmrob73049h09a1
Method
                  BLASTX
NCBI GI
                  q4468981
                  249
BLAST score
                  3.0e-21
E value
                  84
Match length
% identity
                   61
NCBI Description (AL035605) formamidase-like protein [Arabidopsis thaliana]
                   310147
Seq. No.
                   uC-zmrob73050c04a1
Seq. ID
                   BLASTN
Method
                   g1419369
NCBI GI
                   92
BLAST score
                   2.0e-44
E value
                   100
Match length
                   98
% identity
NCBI Description Z.mays ZmABP3 mRNA for actin depolymerizing factor
                   310148
Seq. No.
                   uC-zmrob73050c06a1
Seq. ID
                   BLASTX
Method
                   g3641661
NCBI GI
                   366
BLAST score
                   5.0e-35
E value
Match length
                   87
                   82
% identity
                   (AB008519) high affinity nitrate transporter [Oryza sativa]
NCBI Description
                   310149
Seq. No.
Seq. ID
                   uC-zmrob73050c10a1
                   BLASTN
Method
NCBI GI
                   g1419369
                   43
BLAST score
                   4.0e-15
E value
                   47
Match length
% identity
                   Z.mays ZmABP3 mRNA for actin depolymerizing factor
NCBI Description
                   310150
Seq. No.
                   uC-zmrob73050e12a1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4263716
BLAST score
                   222
                   3.0e-18
E value
Match length
                   82
                   55
% identity
                   (AC006223) putative alanine acetyl transferase [Arabidopsis
NCBI Description
                   thaliana]
```

44172

310151

uC-zmrob73050e12b1

Seq. No.

Seq. ID



```
BLASTX
Method
NCBI GI
                  g4263716
BLAST score
                  155
E value
                  2.0e-10
                  67
Match length
% identity
                  42
NCBI Description
                  (AC006223) putative alanine acetyl transferase [Arabidopsis
                  thaliana]
                  310152
Seq. No.
Seq. ID
                  uC-zmrob73050f01b1
Method
                  BLASTX
NCBI GI
                  q135398
BLAST score
                  238
E value
                  3.0e-20
Match length
                  56
% identity
                  TUBULIN ALPHA-1 CHAIN >gi 82731 pir $15773 tubulin alpha-1
NCBI Description
                  chain - maize >gi 22147 emb CAA33734 (X15704)
                  alphal-tubulin [Zea mays]
                  310153
Seq. No.
                  uC-zmrob73050f07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g464843
BLAST score
                  140
                  8.0e-09
E value
Match length
                  40
                  70
% identity
                  [Segment 1 of 2] TUBULIN ALPHA-4 CHAIN
NCBI Description
                  >gi 22152 emb_CAA44864_ (X63179) alpha-tubulin #4 [Zea
                  mays]
Seq. No.
                  310154
Seq. ID
                  uC-zmrob73050f09b1
Method
                  BLASTX
                  g2832658
NCBI GI
BLAST score
                  231
                  4.0e-19
E value
                  67
Match length
                  67
% identity
                  (AL021710) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  310155
                  uC-zmrob73050g02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2995340
BLAST score
                  147
E value
                  3.0e-09
Match length
                  103
% identity
                  (AL022244) hypothetical protein [Schizosaccharomyces pombe]
```

NCBI Description

Seq. No. 310156

uC-zmrob73050h05b1 Seq. ID

Method BLASTX NCBI GI q2894607



```
BLAST score
                  4.0e-56
E value
Match length
                  131
                  73
% identity
                  (ALO21889) NAM (no apical meristem) - like protein
NCBI Description
                  [Arabidopsis thaliana]
                  310157
Seq. No.
                  uC-zmrob73051b12a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g22176
BLAST score
                  42
                  2.0e-14
E value
                  81
Match length
% identity
NCBI Description Z.mays P gene
Seq. No.
                  310158
                  uC-zmrob73051c12a1
Seq. ID
                  BLASTX
Method
                  g1001630
NCBI GI
                                                        ,*{
BLAST score
                  227
                   1.0e-18
E value
                   67
Match length
% identity
NCBI Description (D64002) hypothetical protein [Synechocystis sp.]
                   310159
Seq. No.
                   uC-zmrob73051h09a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4585901
BLAST score
                   266
E value
                   3.0e-23
Match length
                   126
% identity
                  (AC007133) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   310160
Seq. No.
                   uC-zmrob73052a03a1
Seq. ID
                   BLASTX
Method
                   q3928084
NCBI GI
                   181
BLAST score
                   2.0e-13
E value
                   90
Match length
% identity
                   (AC005770) retrotransposon-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   310161
Seq. No.
                   uC-zmrob73052c12a1
Seq. ID
                   BLASTN
Method
                   g22157
NCBI GI
                   198
BLAST score
                   1.0e-107
E value
                   202
Match length
                   100
% identity
NCBI Description Z.mays mRNA for alpha-tubulin
```

```
310162
Seq. No.
                  uC-zmrob73052h11a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q899607
BLAST score
                  168
E value
                  1.0e-89
                  192
Match length
                  97
% identity
NCBI Description Zea mays polyubiquitin (MubC5) mRNA, complete cds
                  310163
Seq. No.
                  uC\text{-}zmrob73053b03a1
Seq. ID
                  BLASTX
Method
NCBI GI
                   g4510369
BLAST score
                   310
E value
                   2.0e-28
Match length
                   147
% identity
NCBI Description (AC007017) hypothetical protein [Arabidopsis thaliana]
                   310164
Seq. No.
                   uC-zmrob73053b10a1
Seq. ID
                   BLASTX
Method
                   g1723182
NCBI GI
                   210
BLAST score
E value
                   9.0e-17
                   65
Match length
% identity
                   SUGAR CARRIER PROTEIN A >gi_169736 (L08197) sugar carrier
NCBI Description
                   protein [Ricinus communis]
                   310165
Seq. No.
                   uC-zmrob73054c09a1
Seq. ID
                   BLASTN
Method
                   g22292
NCBI GI
                   57
BLAST score
                   2.0e-23
E value
                   165
Match length
                   84
 % identity
NCBI Description Z.mays mRNA for glycine-rich protein
                   310166
Seq. No.
                   uC-zmrob73054d05a1
 Seq. ID
                   BLASTX
Method
                   g2723477
NCBI GI
                   224
BLAST score
                   2.0e-18
E value
                   60
Match length
                   75
 % identity
                   (D89824) GTP-binding protein [Arabidopsis thaliana]
 NCBI Description
                   310167
 Seq. No.
                   uC-zmrob73054g02a1
 Seq. ID
                   BLASTX
 Method
```

44175

g1931652

194

NCBI GI BLAST score



```
6.0e-15
E value
Match length
                  57
% identity
                  61
                  (U95973) phosphatidylinositol-4-phosphate 5-kinase isolog
NCBI Description
                   [Arabidopsis thaliana]
                  310168
Seq. No.
                  uC-zmrob73054h06a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g404688
BLAST score
                  217
                  2.0e-17
E value
Match length
                  63
% identity
                  56
                  (L19074) cytochrome P450 [Catharanthus roseus]
NCBI Description
                  310169
Seq. No.
                  uC-zmrob73054h12a1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2618699
BLAST score
                  410
                  3.0e-40
E value
Match length
                  112
                  65
% identity
NCBI Description
                  (AC002510) unknown protein [Arabidopsis thaliana]
                  310170
Seq. No.
                  uC-zmrob73055a04b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3025189
                  162
BLAST score
                  6.0e-11
E value
Match length
                  114
                  35
% identity
                  HYPOTHETICAL 67.1 KD PROTEIN SLL1770
NCBI Description
                  >gi_1652753_dbj_BAA17672_ (D90908) ABC1-like [Synechocystis
                  sp.]
                  310171
Seq. No.
                  uC-zmrob73055c04b1
Seq. ID
Method
                  BLASTX
                  q3269293
NCBI GI
                  145
BLAST score
                  2.0e-12
E value
Match length
                  81
                  47
% identity
NCBI Description (AL030978) putative protein [Arabidopsis thaliana]
Seq. No.
                  310172
                  uC-zmrob73055c07a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3287696
```

BLAST score 137 E value 1.0e-08 Match length 37 % identity 70

NCBI Description (AC003979) Strong similarity to phosphoribosylanthranilate

transferase gb_D86180 from Pisum sativum. This ORF may be part of a larger gene that lies in the overlapping region. [Arabidopsis thaliana]

```
310173
Seq. No.
                  uC-zmrob73055c10b1
Seq. ID
                  BLASTX
Method
                  q4539422
NCBI GI
                  223
BLAST score
                  7.0e-23
E value
Match length
                  70
                  77
% identity
                  (AL049171) putative protein [Arabidopsis thaliana]
NCBI Description
                   310174
Seq. No.
                   uC-zmrob73055c11b1
Seq. ID
                   BLASTX
Method
                                             4
                   g1438877
NCBI GI
BLAST score
                   351
                   4.0e-33
E value
                   137
Match length
% identity
                   27
                   (U41287) zinc finger protein [Mus musculus]
NCBI Description
                   310175
Seq. No.
                   uC-zmrob73055d08b1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g296593
BLAST score
                   53
                   8.0e-21
E value
                   73
Match length
                   93
% identity
NCBI Description H. vulgare pZE40 gene
                   310176
Seq. No.
                   uC-zmrob73055d11b1
Seq. ID
                   BLASTX
Method
                   g3320104
NCBI GI
                   153
BLAST score
                   3.0e-10
E value
                   92
Match length
                   39
 % identity
                   (AJ007366) calcium-dependent protein kinase [Zea mays]
 NCBI Description
                   310177
 Seq. No.
                   uC-zmrob73055e10a1
 Seq. ID
                   BLASTX
 Method
                   q3075400
 NCBI GI
                   159
 BLAST score
                   8.0e-11
 E value
                   50
 Match length
                   58
 % identity
                   (AC004484) putative thromboxane-A synthase [Arabidopsis
 NCBI Description
                    thaliana] >gi_3413720 (AC004747) putative thromboxin-A
```

Seq. No. 310178

synthase [Arabidopsis thaliana]



```
uC-zmrob73055g04b1
Seq. ID
                   BLASTX
Method
                   g548770
NCBI GI
BLAST score
                   321
E value
                   6.0e - 36
                   143
Match length
                   59
% identity
                   60S RIBOSOMAL PROTEIN L3 >gi_481228_pir__S38359 ribosomal protein L3 - rice >gi_303853_dbj_BAA02155_ (D12630)
NCBI Description
                   ribosomal protein L3 [Oryza sativa]
                    310179
Seq. No.
                   uC-zmrob73055g06b1
Seq. ID
                   BLASTX
Method
                   g2735017
NCBI GI
BLAST score
                   372
E value
                   5.0e-48
Match length
                    140
% identity
                   (U82481) KI domain interacting kinase 1 [Zea mays]
NCBI Description
                    310180
Seq. No.
                    uC-zmrob73055h01a1
Seq. ID
                    BLASTX
Method
                    g1171579
NCBI GI
                    188
BLAST score
E value
                    2.0e-14
                    57
Match length
% identity
                    (X95342) cytochrome P450 [Nicotiana tabacum]
NCBI Description
                    310181
Seq. No.
                    uC-zmrob73055h08b1
Seq. ID
                    BLASTX
Method
                    g1076287
NCBI GI
                    282
BLAST score
                    1.0e-25
E value
                    68
Match length
                    90
 % identity
                    amine acid permease - Arabidopsis thaliana
NCBI Description
                    >gi_510236_emb_CAA50672_ (X71787) amine acid permease
                    [Arabidopsis thaliana]
                    310182
 Seq. No.
                    uC-zmrob73056b04a1
 Seq. ID
                    BLASTN
 Method
                    g514945
 NCBI GI
                    143
 BLAST score
                    1.0e-74
 E value
                    265
 Match length
                    89
 % identity
 NCBI Description Zea mays sucrose synthase (Sus1) mRNA, complete cds
```

44178

310183

BLASTX

g3184289

uC-zmrob73057c11a1

Seq. No.

Seq. ID

Method NCBI GI

Match length

% identity

102

83



```
BLAST score
                   199
                  2.0e-15
E value
                  55
Match length
                  69
% identity
                 (AC004136) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  310184
Seq. No.
Seq. ID
                  uC-zmrob73057e10a1
                  BLASTX
Method
NCBI GI
                  g1944132
BLAST score
                  183
E value
                  2.0e-13
Match length
                  147
                  33
% identity
NCBI Description (AB002560) CUC2 [Arabidopsis thaliana]
Seq. No.
                  310185
Seq. ID
                  uC-zmrob73057g02a1
Method
                  BLASTX
NCBI GI
                  q4263818
BLAST score
                  244
E value
                  1.0e-20
Match length
                  102
% identity
                   40
                  (AC006067) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  310186
                  uC-zmrob73057g12a1
Seq. ID
Method
                  BLASTX
                  g3941480
NCBI GI
BLAST score
                  174
                   4.0e-13
E value
Match length
                  52
% identity
                  58
                   (AF062894) putative transcription factor [Arabidopsis
NCBI Description
                  thaliana]
                   310187
Seq. No.
Seq. ID
                  uC-zmrob73058a09a1
Method
                  BLASTX
NCBI GI
                  g4220528
BLAST score
                  288
E value
                  9.0e-26
                  64
Match length
                  78
% identity
NCBI Description
                   (AL035356) glucose-6-phosphate isomerase [Arabidopsis
                  thaliana]
Seq. No.
                  310188
                  uC-zmrob73058b09a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g294844
BLAST score
                  34
E value
                  7.0e-10
```

NCBI Description Saccharum hybrid cultivar H65-7052 membrane protein mRNA,

NCBI Description

thaliana]



complete cds

310189 Seq. No. uC-zmrob73058d01a1 Seq. ID BLASTX Method g2982452 NCBI GI 430 BLAST score 2.0e-42 E value 130 Match length 66 % identity (AL022223) receptor protein kinase-like protein NCBI Description [Arabidopsis thaliana] 310190 Seq. No. uC-zmrob73058f04a1 Seq. ID BLASTN Method g902585 NCBI GI 39 BLAST score 1.0e-12 E value 175 Match length % identity 81 Zea mays clone MubG9 ubiquitin gene, complete cds NCBI Description 310191 Seq. No. uC-zmrob73058f05a1 Seq. ID BLASTX Method q4218120 NCBI GI 187 BLAST score 4.0e-14 E value 87 Match length 37 % identity (AL035353) Proline-rich APG-like protein [Arabidopsis NCBI Description thaliana] 310192 Seq. No. uC-zmrob73058h07a1 Seq. ID BLASTN Method g22430 NCBI GI 40 BLAST score 4.0e-13 E value 88 Match length 86 % identity Maize pseudo-Gpa2 pseudogene for glyceraldehyde-3-phosphate NCBI Description dehydrogenase subunit A 310193 Seq. No. uC-zmrob73059a10a1 Seq. ID BLASTX Method NCBI GI q2347188 208 BLAST score E value 1.0e-16 Match length 51 73 % identity

(AC002338) laccase isolog [Arabidopsis thaliana]

>gi 3150401 (AC004165) putative laccase [Arabidopsis



55 m

```
Seq. No.
                  uC-zmrob73059b04a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3617770
BLAST score
                  210
E value
                  1.0e-16
                  83
Match length
% identity
                  (Y14329) threonyl-tRNA synthetase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  310195
                  uC-zmrob73059d09a1
Seq. ID
                  BLASTX
Method
NCBI GI
                   g3421109
BLAST score
                  277
E value
                   1.0e-24
Match length
                  72
% identity
                   (AF043533) 20S proteasome beta subunit PBC2 [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   310196
                   uC-zmrob73059h01a1
Seq. ID
                   BLASTX
Method
                   g2252851
NCBI GI
                   244
BLAST score
E value
                   6.0e-21
                   91
Match length
% identity
                  (AF013294) No definition line found [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   310197
                   uC-zmrob73060b03a1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4322331
BLAST score
                   225
E value
                   2.0e-18
Match length
                   169
% identity
                   (AF081514) geranylgeranyl diphosphate synthase [Taxus
NCBI Description
                   canadensis]
Seq. No.
                   310198
                   uC-zmrob73060c04a1
Seq. ID
                   BLASTN
Method
                   g168434
NCBI GI
BLAST score
                   73
                   3.0e-33
E value
                   85
Match length
                   96
% identity
                  Z.mays catalase isozyme 3 (CAT-3) mRNA, complete cds
NCBI Description
Seq. No.
                   310199
                   uC-zmrob73060e10a1
Seq. ID
```

44181

BLASTN

g22320

87

Method

NCBI GI BLAST score



```
E value
                   1.0e-41
Match length
                  184
                  86
% identity
NCBI Description Maize H1 mRNA for H1 histone
                  310200
Seq. No.
Seq. ID
                  uC-zmrob73060f04a1
Method
                  BLASTX
                  q2911082
NCBI GI
BLAST score
                  302
E value
                  2.0e-27
                  104
Match length
% identity
```

NCBI Description (AL021960) hypothetical protein [Arabidopsis thaliana]

Seq. No. 310201 uC-zmrob73060f12a1 Seq. ID Method BLASTX NCBI GI q4249386 BLAST score 585 E value 1.0e-60 Match length 170 % identity 66

(AC005966) Strong similarity to gb_AF061286 gamma-adaptin 1 NCBI Description from Arabidopsis thaliana. EST gb H37393 comes from this

gene. [Arabidopsis thaliana]

310202 Seq. No.

uC-zmrob73060h07a1 Seq. ID

Method BLASTX NCBI GI g2961377 BLAST score 187 1.0e-14 E value Match length 47 % identity 68

NCBI Description (AL022141) putative receptor protein kinase [Arabidopsis

thaliana]

310203

Seq. No. Seq. ID uC-zmrob73061a09a1

Method BLASTN NCBI GI g22330 BLAST score 100 4.0e-49 E value Match length 140 % identity 93

NCBI Description Z.mays Zmhoxla mRNA for homeobox protein

Seq. No. 310204

Seq. ID uC-zmrob73061f05a1

Method BLASTN NCBI GI g22292 BLAST score 135 4.0e-70 E value Match length 195 92 % identity

NCBI Description Z.mays mRNA for glycine-rich protein

Method

NCBI GI

BLASTN

g507844



```
310205
Seq. No.
                  uC-zmrob73062d12a1
Seq. ID
                  BLASTN
Method
                  g2239257
NCBI GI
                  108
BLAST score
                  5.0e-54
E value
Match length
                  176
                  90
% identity
                  Zea mays mRNA for cinnamyl alcohol dehydrogense
NCBI Description
                  310206
Seq. No.
                  uC-zmrob73064b09a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4063750
BLAST score
                  415
                  1.0e-40
E value
                  131
Match length
% identity
                   60
                  (AC005851) putative indole-3-acetate
NCBI Description
                  beta-glucosyltransferase synthetase [Arabidopsis thaliana]
                  310207
Seq. No.
                  uC-zmrob73064b11a1
Seq. ID
                  BLASTX
Method
                  g3759184
NCBI GI
                  231
BLAST score
                  2.0e-19
E value
Match length
                  52
                  81
% identity
NCBI Description (AB018441) phi-1 [Nicotiana tabacum]
                   310208
Seq. No.
                  uC-zmrob73064d01a1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3242708
BLAST score
                   352
                   1.0e-34
E value
Match length
                   131
% identity
                   62
                   (AC003040) putative serine/threonine protein kinase
NCBI Description
                   [Arabidopsis thaliana]
                   310209
Seq. No.
                   uC-zmrob73064d09a1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g168508
BLAST score
                   54
E value
                   2.0e-21
Match length
                   106
% identity
                   89
NCBI Description Maize oleosin KD18 (KD18; L2) gene, complete cds
                   310210
Seq. No.
                   uC-zmrob73064e08a1
Seq. ID
```

44183



```
BLAST score
                   3.0e-41
E value
Match length
                   204
                   85
% identity
```

NCBI Description Zea mays A188 retrotransposon gag gene, complete cds

310211 Seq. No.

uC-zmrob73064g02a1 Seq. ID

BLASTX Method NCBI GI g4249410 266 BLAST score 3.0e-23 E value 122 Match length 47 % identity

(AC006072) unknown protein [Arabidopsis thaliana] NCBI Description

Seq. No.

310212 uC-zmrob73066a07b1 Seq. ID

BLASTX Method NCBI GI g3152598 BLAST score 204 7.0e-16 E value

58 Match length 67 % identity

(AC002986) Contains similarity to C2-HC type zinc finger NCBI Description

protein C.e-MyT1 gb_U67079 from C. elegans and to

hypersensitivity-related gene 201 isolog T28M21.14 from A.

thaliana BAC gb_AF002109. [Arabidopsis thaliana]

310213 Seq. No.

uC-zmrob73066a08b1 Seq. ID

Method BLASTX q3309575 NCBI GI 284 BLAST score 3.0e-25 E value 96 Match length 58

% identity (AF060553) calcium sensor homolog [Arabidopsis thaliana] NCBI Description

>gi_4538989_emb_CAB39731.1_ (Y18870) CBL4 protein

[Arabidopsis thaliana]

310214 Seq. No.

uC-zmrob73066c07b1 Seq. ID

BLASTX Method g3128220 NCBI GI 199 BLAST score 3.0e-15 E value 40 Match length 93 % identity

(AC004077) putative urease accessory protein [Arabidopsis NCBI Description

thaliana] >gi_3337375 (AC004481) putative urease accessory

protein [Arabidopsis thaliana]

310215 Seq. No.

uC-zmrob73066c10b1 Seq. ID

BLASTX Method NCBI GI g3915054



```
192
BLAST score
                  8.0e-29
E value
                  141
Match length
% identity
                  53
                  SUCROSE SYNTHASE 3 (SUCROSE-UDP GLUCOSYLTRANSFERASE 3)
NCBI Description
                  >gi_1196837 (L03366) sucrose synthase 3 [Oryza sativa]
                  >gi_1587663_prf _2207194B sucrose synthase:ISOTYPE=3 [Oryza
                  satīva]
                  310216
Seq. No.
                  uC-zmrob73066e09b1
Seq. ID
                  BLASTX
Method
                  g1549376
NCBI GI
BLAST score
                  274
                  4.0e-24
E value
Match length
                  170
% identity
                  42
NCBI Description (U62616) putative protein [Synechococcus PCC7942]
                  310217
Seq. No.
                  uC-zmrob73066f01b1
Seq. ID
                  BLASTX
Method
                   g585960
NCBI GI
                  153
BLAST score
                   8.0e-10
E value
                   40
Match length
                   78
% identity
                   PROTEIN TRANSPORT PROTEIN SEC61 BETA SUBUNIT
NCBI Description
                   >gi 433665_emb_CAA81412_ (Z26753) Sec61 beta-subunit
                   homolog [Arabidopsis thaliana]
                   310218
Seq. No.
                   uC-zmrob73066f08b1
Seq. ID
                   BLASTX
Method
                   g1710521
NCBI GI
                   265
BLAST score
                   6.0e-29
E value
                   109
Match length
                   66
% identity
                   60S RIBOSOMAL PROTEIN L24 >gi 1154859 emb_CAA63960_
NCBI Description
                   (X94296) L24 ribosomal protein [Hordeum vulgare]
                   310219
Seq. No.
                   uC-zmrob73066h05b1
Seq. ID
                   BLASTX
Method
                   g2961285
NCBI GI
                   186
BLAST score
                   7.0e-14
E value
                   95
Match length
                   43
 % identity
                   (Y16848) cinnamyl alcohol dehydrogenase-like protein,
NCBI Description
                   subunit b [Arabidopsis thaliana]
```

Seq. No. 310220

Seq. ID uC-zmrob73068a02b1

Method BLASTX NCBI GI g3242717



```
BLAST score
                  3.0e-19
E value
                  142
Match length
                  42
% identity
NCBI Description (AC003040) putative APG protein [Arabidopsis thaliana]
Seq. No.
                  310221
Seq. ID
                  uC-zmrob73068a12b1
Method
                  BLASTX
                  g1707642
NCBI GI
BLAST score
                  178
E value
                  6.0e-13
Match length
                  82
                  48
% identity
NCBI Description (Y07748) TMK [Oryza sativa]
                  310222
Seq. No.
Seq. ID
                  uC-zmrob73068b06b1
Method
                  BLASTN
                  q4185305
NCBI GI
BLAST score
                  103
                   9.0e-51
E value
Match length
                   279
                   84
% identity
                  Zea mays cosmid IV.1E1 22-kDa alpha zein protein 21
NCBI Description
                   (sz22-21) gene, complete cds; retrotransposon Opie-2 gag
                  protein, polyprotein, and copia protein genes, complete
                  cds; and unknown genes
Seq. No.
                   310223
                   uC-zmrob73068b07b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3004565
                   253
BLAST score
                   4.0e-36
E value
                   154
Match length
% identity
                   (AC003673) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                   310224
Seq. No.
Seq. ID
                   uC-zmrob73068c09b1
Method
                   BLASTX
NCBI GI
                   g2465923
BLAST score
                   226
E value
                   1.0e-18
Match length
                   140
                   41
% identity
                   (AF024648) receptor-like serine/threonine kinase
NCBI Description
                   [Arabidopsis thaliana]
                   310225
Seq. No.
```

uC-zmrob73068g11b1 Seq. ID

Method BLASTX NCBI GI q1491776 225 BLAST score 3.0e-21E value 82 Match length

NCBI Description



```
% identity
                   (M37636) cationic peroxidase [Arachis hypogaea]
NCBI Description
                   310226
Seq. No.
Seq. ID
                  uC-zmrob73071c02b1
Method
                  BLASTX
                   g2088656
NCBI GI
BLAST score
                   160
                   1.0e-10
E value
Match length
                   156
% identity
                   29
                   (AF002109) DNA-directed RNA polymerase II isolog
NCBI Description
                   [Arabidopsis thaliana]
                   310227
Seq. No.
Seq. ID
                   uC-zmrob73071c05b1
Method
                   BLASTX
NCBI GI
                   g1176658
BLAST score
                   147
E value
                   3.0e-09
Match length
                   134
% identity
                   33
                   HYPOTHETICAL 200.6 KD PROTEIN B0228.2 IN CHROMOSOME II
NCBI Description
                   >gi 726363 (U23168) No definition line found
                   [Caenorhabditis elegans]
                   310228
Seq. No.
Seq. ID
                   uC-zmrob73071g03b1
Method
                   BLASTX
NCBI GI
                   q4104060
BLAST score
                   352
                   3.0e-33
E value
Match length
                   113
% identity
                   62
NCBI Description
                   (AF031231) S222 [Triticum aestivum]
Seq. No.
                   310229
Seq. ID
                   uC-zmrob73071g10b1
Method
                   BLASTX
NCBI GI
                   g2062176
BLAST score
                   160
E value
                   5.0e-11
Match length
                   89
% identity
                   43
NCBI Description
                   (AC001645) Myb-related transcription activator (MybSt1)
                   isolog [Arabidopsis thaliana]
Seq. No.
                   310230
                   uC-zmrob73071h06b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1176658
BLAST score
                   153
E value
                   2.0e-13
Match length
                   127
% identity
                   43
                   HYPOTHETICAL 200.6 KD PROTEIN B0228.2 IN CHROMOSOME II
```

>gi 726363 (U23168) No definition line found



[Caenorhabditis elegans]

```
Seq. No.
                  310231
Seq. ID
                  uC-zmrob73075a06b1
Method
                  BLASTX
NCBI GI
                  q4567303
BLAST score
                  266
                  2.0e-23
E value
Match length
                 √68
% identity
                  74
NCBI Description (AC005956) unknown protein [Arabidopsis thaliana]
Seq. No.
                  310232
Seq. ID
                  uC-zmrob73075a10b1
Method
                  BLASTX
NCBI GI
                  q2980641
BLAST score
                  290
E value
                  4.0e-26
Match length
                  140
% identity
                  41
NCBI Description (Y11250) multi resistance protein [Arabidopsis thaliana]
Seq. No.
                  310233
Seq. ID
                  uC-zmrob73075e05b1
Method
                  BLASTX
NCBI GI
                  q1531760
BLAST score
                  169
E value
                  1.0e-19
Match length
                  94
% identity
                  49
                  (X97075) proline oxidase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  310234
                  uC-zmrob73075e07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4249419
BLAST score
                  336
                  1.0e-31
E value
Match length
                  92
% identity
                  64
                   (AC006072) hypothetical protein, 3' partial [Arabidopsis
NCBI Description
                  thaliana]
                  310235
Seq. No.
                  uC-zmrob73075f05b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1149569
BLAST score
                  651
                  2.0e-68
E value
Match length
                  154
% identity
                  83
NCBI Description
                  (Z50851) HD-zip [Arabidopsis thaliana]
                  310236
Seq. No.
                  uC-zmrob73075f06b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2511541
```

44188

>.



BLAST score 3.0e-34 E value Match length 90 % identity 87

(AF020787) DNA-binding protein GBP16 [Oryza sativa] NCBI Description

Seq. No. Seq. ID

310237 uC-zmrob73075g02b1

Method NCBI GI

BLASTN g3342803 126

BLAST score E value 2.0e-64 Match length 251 87 % identity

NCBI Description

Zea mays strain B73 putative 6-phosphogluconate

dehydrogenase mRNA, nuclear gene encoding putative plastid

protein, partial cds

Seq. No.

310238

Seq. ID uC-zmrob73075g07b1 Method BLASTX

NCBI GI q549063 BLAST score 161 E value 3.0e-14 Match length 73 % identity

TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP) NCBI Description

>gi 1072464 pir A38958 IgE-dependent histamine-releasing factor homolog - rice >gi 303835 dbj BAA02151 (D12626)

21kd polypeptide [Oryza sativa]

Seq. No.

310239

Seq. ID

uC-zmrob73075g11b1

Method BLASTX NCBI GI q3096919 BLAST score 488 E value 3.0e-49 Match length 126 % identity 79

(AL023094) putative serine/threonine protein kinase NCBI Description

[Arabidopsis thaliana]

Seq. No.

310240

Seq. ID

uC-zmrob73075h01b1

BLASTN Method g902585 NCBI GI 242 BLAST score 1.0e-133 E value 277 Match length 97 % identity

NCBI Description Zea mays clone MubG9 ubiquitin gene, complete cds

Seq. No.

310241

Seq. ID

uC-zmrob73075h04b1

BLASTX Method g2827536 NCBI GI BLAST score 162

```
E value
                  6.0e-11
Match length
                  77
% identity
                  39
NCBI Description (AL021633) hypothetical protein [Arabidopsis thaliana]
                  310242
Seq. No.
                  uC-zmrob73076a11b1
Seq. ID
                  BLASTX
Method
                  g3335366
NCBI GI
BLAST score
                  161
                  6.0e-11
E value
                  53
Match length
                  55
% identity
NCBI Description (AC003028) unknown protein [Arabidopsis thaliana]
Seq. No.
                  310243
                  uC-zmrob73076b06b1
Seq. ID
                  BLASTX
Method
                  g3043428
NCBI GI
                  214
BLAST score
E value
                  3.0e-17
                  106
Match length
% identity
                  43
NCBI Description (AJ005346) 40S ribosomal protein S5 [Cicer arietinum]
Seq. No.
                  310244
                  uC-zmrob73076b09b1
Seq. ID
                  BLASTX
Method
                  g1946265
NCBI GI
BLAST score
                  380
                  1.0e-36
E value
Match length
                  112
% identity
                  66
NCBI Description (Y11414) myb [Oryza sativa]
                  310245
Seq. No.
                  uC-zmrob73076b11b1
Seq. ID
                  BLASTX
Method
                  g3928543
NCBI GI
BLAST score
                   347
E value
                  1.0e-32
Match length
                  151
                   43
% identity
                  (AB016819) UDP-glucose glucosyltransferase [Arabidopsis
NCBI Description
                   thaliana]
```

Seq. No. 310246

Seq. ID uC-zmrob73076c04b1

Method BLASTX
NCBI GI g4115379
BLAST score 238
E value 6.0e-20
Match length 80
% identity 60

NCBI Description (AC005967) putative carbonyl reductase [Arabidopsis

thaliana]



```
310247
Seq. No.
Seq. ID
                  uC-zmrob73076e12b1
Method
                  BLASTX
NCBI GI
                  q1170937
BLAST score
                  322
                  2.0e-35
E value
                  82
Match length
                  95
% identity
                  S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
NCBI Description
                  ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                  >gi_450549_emb_CAA81481_ (Z26867) S-adenosyl methionine
                  synthetase [Oryza sativa]
                  310248
Seq. No.
                  uC-zmrob73076f12b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4191775
BLAST score
                  220
                  7.0e-18
E value
                   132
Match length
% identity
                   (AC005917) putative acyl-CoA cholesterol acyltransferase
NCBI Description
                   [Arabidopsis thaliana]
                   310249
Seq. No.
Seq. ID
                   uC-zmrob73076g09b1
Method
                   BLASTX
                   q4371296
NCBI GI
BLAST score
                   149
E value
                   2.0e-09
                   81
Match length
                   42
% identity
                   (AC006260) putative receptor protein kinase [Arabidopsis
NCBI Description
                   thaliana]
                   310250
Seq. No.
                   uC-zmrob73076h08b1
Seq. ID
                   BLASTX
Method
                   q118104
NCBI GI
                   461
BLAST score
                   3.0e-68
E value
Match length
                   143
% identity
                   90
                   PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE)
NCBI Description
                   (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN)
                   >gi_68408_pir__CSZM peptidylprolyl isomerase (EC 5.2.1.8) -
                   maize >gi_168461 (M55021) cyclophilin [Zea mays]
                   >gi 829148_emb_CAA48638_ (X68678) cyclophilin [Zea mays]
                   310251
Seq. No.
                   uC-zmrob73076h09b1
Seq. ID
Method
                   BLASTX
                   g3080389
NCBI GI
                   267
BLAST score
```

2.0e-23

56

88

E value

Match length % identity



NCBI Description (AL022603) putative membrane associated protein

[Arabidopsis thaliana]

Seq. No. 310252

Seq. ID uC-zmrob73077a01b1

Method BLASTX
NCBI GI g1171579
BLAST score 234
E value 2.0e-19
Match length 71
% identity 61

NCBI Description (X95342) cytochrome P450 [Nicotiana tabacum]

Seq. No. 310253

Seq. ID uC-zmrob73077a04b1

Method BLASTX
NCBI GI g100490
BLAST score 651
E value 2.0e-68
Match length 140
% identity 27

NCBI Description polyubiquitin - garden snapdragon (fragment)

>gi 16071 emb CAA48140 (X67957) ubiquitin [Antirrhinum

majus]

Seq. No. 310254

Seq. ID uC-zmrob73077b07b1

Method BLASTX
NCBI GI g4262162
BLAST score 338
E value 1.0e-31
Match length 129
% identity 48

NCBI Description (AC005275) putative glycosylation enzyme [Arabidopsis

thaliana]

Seq. No. 310255

Seq. ID uC-zmrob73077c01b1

Method BLASTX
NCBI GI g282994
BLAST score 550
E value 2.0e-56
Match length 142
% identity 78

NCBI Description Sip1 protein - barley >gi_167100 (M77475) seed imbibition

protein [Hordeum vulgare]

Seq. No. 310256

Seq. ID uC-zmrob73077d04b1

Method BLASTX
NCBI GI g4006829
BLAST score 605
E value 6.0e-63
Match length 154
% identity 75

NCBI Description (AC005970) putative protein kinase [Arabidopsis thaliana]



```
310257
Seq. No.
                  uC-zmrob73077d07b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g312180
BLAST score
                  40
                  5.0e-13
E value
                  56
Match length
                  93
% identity
                  Z.mays GapC4 gene
NCBI Description
Seq. No.
                  310258
                  uC-zmrob73077e05b1
Seq. ID
                  BLASTX
Method
                   g3056595
NCBI GI
BLAST score
                   190
E value
                   6.0e-15
Match length
                   141
% identity
                   38
                  (AC004255) T1F9.16 [Arabidopsis thaliana]
NCBI Description
                   310259
Seq. No.
Seq. ID
                   uC-zmrob73077g01b1
Method
                   BLASTX
NCBI GI
                   g1171579
BLAST score
                   471
E value
                   2.0e-47
Match length
                   126
                   69
% identity
                  (X95342) cytochrome P450 [Nicotiana tabacum]
NCBI Description
                   310260
Seq. No.
                   uC-zmrob73078a02b1
Seq. ID
                   BLASTX
Method
                   g4490301
NCBI GI
                   156
BLAST score
                   2.0e-10
E value
Match length
                   64
                   44
% identity
                  (AL035678) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   310261
Seq. No.
                   uC-zmrob73078a08b1
Seq. ID
                   BLASTX
Method
                   g282881
NCBI GI
                   453
BLAST score
                   5.0e-45
E value
                   154
Match length
                   56
% identity
                   receptor-like protein kinase precursor - Arabidopsis
NCBI Description
                   thaliana >gi_166846 (M84658) receptor-like protein kinase
                   [Arabidopsis thaliana]
                   310262
Seq. No.
```

uC-zmrob73078a09b1 Seq. ID

Method BLASTX NCBI GI g2739008 BLAST score 181



```
2.0e-13
E value
Match length
                  72
% identity
                  43
NCBI Description (AF022463) CYP78A3p [Glycine max]
Seq. No.
                  310263
                  uC-zmrob73078a10b1
Seq. ID
Method .
                  BLASTX
NCBI GI
                  g2505874
BLAST score
                  475
                  1.0e-47
E value
Match length
                  121
                  76
% identity
NCBI Description (Y12776) putative kinase [Arabidopsis thaliana]
                  310264
Seq. No.
                  uC-zmrob73078c10b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4539386
BLAST score
                  345
                  2.0e-32
E value
Match length
                  109
                  59
% identity
NCBI Description (AL035526) extensin-like protein [Arabidopsis thaliana]
                  310265
Seq. No.
                  uC-zmrob73078d07b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2239259
BLAST score
                  105
E value
                  5.0e-52
Match length
                  269
                  85
% identity
NCBI Description Zea mays mRNA for cinnamoyl CoA reductase
Seq. No.
                  310266
Seq. ID
                  uC-zmrob73078q10b1
Method
                  BLASTX
NCBI GI
                  g2920654
BLAST score
                  249
E value
                  6.0e-22
Match length
                  111
% identity
                  58
                  (AF047697) putative high-pI laccase [Oryza sativa]
NCBI Description
                  310267
Seq. No.
                  uC-zmrob73078h03b1
Seq. ID
```

Method BLASTX NCBI GI q4510345 BLAST score 150 E value 1.0e-09 Match length 57 % identity 47

NCBI Description (AC006921) unknown protein [Arabidopsis thaliana]

310268 Seq. No.

uC-zmrob73078h10b1 Seq. ID



```
Method
                  BLASTX
                  g625973
NCBI GI
BLAST score
                  212
E value
                  5.0e-17
                  114
Match length
                  46
% identity
                  disease resistance protein RPS2 - Arabidopsis thaliana
NCBI Description
                  >gi 548086 (U14158) RPS2 [Arabidopsis thaliana] >gi_549979
                  (U12860) RPS2 [Arabidopsis thaliana]
                  >gi_4538938_emb_CAB39674.1_ (AL049483) disease resistance
                  protein RPS2 [Arabidopsis thaliana]
                  310269
Seq. No.
                  uC-zmrob73078h11b1
Seq. ID
```

Seq. ID uC-zmrob73078h11

Method BLASTX

NCBI GI g3811007

BLAST score 193

E value 1.0e-14

Match length 83

% identity 52

NCBI Description (AB019327) NADP specific isocitrate dehydrogenase [Daucus

4.

carota]

Seq. No. 310270

Seq. ID uC-zmrob73079b04b1

Method BLASTX
NCBI GI g3522937
BLAST score 204
E value 5.0e-16
Match length 77
% identity 49

NCBI Description (AC004411) unknown protein [Arabidopsis thaliana]

Seq. No. 310271

Seq. ID uC-zmrob73079c04b1

Method BLASTX
NCBI GI g2598575
BLAST score 375
E value 5.0e-36
Match length 136
% identity 56

NCBI Description (Y15293) MtN21 [Medicago truncatula]

Seq. No. 310272

Seq. ID uC-zmrob73079f04b1

Method BLASTX
NCBI GI g3355308
BLAST score 292
E value 3.0e-26
Match length 150
% identity 45

NCBI Description (AJ009695) wall-associated kinase 4 [Arabidopsis thaliana]

Seq. No. 310273

Seq. ID uC-zmrob73079f07b1

Method BLASTX NCBI GI g585661

E value

Match length

70

```
BLAST score
                  1.0e-53
E value
                  132
Match length
                  74
% identity
NCBI Description PEROXIDASE PRECURSOR >gi_287401_dbj_BAA03644_ (D14997)
                  peroxidase [Oryza sativa]
                  310274
Seq. No.
                  uC-zmrob73079h02b1
Seq. ID
                  BLASTX
Method
                  q1206013
NCBI GI
BLAST score
                  442
                   6.0e-44
E value
                  131
Match length
% identity
                  (U44087) beta-D-glucosidase precursor [Zea mays]
NCBI Description
                   310275
Seq. No.
                   uC-zmrob73080a04b1
Seq. ID
                   BLASTX
Method
                   g135398
NCBI GI
BLAST score
                   497
                   2.0e-50
E value
                   98
Match length
                   94
% identity
                   TUBULIN ALPHA-1 CHAIN >gi_82731_pir _S15773 tubulin alpha-1
NCBI Description
                   chain - maize >gi_22147_emb_CAA33734_ (X15704)
                   alphal-tubulin [Zea mays]
                   310276
Seq. No.
                   uC-zmrob73080a06b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3643596
                   252
BLAST score
                   8.0e-22
E value
                   95
Match length
% identity
                  (AC005395) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   310277
Seq. No.
                   uC-zmrob73080e01b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2252844
BLAST score
                   159
                   3.0e-23
E value
Match length
                   82
                   71
 % identity
                   (AF013293) belongs to the cytochrome p450 family
NCBI Description
                   [Arabidopsis thaliana]
                   310278
 Seq. No.
                   uC-zmrob73080f01b1
 Seq. ID
                   BLASTX
Method
                   g3746060
NCBI GI
                   324
BLAST score
                   5.0e-30
```

% identity (AC005311) unknown protein [Arabidopsis thaliana] NCBI Description 310279 Seq. No. uC-zmrob73080f02b1 Seq. ID BLASTX Method g3687250 NCBI GI 150 BLAST score 1.0e-09 E value 119 Match length 38 % identity (AC005169) putative arginine n-methyltransferase NCBI Description [Arabidopsis thaliana] Seq. No. 310280 uC-zmrob73080g04b1 Seq. ID BLASTX Method q2935342 NCBI GI BLAST score 164 2.0e-11 E value Match length 49 57 % identity (AF044216) steroid 22-alpha-hydroxylase; DWF4; CYP90B1 NCBI Description [Arabidopsis thaliana] Seq. No. 310281 uC-zmrob73080g08b1 Seq. ID Method BLASTX NCBI GI q4587525 177 BLAST score 1.0e-12 E value Match length 80 42 % identity (AC007060) Contains the PF_00650 CRAL/TRIO NCBI Description phosphatidyl-inositol-transfer protein domain. ESTs

phosphatidyl-inositol-transfer protein domain. ESTs gb_T76582, gb_N06574 and gb_Z25700 come from this gene.

[Arabidopsis thaliana]

Seq. No. 310282

Seq. ID uC-zmrob73080h06b1

Method BLASTX
NCBI GI g2213615
BLAST score 287
E value 1.0e-25
Match length 138
% identity 46

NCBI Description (AC000103) F21J9.9 [Arabidopsis thaliana]

Seq. No. 310283

Seq. ID uC-zmrob73080h10b1

Method BLASTX
NCBI GI g4415934
BLAST score 323
E value 7.0e-30
Match length 130
% identity 51

NCBI Description (AC006418) putative auxin response factor 1 [Arabidopsis



thaliana]

```
Seq. No.
                  310284
Seq. ID
                  uC-zmromo17006h04a1
Method
                  BLASTX
                  g3096935
NCBI GI
BLAST score
                  209
E value
                  1.0e-16
Match length
                  72
% identity
                  61
                  (AL023094) putative protein [Arabidopsis thaliana]
NCBI Description
                  310285
Seq. No.
Seq. ID
                  uC-zmromo17007a01a1
Method
                  BLASTN
NCBI GI
                  g433037
BLAST score
                  87
E value
                  2.0e-41
Match length
                  246
% identity
                  88
NCBI Description
                  Zea mays W-22 clone cDNA4 retroelement PREM-1-containing
                  310286
Seq. No.
Seq. ID
                  uC-zmromo17007a04a1
Method
                  BLASTX
NCBI GI
                  g4098250
BLAST score
                  166
                  9.0e-12
E value
Match length
                  40
% identity
                  72
NCBI Description
                  (U76611) similar to Solanum tuberosum ci21A gene product
                  encoded by the sequence presented in GenBank Accession
                  Number U76610 [Solanum tuberosum]
Seq. No.
                  310287
                  uC-zmromo17007b01a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1498053
BLAST score
                  248
E value
                  4.0e-21
Match length
                  48
% identity
                  100
NCBI Description (U64436) ribosomal protein S8 [Zea mays]
Seq. No.
                  310288
                  uC-zmromo17007f02a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g475252
BLAST score
                  81
                  4.0e-38
E value
Match length
                  125
% identity
                  91
NCBI Description Z.mays MPI gene
```

Seq. No. 310289

Seq. ID uC-zmromo17008a10a1



38 4.0e-12

- 74

E value Match length

```
BLASTN
Method
NCBI GI
                  g435542
BLAST score
                  126
E value
                  1.0e-64
Match length
                  134
                  99
% identity
NCBI Description Z.mays mRNA for calmodulin
                  310290
Seq. No.
                  uC-zmromo17008c09a1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g1491773
BLAST score
                  37
                  1.0e-11
E value
Match length
                  61
% identity
                  90
                  Z.mays mRNA for cysteine proteinase, See1
NCBI Description
                  310291
Seq. No.
                  uC-zmromo17009a01a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4263775
BLAST score
                  144
E value
                  3.0e-09
Match length
                  36
% identity
                  72
                  (AC006068) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  310292
                  uC-zmromo17009a07a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3822225
BLAST score
                  288
                  8.0e-26
E value
                  106
Match length
% identity
                  50
                  (AF079183) RING-H2 finger protein RHG1a [Arabidopsis
NCBI Description
                  thaliana]
                  310293
Seq. No.
                  uC-zmromo17009a09a1
Seq. ID
Method
                  BLASTN
                  g3342801
NCBI GI
BLAST score
                  59
E value
                  1.0e-24
Match length
                  174
% identity
                  84
                  Zea mays strain W64A x A182E putative cytosolic
NCBI Description
                  6-phosphogluconate dehydrogenase (pdh2) mRNA, complete cds
Seq. No.
                  310294
                  uC-zmromo17009c06a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1848280
BLAST score
```



```
% identity
                  Sorghum bicolor membrane intrinsic protein (Mip1) mRNA,
NCBI Description
                  partial cds
                  310295
Seq. No.
                  uC-zmromo17009e07a1
Seq. ID
                  BLASTX
Method
                  g1945609
NCBI GI
BLAST score
                  240
                  3.0e-20
E value
                  127
Match length
                  42
% identity
                  (AB003102) 26S proteasome subunit p44.5 [Homo sapiens]
NCBI Description
Seq. No.
                  310296
                  uC-zmromo17010d11a1
Seq. ID
                  BLASTX
Method
                  q1076579
NCBI GI
                  187
BLAST score
                   5.0e-14
E value
Match length
                  53
                   60
% identity
                  alcohol dehydrogenase homolog ADH3a - tomato
NCBI Description
                   310297
Seq. No.
                  uC-zmromo17010g04a1
Seq. ID
Method
                  BLASTX
                   g3335366
NCBI GI
                   160
BLAST score
                   7.0e-11
E value
Match length
                   48
                   69
% identity
                  (AC003028) unknown protein [Arabidopsis thaliana]
NCBI Description
                   310298
Seq. No.
                   uC-zmromo17011a06a1
Seq. ID
                   BLASTX
Method
                   g4455366
NCBI GI
BLAST score
                   158
                   1.0e-10
E value
Match length
                   40
                   78
% identity
                  (AL035524) putative protein [Arabidopsis thaliana]
NCBI Description
                   310299
Seq. No.
                   uC-zmromo17011b12a1
Seq. ID
Method
                   BLASTX
                   g262391
NCBI GI
BLAST score
                   421
```

1.0e-41 E value Match length 91 85 % identity

NCBI Description Rig homolog [human, brain, Peptide Partial, 135 aa]

310300 Seq. No.

Seq. ID uC-zmromo17011c08a1

Method BLASTN

```
g433044
NCBI GI
BLAST score
                   112
                   3.0e-56
E value
Match length
                   179
 % identity
                   91
                   Zea mays W-22 clone PREM-1D retroelement PREM-1, partial
NCBI Description
                   sequence
Seq. No.
                   310301
                   uC-zmromo17011d03a1
Seq. ID
                   BLASTX
Method
                   g132935
NCBI GI
BLAST score
                   294
                   1.0e-26
E value
Match length
                   98
 % identity
                   56
                   60S RIBOSOMAL PROTEIN L37A (YL37) (RP47)
- NCBI Description
                   >gi 101568 pir S18431 ribosomal protein L35a.e.c16 - yeast
                   (Saccharomyces cerevisiae) >gi 4392 emb CAA41035 (X57969)
                   ribosomal protein L37a [Saccharomyces cerevisiae]
                   >qi 1244773 (U43703) Lpi4p [Saccharomyces cerevisiae]
                   >qi 1370305 emb CAA97847 (Z73499) ORF YPL143w
                   [Saccharomyces cerevisiae]
                   310302
 Seq. No.
 Seq. ID
                   uC-zmromo17017h06a1
Method
                   BLASTX
NCBI GI
                   g2213632
BLAST score
                   348
E value
                   3.0e - 33
Match length
                   95
 % identity
                   66
                   (AC000103) F21J9.24 [Arabidopsis thaliana]
 NCBI Description
                   310303
 Seq. No.
                   uC-zmromo17023b06a1
 Seq. ID
Method
                   BLASTN
 NCBI GI
                   g433038
 BLAST score
                   72
                   2.0e-32
 E value
Match length
                   205
 % identity
                   83
                   Zea mays W-22 clone cDNA7 retroelement PREM-1-containing
 NCBI Description
 Seq. No.
                   310304
                   uC-zmromo17023f08a1
 Seq. ID
 Method
                   BLASTN
 NCBI GI
                   g4416300
 BLAST score
                   67
 E value
                   3.0e-29
```

Match length 146 44

% identity

Zea mays chromosome 4 22 kDa zein-associated intercluster NCBI Description

region, complete sequence

Seq. No. 310305



```
uC-zmromo17025c02a1
Seq. ID
Method
                   BLASTX
                   g3386596
NCBI GI
BLAST score
                   180
                   1.0e-13
E value
Match length
                   51
% identity
                   (AC004665) unknown protein [Arabidopsis thaliana]
NCBI Description
                   >gi 3702346 (AC005397) unknown protein [Arabidopsis
                   thaliana]
                   310306
Seq. No.
Seq. ID
                   uC-zmromo17026d05a1
Method
                   BLASTN
NCBI GI
                   g4514634
BLAST score
                   129
E value
                   2.0e-66
Match length
                   157
% identity
                   96
NCBI Description Zea mays ZmRCP1 mRNA for root cap protein 1, complete cds
Seq. No.
                   310307
Seq. ID
                   uC-zmromo17027c04a1
Method
                   BLASTX
NCBI GI
                   g549063
BLAST score
                   148
E value
                   1.0e-09
Match length
                   38
% identity
                   74
                   TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)
NCBI Description
                   >gi 1072464 pir A38958 IgE-dependent histamine-releasing
                   factor homolog - rice >gi 303835 dbj BAA02151 (D12626)
                   21kd polypeptide [Oryza sativa]
                   310308
Seq. No.
Seq. ID
                   uC-zmromo17027h01a1
Method
                   BLASTN
NCBI GI
                   g639494
                   56
BLAST score
E value
                   8.0e-23
Match length
                   120
% identity
                   45
                   Zea mays Mu3 transposon in alcohol dehydrogenase (adh1)
NCBI Description
                   gene
Seq. No.
                   310309
                   uC-zmromo17028c07a1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g22292
BLAST score
                   62
E value
                   9.0e-27
Match length
                   102
% identity
                   90
```

Seq. No. 310310

Seq. ID uC-zmromo17028f04a1

NCBI Description Z.mays mRNA for glycine-rich protein



```
Method
                   BLASTN
NCBI GI
                   g2997588
BLAST score
                   67
                   1.0e-29
E value
                   135
Match length
                   87
% identity
```

Zea mays glucose-6-phosphate/phosphate-translocator NCBI Description precursor (qpt) mRNA, nuclear gene encoding plastid

protein, complete cds

```
310311
Seq. No.
```

uC-zmromo17029d01a1 Seq. ID

Method BLASTX NCBI GI g4506621 BLAST score 324 3.0e-30 E value Match length 87 75 % identity

ribosomal protein L26 >gi 400990 sp Q02877_RL26_HUMAN 60S NCBI Description

RIBOSOMAL PROTEIN L26 >gi 423068 pir S33713 ribosomal protein L26 - human >gi 1071990 pir S48864 gene L26 protein - mouse >gi 36115 emb CAA49189 (X69392) ribosomal

protein L26 [Homo sapiens] >gi_565624_emb_CAA56716_

(X80699) L26 [Mus musculus]

Seq. No. 310312

uC-zmromo17029e02a1 Seq. ID

BLASTN Method g1574937 NCBI GI BLAST score 35 3.0e-10 E value Match length 72 88 % identity

Zea mays superoxide dismutase 4 (sod4) gene, partial cds NCBI Description

Seq. No. 310313

uC-zmromo17029e06a1 Seq. ID

Method BLASTN g1845196 NCBI GI BLAST score 71 E value 8.0e-32 Match length 234

89 % identity

NCBI Description Z.mays mRNA for HMGc2 protein

Seq. No. 310314

uC-zmromo17029e07a1 Seq. ID

Method BLASTN NCBI GI g3318612 BLAST score 45 E value 2.0e-16 Match length 122 % identity 83

Zea mays mRNA for mitochondrial phosphate transporter, NCBI Description

complete cds

Seq. No. 310315



```
uC-zmromo17030h10a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3776573
BLAST score
                  185
                  5.0e-14
E value
Match length
                  51
% identity
                  61
NCBI Description
                  (AC005388) Similar to nodulins and lipase homolog F14J9.5
                  gi_3482914 from Arabidopsis thaliana BAC gb_AC003970.
                  Alternate first exon from 72258 to 72509. [Arabidopsis
                  thaliana]
Seq. No.
                  310316
                  uC-zmromo17031e03a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3868758
BLAST score
                  260
E value
                  2.0e-22
Match length
                  53
% identity
                  92
NCBI Description
                  (D89802) elongation factor 1B gamma [Oryza sativa]
Seq. No.
                  310317
Seq. ID
                  uC-zmromo17055h05a1
Method
                  BLASTN
                  g168508
NCBI GI
BLAST score
                  50
E value
                  2.0e-19
Match length
                  74
% identity
                  93
NCBI Description Maize oleosin KD18 (KD18; L2) gene, complete cds
Seq. No.
                  310318
                  uC-zmromo17067c12a1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g998429
BLAST score
                  110
E value
                  3.0e-55
Match length
                  211
% identity
                  96
                  GRF1=general regulatory factor [Zea mays, XL80, Genomic,
NCBI Description
                  5348 nt]
Seq. No.
                  310319
Seq. ID
                  uC-zmromo17067h09a1
Method
                  BLASTN
NCBI GI
                  q2668739
BLAST score
                  129
E value
                  1.0e-66
Match length
                  148
% identity
                  97
```

NCBI Description

Zea mays translation initiation factor GOS2 (TIF) mRNA,

complete cds

Seq. No.

310320

Seq. ID

uC-zmromo17068a01a1

Method

BLASTX



```
NCBI GI
                  q3334441
BLAST score
                  182
E value
                  2.0e-13
Match length
                  90
% identity
                  42
                  HYPOTHETICAL 47.9 KD PROTEIN T517.9 IN CHROMOSOME II
NCBI Description
                  >gi 2642161 (AC003000) hypothetical protein [Arabidopsis
                  thaliana]
                  310321
Seq. No.
                  uC-zmromo17068c07a1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2194117
BLAST score
                  168
E value
                  9.0e-12
Match length
                  76
% identity
                  39
                  (AC002062) Strong similarity to Arabidopsis receptor
NCBI Description
                  protein kinase PR5K (gb ATU48698). [Arabidopsis thaliana]
Seq. No.
                  310322
                  uC-zmromo17068d07a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g464621
BLAST score
                  160
E value
                  4.0e-11
Match length
                  57
% identity
NCBI Description
                  60S RIBOSOMAL PROTEIN L6 (YL16-LIKE) >qi 280374 pir S28586
                  ribosomal protein ML16 - common ice plant
                  >qi 19539 emb CAA49175 (X69378) ribosomal protein YL16
                  [Mesembryanthemum crystallinum]
                  310323
Seq. No.
                  uC-zmromo17068h05a1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g596079
BLAST score
                  70
                  3.0e-31
E value
Match length
                  160
% identity
                  87
NCBI Description
                  Zea mays thiamine biosynthetic enzyme (thi1-2) mRNA,
                  complete cds
Seq. No.
                  310324
                  uC-zmromo17071b02a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2914700
BLAST score
                  146
E value
                  3.0e-09
Match length
                  39
% identity
                  67
                  (AC003974) tRNA-processing protein SEN3-like [Arabidopsis
NCBI Description
```

Seq. No. 310325

Seq. ID uC-zmromo17071d02a1

thalianal



```
BLASTX
Method
                  g480450
NCBI GI
BLAST score
                  201
                  9.0e-16
E value
                  42
Match length
                  93
% identity
                  ketol-acid reductoisomerase (EC 1.1.1.86) - Arabidopsis
NCBI Description
                  thaliana >gi_402552_emb_CAA49506_ (X69880) ketol-acid
                  reductoisomerase [Arabidopsis thaliana]
                  310326
Seq. No.
                  uC-zmromo17072d08a1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4512651
BLAST score
                  234
                  1.0e-19
E value
                  82
Match length
                   45
% identity
                   (AC007048) putative tyrosine transaminase [Arabidopsis
NCBI Description
                  thaliana]
                   310327
Seq. No.
                  uC-zmromo17085c03a1
Seq. ID
                  BLASTN
Method
                   g236729
NCBI GI
                   103
BLAST score
                   7.0e-51
E value
Match length
                   143
                   93
% identity
                  metallothionein homologue [Zea mays, Genomic/mRNA, 1859 nt]
NCBI Description
                   310328
Seq. No.
                   uC-zmromo17085c05a1
Seq. ID
                   BLASTX
Method
                   g445612
NCBI GI
                   184
BLAST score
                   1.0e-13
E value
Match length
                   39
                   92
% identity
NCBI Description ribosomal protein S19 [Solanum tuberosum]
                   310329
Seq. No.
                   uC-zmromo17088e07a1
Seq. ID
                   BLASTN
Method
NCBI GI
                   q4185305
                   84
BLAST score
                   1.0e-39
E value
                   253
Match length
```

% identity

NCBI Description

Zea mays cosmid IV.1E1 22-kDa alpha zein protein 21 (sz22-21) gene, complete cds; retrotransposon Opie-2 gag protein, polyprotein, and copia protein genes, complete

cds; and unknown genes

Seq. No.

310330

Seq. ID

uC-zmromo17089f10a1

Method

BLASTN

Match length

% identity

120

39



```
g4160401
NCBI GI
BLAST score
                  45
                  3.0e-16
E value
Match length
                  124
                  85
% identity
NCBI Description Zea mays eIF-5 gene, exons 1-2
                  310331
Seq. No.
                  uC-zmromo17089g02a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4234852
BLAST score
                  378
                  2.0e-39
E value
                  91
Match length
% identity
                  96
                  (AF082133) gag-pol polyprotein [Zea mays]
NCBI Description
                  310332
Seq. No.
                  uC-zmromo17089g09a1
Seq. ID
                  BLASTN
Method
                  g1800218
NCBI GI
                  92
BLAST score
                  2.0e-44
E value
Match length
                  112
                  96
% identity
                  Sorghum bicolor phytochrome C (PHYC) mRNA, complete cds
NCBI Description
                  310333
Seq. No.
                  uC-zmromo17091a09a1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g626042
BLAST score
                  301
                  2.0e-27
E value
                  77
Match length
                  66
% identity
                  beta-glucosidase, root meristem (EC 3.2.1.-) precursor -
NCBI Description
                  maize >gi_435313_emb_CAA52293_ (X74217) beta-glucosidase
                   [Zea mays]
                   310334
Seq. No.
                  uC-zmromo17091b03a1
Seq. ID
Method
                  BLASTN
NCBI GI
                   g22292
                   173
BLAST score
E value
                   1.0e-92
Match length
                  262
% identity
                   92
NCBI Description Z.mays mRNA for glycine-rich protein
                   310335
Seq. No.
Seq. ID
                   uC-zmromo17096b02a1
Method ·
                  BLASTX
                   q1086989
NCBI GI
BLAST score
                   215
E value
                   2.0e-17
```



NCBI Description (S79323) plasma membrane H(+)-ATPase [Vicia faba, Otafuku, abaxial epidermis, guard cell protoplasts, Peptide, 963 aa] [Vicia faba]

Seq. No. 310336

Seq. ID uC-zmromo17096d01a1

Method BLASTN
NCBI GI g416148
BLAST score 65
E value 3.0e-28
Match length 208
% identity 82

NCBI Description Zea mays beta-7 tubulin (tub7) mRNA, complete cds

Seq. No. 310337

Seq. ID uC-zmromo17096d03a1

Method BLASTN
NCBI GI g3511235
BLAST score 34
E value 1.0e-09
Match length 70

Match length 70 % identity 87

NCBI Description Zea mays starch branching enzyme IIb (ae) gene, complete

يمئن

cds

Seq. No. 310338

Seq. ID uC-zmromo17098d10a1

Method BLASTN
NCBI GI g2529386
BLAST score 71
E value 6.0e-32
Match length 127
% identity 89

NCBI Description Zea mays triosephosphate isomerase 1 gene, exon 2-9 and

complete cds

Seq. No. 310339

Seq. ID uC-zmromo17100d05a1

Method BLASTN
NCBI GI g397395
BLAST score 53
E value 3.0e-21
Match length 133
% identity 85

NCBI Description Z.mays MNB1b mRNA for DNA-binding protein

Seq. No. 310340

Seq. ID uC-zmromo17102b07a1

Method BLASTN
NCBI GI g886820
BLAST score 75
E value 3.0e-34
Match length 189
% identity 83

NCBI Description Zea mays calcium-dependent protein kinase (MZECDPK2) mRNA,

complete cds

% identity

NCBI Description

81

```
Seq. No.
Seq. ID
                  uC-zmromo17104f03a1
Method
                  BLASTN
NCBI GI
                  q1657766
BLAST score
                  36
E value
                  3.0e-11
Match length
                  84
                  43
% identity
                  Zea mays retrotransposon Opie-2 5' LTR, primer binding
NCBI Description
                  site, gag gene, pol gene, complete cds, polypurine tract
                  and 3' LTR
Seq. No.
                  310342
Seq. ID
                  uC-zmromo17104g01a1
Method
                  BLASTN
NCBI GI
                  g3511235
BLAST score
                  46
E value
                  1.0e-16
Match length
                  50
% identity
                  98
NCBI Description
                  Zea mays starch branching enzyme IIb (ae) gene, complete
Seq. No.
                  310343
Seq. ID
                  uC-zmromo17112g08a1
Method
                  BLASTX
NCBI GI
                  q4416302
BLAST score
                  402
E value
                  3.0e-39
Match length
                  107
                  73
% identity
NCBI Description (AF105716) copia-type pol polyprotein [Zea mays]
Seq. No.
                  310344
Seq. ID
                  uC-zmromo17113g03a1
Method
                  BLASTN
NCBI GI
                  q899607
BLAST score
                  143
E value
                  8.0e-75
Match length
                  207
% identity
                  92
NCBI Description Zea mays polyubiquitin (MubC5) mRNA, complete cds
Seq. No.
                  310345
Seq. ID
                  uC-zmromo17114a10a1
Method
                  BLASTX
NCBI GI
                  g133902
BLAST score
                  292
                  2.0e-26
E value
Match length
                  64
```

protein S27 - rat >gi_57741_emb_CAA42019_ (X59375) ribosomal protein S27 [Rattus rattus]

>gi 4454712 gb AAD20974 (AF070668) 40S ribosomal protein

40S RIBOSOMAL PROTEIN S27 >gi_71056_pir__R3RT27 ribosomal

S27 isoform [Homo sapiens]



```
Seq. No.
                  310346
                  uC-zmromo17119g02a1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1076390
BLAST score
                  222
E value
                  3.0e-18
Match length
                  50
                  84
% identity
                  protein phosphatase 2A pDF2 - Arabidopsis thaliana
NCBI Description
                  >gi 683504 emb CAA57529 (X82003) protein phosphatase 2A 65
                  kDa regulatory subunit [Arabidopsis thaliana]
Seq. No.
                  310347
Seq. ID
                  uC-zmroteosinte001c07b1
Method
                  BLASTX
NCBI GI
                  q4204265
BLAST score
                  270-
E value
                  1.0e-23
Match length
                  71
% identity
                  73
NCBI Description
                  (AC005223) 45643 [Arabidopsis thaliana]
Seq. No.
                  310348
Seq. ID
                  uC-zmroteosinte001e05b1
Method
                  BLASTX
NCBI GI
                  q1352613
BLAST score
                  288
E value
                  8.0e-26
Match length
                  72
% identity
                  78
NCBI Description
                  OCS-ELEMENT BINDING FACTOR 1 (OCSBF-1)
                  >gi 444047 emb CAA44607 (X62745) ocs-binding factor 1 [Zea
                  mays]
Seq. No.
                  310349
Seq. ID
                  uC-zmroteosinte001f01b1
Method
                  BLASTX
NCBI GI
                  g2408051
BLAST score
                  344
E value
                  2.0e-32
Match length
                  157
% identity
                  40
NCBI Description
                  (Z99164) hypothetical protein [Schizosaccharomyces pombe]
Seq. No.
                  310350
                  uC-zmroteosinte001f07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4505417
BLAST score
                  242
E value
                  2.0e-20
Match length
                  121
% identity
                  44
NCBI Description
                  NAD(P)H menadione oxidoreductase 2, dioxin-inducible
                  >gi 107157 pir A32667 NAD(P)H dehydrogenase (quinone) (EC
```

oxidoreductase [Homo sapiens] >gi_516534 (U07736) quinone oxidoreductase2 [Homo sapiens]

1.6.99.2) 2 - human >gi_190818 (J02888) quinone

NCBI GI

BLAST score

g1019946

387

```
310351
Seq. No.
Seq. ID
                  uC-zmroteosinte001f12b1
Method
                  BLASTX
NCBI GI
                  q2623295
BLAST score
                  215
E value
                  3.0e-17
Match length
                  92
% identity
                  47
                  (AC002409) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  310352
Seq. No.
                  uC-zmroteosinte002b07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2342690
BLAST score
                   413
E value
                  2.0e-40
Match length
                  151
                   54
% identity
                   (AC000106) Similar to Homo copine I (gb U83246).
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   310353
                  uC-zmroteosinte002c01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q4544440
BLAST score
                   261
E value
                   4.0e-26
Match length
                   102
% identity
                   59
                  (AC006592) unknown protein [Arabidopsis thaliana]
NCBI Description
                   310354
Seq. No.
                   uC-zmroteosinte002g07b1
Seq. ID
Method
                  BLASTN
NCBI GI
                   g3057121
BLAST score
                   52
                   3.0e-20
E value
Match length
                   60
% identity
                   97
                  Zea mays starch synthase DULL1 (dull1) gene, partial cds
NCBI Description
                   310355
Seq. No.
                   uC-zmroteosinte003a09b1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g22378
BLAST score
                   37
                   3.0e-11
E value
Match length
                   124
                   84
% identity
NCBI Description Z.mays gene for nucleic acid binding protein
Seq. No.
                   310356
                   uC-zmroteosinte003c02b1
Seq. ID
Method
                   BLASTX
```

NCBI GI

E value

BLAST score

Match length

g3925233

1.0e-82

599

160



```
E value
                  2.0e-37
Match length
                  95
                  76
% identity
                  (U37060) ascorbate peroxidase [Gossypium hirsutum]
NCBI Description
Seq. No.
                  310357
                  uC-zmroteosinte003d01b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1750404
BLAST score
                  160
                  9.0e-11
E value
                  53
Match length
                  57
% identity
                  (U80953) Similar to 40S ribosomal protein S29; coded for by
NCBI Description
                  C. elegans cDNA cm10c2; coded for by C. elegans cDNA
                  yk61d8.5; coded for by C. elegans cDNA yk107e8.5; coded for
                  by C. elegans cDNA CEESF55F; coded for by C. elegans cDNA
                  yk107e8.3;
Seq. No.
                  310358
                  uC-zmroteosinte003d04b1
Seq. ID
                  BLASTN
Method
                  g454880
NCBI GI
                  58
BLAST score
                  1.0e-23
E value
Match length
                  126
                  94
% identity
                  Rice mRNA for WSI724 protein induced by water stress,
NCBI Description
                  complete cds
Seq. No.
                  310359
                  uC-zmroteosinte003e08b1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g4321977
BLAST score
                  98
                  1.0e-47
E value
                  226
Match length
                  86
% identity
NCBI Description Zea mays beta-amylase (Amy2) gene, complete cds
Seq. No.
                   310360
                  uC-zmroteosinte003q02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4510346
BLAST score
                   251
                  1.0e-21
E value
Match length
                  77
% identity
                   61
                  (AC006921) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   310361
                  uC-zmroteosinte003h12b1
Seq. ID
Method
                  BLASTX
```



```
% identity
NCBI Description
                   (AF037034) putative peroxidase P7X [Zea mays]
Seq. No.
                   310362
                   uC-zmroteosinte004a06b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4490310
BLAST score
                   156
E value
                   1.0e-10
Match length
                   42
                   71
% identity
NCBI Description
                   (AL035678) somatic embryogenesis receptor-like kinase-like
                   protein [Arabidopsis thaliana]
Seq. No.
                   310363
Seq. ID
                   uC-zmroteosinte004a10b1
Method
                   BLASTX
NCBI GI
                   g4519936
BLAST score
                   182
E value
                   6.0e-14
Match length
                   69
                   49
% identity
NCBI Description
                   (AB019186) RPR1 [Oryza sativa]
Seq. No.
                   310364
                   uC-zmroteosinte004c10b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1546696
BLAST score
                   168
E value
                   7.0e-12
Match length
                   52
% identity
                   63
NCBI Description
                   (X98807) peroxidase ATP21a [Arabidopsis thaliana]
Seq. No.
                   310365
                   uC-zmroteosinte004d02b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2130151
BLAST score
                   426
E value
                   2.0e-51
Match length
                   103
% identity
NCBI Description
                   hypothetical protein 139 - maize chloroplast
                   >gi_902269_emb_CAA60334_ (X86563) ORF139 [Zea mays]
>gi_902302_emb_CAA60366_ (X86563) ORF139 [Zea mays]
Seq. No.
                   310366
Seq. ID
                   uC-zmroteosinte004f09b1
Method
                   BLASTX
```

310367

NCBI GI q3687230 BLAST score 262 E value 1.0e-22 Match length 128 % identity 55

NCBI Description (AC005169) hypothetical protein [Arabidopsis thaliana]

Seq. No.



```
uC-zmroteosinte005c11b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g416615
BLAST score
                  721
E value
                  1.0e-76
Match length
                  153
% identity
                  91
                  ALKALINE PROTEINASE PRECURSOR (ALP) >qi 419912 pir S32905
NCBI Description
                  serine proteinase (EC 3.4.21.-) prb1 precursor - fungus
                  (Trichoderma harzianum) >gi 170539 (M87516) alkaline
                  proteinase [Trichoderma harzianum] >gi 170545 (M87518)
                  alkaline proteinase [Trichoderma harzianum]
Seq. No.
                  310368
Seq. ID
                  uC-zmroteosinte005d12b1
Method
                  BLASTX
NCBI GI
                  g2505876
BLAST score
                  235
E value
                  1.0e-19
Match length
                  69
% identity
                  68
NCBI Description
                  (Y12776) MYB-related protein [Arabidopsis thaliana]
Seq. No.
                  310369
Seq. ID
                  uC-zmroteosinte005e07b1
Method
                  BLASTX
NCBI GI
                  q3641870
BLAST score
                  223
E value
                  2.0e-18
Match length
                  106
% identity
                  43
NCBI Description
                  (AJ011013) hypothetical protein [Cicer arietinum]
                  310370
Seq. No.
                  uC-zmroteosinte006a08b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g485518
BLAST score
                  255
E value
                  1.0e-22
Match length
                  67
% identity
                  79
NCBI Description
                  ubiquitin / ribosomal protein CEP52 - rice
                  >gi 303857 dbj BAA02154 (D12629) ubiquitin/ribosomal
                  polyprotein [Oryza sativa]
Seq. No.
                  310371
                  uC-zmroteosinte006a12b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2832629
BLAST score
                  179
E value
                  5.0e-13
Match length
                  70
```

Seq. No. 310372

51

thalianal

% identity

NCBI Description

(AL021711) 4-coumarate-CoA ligase - like [Arabidopsis



```
Seq. ID
                  uC-zmroteosinte006b04b1
Method
                  BLASTX
NCBI GI
                  g4056432
BLAST score
                  380
                  2.0e-36
E value
                  170
Match length
                  49
% identity
                  (AC005990) Similar to gi_2245014 glucosyltransferase
NCBI Description
                  homolog from Arabidopsis thaliana chromosome 4 contig
                  gb_Z97341. ESTs gb_T20778 and gb_AA586281 come from this
                  gene. [Arabidopsis thaliana]
                  310373
Seq. No.
Seq. ID
                  uC-zmroteosinte006e01b1
Method
                  BLASTX
NCBI GI
                  g767869
BLAST score
                  524
E value
                  5.0e-55
Match length
                  159
% identity
                  81
                  (U20140) elongation factor 1-alpha [Trichoplusia ni]
NCBI Description
                  310374
Seq. No.
                  uC-zmroteosinte006e02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2117501
BLAST score
                  361
E value
                  3.0e - 34
Match length
                  137
                  48
% identity
NCBI Description
                  xanthine dehydrogenase (EC 1.1.1.204) - fruit fly
                  (Drosophila melanogaster)
                  310375
Seq. No.
                  uC-zmroteosinte006h02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1346113
                  182
BLAST score
E value
                  2.0e-13
Match length
                  81
% identity
                  77
                  GTP CYCLOHYDROLASE II >gi_1084339_pir__JC4209 GTP
NCBI Description
                  cyclohydrolase II (EC 3.5.4.25) - Arabidopsis thaliana
                  >gi_940383_dbj_BAA08113_ (D45165) GTP cyclohydrolase II
                  [Arabidopsis thaliana]
Seq. No.
                  310376
```

Seq. ID uC-zmroteosinte006h04b1

Method BLASTX NCBI GI q1877193 BLAST score 354 2.0e-33 E value Match length 113 % identity 57

NCBI Description (Y10911) NADH-ubiquinone oxidoreductase 42 kDa subunit

[Drosophila melanogaster]



```
310377
Seq. No.
                   uC-zmroteosinte007a01b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2754812
BLAST score
                   253
E value
                   1.0e-21
Match length
                   135
% identity
NCBI Description (AF010309) Pig3 [Homo sapiens]
Seq. No.
                   310378
Seq. ID
                   uC-zmroteosinte007d02b1
Method
                   BLASTX
NCBI GI
                   q3063467
BLAST score
                   185
E value
                   9.0e-14
Match length
                   80
% identity
NCBI Description (AC003981) F22013.29 [Arabidopsis thaliana]
Seq. No.
                   310379
Seq. ID
                   uC-zmroteosinte007e12b1
Method
                   BLASTX
NCBI GI
                   q1711535
BLAST score
                   201
E value
                   1.0e-15
Match length
                   90
                   49
% identity
NCBI Description
                   SUCCINATE SEMIALDEHYDE DEHYDROGENASE (NAD (+) - DEPENDENT
                   SUCCINIC SEMIALDEHYDE DEHYDROGENASE)
                   >gi 2143986 pir I61704 succinate-semialdehyde
                   dehydrogenase (EC 1.2.1.24) - rat (fragment) >gi 556395
                   (L34821) succinate semialdehyde dehydrogenase [Rattus
                   norvegicus]
Seq. No.
                   310380
Seq. ID
                   uC-zmroteosinte007f01b1
Method
                   BLASTX
NCBI GI
                   g2618684
                   385
BLAST score
E value
                   3.0e-37
Match length
                   140
                   58
% identity
NCBI Description
                   (AC002510) putative
                   UDP-N-acetylglucosamine--dolichyl-phosphate
                   N-acetylglucosaminephosphotransferase [Arabidopsis
                   thaliana] >gi 3241947 (AC004625) putative
                   UDP-N-acetylglucosamine--dolichyl-phosphate
                   N-acetylglucosaminephosphotransferase [Arabidopsis
                   thaliana]
Seq. No.
                   310381
                   uC-zmroteosinte007h05b1
Seq. ID
Method
                   BLASTX
```

44216

g3157946

1.0e-20

244

NCBI GI BLAST score

E value



Match length 156 % identity 38

NCBI Description (AC002131) Similar to salt-inducible membrane protein

gb_U08285 from Nicotiana tabacum. EST gb_F14010 comes from

this gene. [Arabidopsis thaliana]

Seq. No. 310382

Seq. ID uC-zmroteosinte008a11b1

Method BLASTX
NCBI GI g3080427
BLAST score 577
E value 1.0e-59
Match length 158
% identity 72

NCBI Description (AL022604) putative protein [Arabidopsis thaliana]

Seq. No. 310383

Seq. ID uC-zmroteosinte008d07b1

Method BLASTX
NCBI GI g1709000
BLAST score 452
E value 6.0e-45
Match length 90
% identity 93

NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE

ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)

 $>gi_960357_dbj_BAA09895_ (D63835)$ S-adenosylmethionine

synthetase [Hordeum vulgare]

Seq. No. 310384

Seq. ID uC-zmroteosinte008f01b1

Method BLASTX
NCBI GI g4105101
BLAST score 186
E value 9.0e-14
Match length 96
% identity 46

NCBI Description (AF043086) dehydrin 11 [Hordeum vulgare]

Seq. No. 310385

Seq. ID uC-zmroteosinte008f10b1

Method BLASTX
NCBI GI g2980780
BLAST score 533
E value 2.0e-54
Match length 154
% identity 62

NCBI Description (AL022198) putative protein [Arabidopsis thaliana]

Seq. No. 310386

Seq. ID uC-zmroteosinte009b10b1

Method BLASTX
NCBI GI g129881
BLAST score 347
E value 1.0e-32
Match length 139
% identity 61



NCBI Description PYROPHOSPHATE--FRUCTOSE 6-PHOSPHATE 1-PHOSPHOTRANSFERASE ALPHA SUBUNIT (PFP) (6-PHOSPHOFRUCTOKINASE (PYROPHOSPHATE)) (PYROPHOSPHATE-DEPENDENT 6-PHOSPHOFRUCTOSE-1-KINASE) (PPI-PFK) >gi_482294_pir__A36094

pyrophosphate--fructose-6-phosphate 1-phosphotransferase
(EC 2.7.1.90) alpha chain - potato (cv. Kennebec)
>gi_169538 (M55190) pyrophosphate-fructose 6-phosphate
1-phosphotransferase alpha-subunit [Solanum tuberosum]

Seq. No. 310387

Seq. ID uC-zmroteosinte009d02b1

Method BLASTX
NCBI GI g3292831
BLAST score 625
E value 3.0e-65
Match length 164
% identity 68

NCBI Description (AL031018) putative serine/threonine kinase [Arabidopsis

thaliana]

Seq. No. 310388

Seq. ID uC-zmroteosinte009d10b1

Method BLASTX
NCBI GI g2731377
BLAST score 282
E value 5.0e-25
Match length 142
% identity 44

NCBI Description (U28739) similar to alcohol dehydrogenase/ribitol

dehydrogenase [Caenorhabditis elegans]

Seq. No. 310389

Seq. ID uC-zmroteosinte009h03b1

Method BLASTX
NCBI GI g2668742
BLAST score 332
E value 3.0e-31
Match length 73
% identity 89

NCBI Description (AF034945) glycine-rich RNA binding protein [Zea mays]

Seq. No. 310390

Seq. ID uC-zmroteosinte010b08b1

Method BLASTN
NCBI GI g22260
BLAST score 295
E value 1.0e-165
Match length 367
% identity 95

NCBI Description Maize DNA for Ds101 controlling element (Ds1-related)

Seq. No. 310391

Seq. ID uC-zmroteosinte010f03b1

Method BLASTX
NCBI GI g1170434
BLAST score 782
E value 1.0e-83

```
173
Match length
% identity
                  88
                  HOMEOBOX PROTEIN HOX1A >gi 283057 pir S25237 homeotic
NCBI Description
                  protein Hoxla - maize >gi 22331 emb CAA47859 (X67561)
                  Zmhoxla homeobox protein [Zea mays]
                  310392
Seq. No.
                  uC-zmroteosinte011c06b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3228517
BLAST score
                  179
                  5.0e-13
E value
Match length
                  67
% identity
                  55
NCBI Description
                  (AF007788) ETTIN [Arabidopsis thaliana]
Seq. No.
                  310393
                  uC-zmroteosinte011d07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q509810
BLAST score
                  554
E value
                  7.0e-57
Match length
                  174
% identity
                  61
                  (L08468) envelope Ca2+-ATPase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  310394
                  uC-zmroteosinte011e01b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q532622
BLAST score
                  106
E value
                  9.0e-53
Match length
                  210
% identity
                  88
NCBI Description Zea mays lipase (LIP) mRNA, complete cds
                  310395
Seq. No.
Seq. ID
                  uC-zmroteosinte011f09b1
Method
                  BLASTX
NCBI GI
                  g3319372
BLAST score
                  160
E value
                  1.0e-10
Match length
                  102
% identity
                  34
NCBI Description
                  (AF077409) similar to reverse transcriptases (PFam:
                  rvt.hmm, score: 60.13) [Arabidopsis thaliana]
                  310396
Seq. No.
                  uC-zmroteosinte011h07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g118498
BLAST score
                  530
E value
                  3.0e-54
```

Match length 124
% identity 82
NCBI Description ALDEHYDE DEHYDROGENASE (ALDDH) >gi_83694_pir_A29055

aldehyde dehydrogenase (NAD+) (EC 1.2.1.3) - Emericella

% identity

91



nidulans >gi_168011 (M16197) aldehyde dehydrogenase [Emericella nidulans] >gi_225561_prf__1306289A dehydrogenase,aldehyde [Emericella nidulans]

Seq. No. Seq. ID uC-zmroteosinte012a11b1 Method BLASTX NCBI GI q3386615 BLAST score 280 E value 6.0e-25 Match length 105 % identity 56 NCBI Description (AC004665) putative phosphomannomutase [Arabidopsis thaliana] Seq. No. 310398 Seq. ID uC-zmroteosinte012d11b1 Method BLASTX NCBI GI g2653285 BLAST score 402 4.0e-54 E value 1200 Match length 138 % identity 78 NCBI Description (AJ003025) enoyl-ACP reductase [Oryza sativa] Seq. No. 310399 Seq. ID uC-zmroteosinte012e02b1 Method BLASTX g2078350 NCBI GI BLAST score 151 E value 2.0e-10 Match length 37 % identity NCBI Description (U95923) transaldolase [Solanum tuberosum] Seq. No. 310400 Seq. ID uC-zmroteosinte012f02b1 Method BLASTX NCBI GI g2335108 BLAST score 145 E value 6.0e-09 Match length 42 % identity NCBI Description (AC002339) putative isulinase [Arabidopsis thaliana] Seq. No. 310401 Seq. ID uC-zmroteosinte012f06b1 Method BLASTX NCBI GI g112994 BLAST score 393 E value 3.0e-38 Match length 85

NCBI Description GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN

>gi_82685_pir__S04536 embryonic abundant protein,
glycine-rich - maize >gi_22313_emb_CAA31077_ (X12564)

ABA-inducible gene protein [Zea mays]



>gi_226091_prf__1410284A abscisic acid inducible gene [Zea mays]

Seq. No. 310402

Seq. ID uC-zmroteosinte012f08b1

Method BLASTX
NCBI GI g4510346
BLAST score 248
E value 1.0e-34
Match length 144
% identity 60

NCBI Description (AC006921) hypothetical protein [Arabidopsis thaliana]

Seq. No. 310403

Seq. ID uC-zmroteosinte012g04b1

Method BLASTX
NCBI GI g161752
BLAST score 177
E value 1.0e-12
Match length 97
% identity 10

NCBI Description (L03710) cnjB [Tetrahymena thermophila]

>gi_737494_prf__1922371A cnjB gene [Tetrahymena

thermophila]

Seq. No. 310404

Seq. ID uC-zmroteosinte012h10b1

Method BLASTX
NCBI GI g1001430
BLAST score 255
E value 8.0e-22
Match length 126
% identity 41

NCBI Description (D63999) ORF1 [Synechocystis sp.]

Seq. No. 310405

Seq. ID uC-zmroteosinte013b07b1

Method BLASTX
NCBI GI g2505877
BLAST score 559
E value 2.0e-57
Match length 159
% identity 70

NCBI Description (Y12776) dehydrogenase [Arabidopsis thaliana]

Seq. No. 310406

Seq. ID uC-zmroteosinte013c05b1

Method BLASTX
NCBI GI g1168609
BLAST score 149
E value 1.0e-09
Match length 122
% identity 31

NCBI Description AUXIN-RESISTANCE PROTEIN AXR1 >gi_479664_pir__S35071

auxin-resistance protein AXR1 - Arabidopsis thaliana >gi_304104 (L13922) ubiquitin-activating enzyme E1 [Arabidopsis thaliana] >gi_2388579 (AC000098) Match to



Arabidopsis AXR1 (gb_ATHAXR1122). [Arabidopsis thaliana] >gi_448755_prf__1917337A ubiquitin-activating enzyme E1 [Arabidopsis thaliana]

```
310407
Seq. No.
Seq. ID
                  uC-zmroteosinte013d10b1
Method
                  BLASTX
NCBI GI
                  q99741
BLAST score
                  388
                  2.0e-37
E value
Match length
                  176
% identity
                  23
NCBI Description P-glycoprotein pgp1 - Arabidopsis thaliana
                  310408
Seq. No.
                  uC-zmroteosinte013d11b1
Seq. ID
Method
                 - BLASTN
NCBI GI
                  g3511235
BLAST score
                  112
E value
                  5.0e-56
Match length
                  305
                  85
% identity
                  Zea mays starch branching enzyme IIb (ae) gene, complete
NCBI Description
Seq. No.
                   310409
                  uC-zmroteosinte013f08b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g100226
BLAST score
                   261
                   1.0e-22
E value
Match length
                   160
% identity
                   37
NCBI Description
                  hypothetical protein - tomato >gi_19275_emb_CAA78112_
                   (Z12127) protein of unknown function [Lycopersicon
                   esculentum] >gi_445619_prf__1909366A Leu zipper protein
                   [Lycopersicon esculentum]
                   310410
Seq. No.
Seq. ID
                   uC-zmroteosinte013h05b1
Method
                   BLASTX
NCBI GI
                   g3241943
BLAST score
                   452
E value
                   5.0e-45
Match length
                   134
                   63
% identity
NCBI Description
                  (AC004625) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   310411
Seq. ID
                   uC-zmroteosinte013h07b1
Method
                   BLASTX
NCBI GI
                   q560610
BLAST score
                   170
                   5.0e-12
E value
Match length
                   45
% identity
                   58
```

NCBI Description trypsin inhibitor, WTI [Triticum aestivum=wheat, variety





San Pastore, endosperm, Peptide, 71 aa]

Seq. No. 310412 Seq. ID uC-zmroteosinte014a12b1 Method BLASTN NCBI GI g407411 BLAST score 46 6.0e-17 E value Match length 114 % identity 86 NCBI Description C.roseus SAHH gene for S-adenosyl-L-homocysteine hydrolase Seq. No. 310413 Seq. ID uC-zmroteosinte014c06b1 Method BLASTN NCBI GI q551482 BLAST score 239 E value 1.0e-132 Match length 411 % identity 93 NCBI Description Zea mays ABA- and ripening-inducible-like protein mRNA, complete cds Seq. No. 310414 Seq. ID uC-zmroteosinte014g02b1 Method BLASTX NCBI GI q4263820 BLAST score 176 E value 2.0e-13 Match length 60 % identity 55 NCBI Description (AC006067) hypothetical protein [Arabidopsis thaliana] Seq. No. 310415 uC-zmroteosinte014h05b1 Seq. ID Method BLASTX NCBI GI g3757529 BLAST score 150 E value 1.0e-09 Match length 82 % identity 39 NCBI Description (AC005167) tetracycline transporter-like protein [Arabidopsis thaliana] Seq. No. 310416 uC-zmroteosinte015b01b1 Seq. ID Method BLASTX NCBI GI g1946361 BLAST score 151 E value 1.0e-09 Match length 166 % identity 31 NCBI Description (U93215) C3HC4 zinc finger protein isolog [Arabidopsis

Seq. No.

310417

thaliana]

Seq. ID

uC-zmroteosinte015c08b1



```
Method
                  BLASTX
NCBI GI
                  g1244566
BLAST score
                  521
E value
                   9.0e-69
Match length
                  153
% identity
                  87
NCBI Description
                  (U39321) acetyl-CoA carboxylase [Triticum aestivum]
                  >gi 1588584 prf 2208491A Ac-CoA carboxylase [Triticum
                  aestivum]
Seq. No.
                  310418
Seq. ID
                  uC-zmroteosinte015d07b1
Method
                  BLASTX
NCBI GI
                  q4587685
BLAST score
                  327
E value
                  3.0e-30
Match length
                  77
% identity
                  82
NCBI Description
                  (AC007197) putative methylmalonate semi-aldehyde
                  dehydrogenase [Arabidopsis thaliana]
Seq. No.
                  310419
                  uC-zmroteosinte015f04b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3355466
BLAST score
                  253
E value
                  1.0e-21
Match length
                  173
% identity
                  41
NCBI Description
                  (AC004218) unknown protein [Arabidopsis thaliana]
Seq. No.
                  310420
Seq. ID
                  uC-zmroteosinte015f07b1
Method
                  BLASTX
NCBI GI
                  g3309575
BLAST score
                  413
E value
                  2.0e-40
Match length
                  122
% identity
                  66
NCBI Description
                  (AF060553) calcium sensor homolog [Arabidopsis thaliana]
                  >gi_4538989_emb_CAB39731.1 (Y18870) CBL4 protein
                  [Arabidopsis thaliana]
Seq. No.
                  310421
Seq. ID
                  uC-zmroteosinte016a05b1
Method
                  BLASTX
NCBI GI
                  g121695
BLAST score
                  197
E value
                  2.0e-24
```

Match length 94 % identity 62

NCBI Description GLUTATHIONE S-TRANSFERASE I (GST-I) (GST-29) (CLASS-PHI)

>gi 22315 emb CAA29928 (X06754) GST I (AA 1-214) [Zea

mays]

Seq. No. - 310422

Seq. ID uC-zmroteosinte016a12b1

Seq. No.

Seq. ID

Method

310427

BLASTX

uC-zmroteosinte017b09b1



```
BLASTX
Method
NCBI GI
                  q3421104
BLAST score
                  303
                  1.0e-27
E value
Match length
                  86
                  69
% identity
                  (AF043531) 20S proteasome beta subunit PBB2 [Arabidopsis
NCBI Description
                  thaliana]
                  310423
Seq. No.
                  uC-zmroteosinte016c03b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3080420
BLAST score
                  188
E value
                  3.0e-14
Match length
                  78
                  50
% identity
                  (AL022604) putative sugar transporter protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  310424
Seq. ID
                  uC-zmroteosinte016g10b1
Method
                  BLASTN
NCBI GI
                  g433040
BLAST score
                  102
E value
                  5.0e-50
Match length
                  122
                  96
% identity
                  Zea mays W-22 clone PREM-1A retroelement PREM-1, partial
NCBI Description
                  sequence
                  310425
Seq. No.
                  uC-zmroteosinte017a10b1
Seq. ID
Method
                  BLASTX
                  g416581
NCBI GI
BLAST score
                  223
E value
                  7.0e-21
Match length
                  93
% identity
                  50
NCBI Description
                  ACTIN-LIKE PROTEIN 3 >gi 283066 pir A41790 actin like
                  protein act2 - fission yeast (Schizosaccharomyces pombe)
Seq. No.
                  310426
Seq. ID
                  uC-zmroteosinte017b01b1
Method
                  BLASTX
NCBI GI
                  g1723232
BLAST score
                  143
E value
                  1.0e-08
Match length
                  52
                  60
% identity
NCBI Description
                  HYPOTHETICAL 90.6 KD PROTEIN C1D4.10 IN CHROMOSOME I
                  >gi_1177343_emb_CAA93219_ (Z69239) unknown
                  [Schizosaccharomyces pombe]
```



```
g2088643
NCBI GI
BLAST score
                  157
                  2.0e-10
E value
Match length
                  148
% identity
                  26
                  (AF002109) transcription factor SF3 isolog [Arabidopsis
NCBI Description
                  thaliana]
                  310428
Seq. No.
                  uC-zmroteosinte017c07b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1172635
BLAST score
                  212
                  9.0e-31
E value
Match length
                  118
% identity
                  68
                  26S PROTEASE REGULATORY SUBUNIT 4 HOMOLOG (TAT-BINDING
NCBI Description
                  PROTEIN HOMOLOG 2) >gi 556558 dbj BAA04615 (D17789) rice
                  homologue of Tat binding protein [Oryza sativa]
Seq. No.
                  310429
                  uC-zmroteosinte017e02b1
Seq. ID
                  BLASTX
Method
                  g2499932
NCBI GI
BLAST score
                  154
E value
                  7.0e-23
Match length
                  79
% identity
                  78
                  ADENINE PHOSPHORIBOSYLTRANSFERASE 1 (APRT) >gi 726305
NCBI Description
                   (U22442) adenine phosphoribosyltransferase form 1 [Triticum
                  aestivum]
                  310430
Seq. No.
                  uC-zmroteosinte017f10b1
Seq. ID
Method
                  BLASTX
                  g4090257
NCBI GI
                  194
BLAST score
E value
                  4.0e-15
Match length
                  73
% identity
                  62
NCBI Description (AJ131732) ribosomal protein L37A [Pseudotsuga menziesii]
                  310431
Seq. No.
                  uC-zmroteosinte018f10b1
Seq. ID
Method
                  BLASTX
                  g2651300
NCBI GI
BLAST score
                  156
                  6.0e-21
E value
                  98
Match length
```

51 % identity

NCBI Description (AC002336) putative initiator tRNA

phosphoribosyl-transferase [Arabidopsis thaliana]

310432 Seq. No.

uC-zmroteosinte018g09b1 Seq. ID

Method BLASTX NCBI GI g1353239



BLAST score E value 4.0e-49157 Match length % identity 65

(U10245) putative RNA helicase A [Arabidopsis thaliana] NCBI Description

Seq. No.

310433 uC-zmroteosinte019a02b1 Seq. ID

Method BLASTX NCBI GI g4038471 BLAST score 354 E value 2.0e-33 Match length 86 77 % identity

NCBI Description (AF111029) 40S ribosomal protein S27 homolog [Zea mays]

Seq. No.

310434 Seq. ID uC-zmroteosinte019a05b1

Method BLASTX NCBI GI q4204695 BLAST score 494 E value 6.0e-50 Match length 147 % identity 64

NCBI Description (AF117062) putative inositol polyphosphate 5-phosphatase

At5P1 [Arabidopsis thaliana]

Seq. No.

310435 Seq. ID uC-zmroteosinte019c02b1

Method BLASTX NCBI GI g2499819 BLAST score 344 1.0e-32 E value Match length 114 56 % identity

NCBI Description ASPARTIC PROTEINASE ORYZASIN 1 PRECURSOR

> >gi 2130068 pir S66516 aspartic proteinase 1 precursor rice >gi 1030715 dbj BAA06876 (D32165) aspartic protease [Oryza sativa] >gi 1711289 dbj BAA06875 (D32144) aspartic

protease [Oryza sativa]

Seq. No. 310436

uC-zmroteosinte019c05b1 Seq. ID

BLASTX Method NCBI GI g3132310 BLAST score 327 8.0e-35 E value Match length 140 % identity 65

NCBI Description (AB012228) phosphoenolpyruvate carboxylase [Zea mays]

Seq. No. 310437

Seq. ID uC-zmroteosinte019d05b1

Method BLASTX g3122858 NCBI GI BLAST score 264 E value 4.0e-23



Match length 89 % identity 60

NCBI Description D-3-PHOSPHOGLYCERATE DEHYDROGENASE PRECURSOR

>gi_2189964_dbj_BAA20405_ (AB003280) Phosphoglycerate

dehydrogenase [Arabidopsis thaliana]

>gi_2804258_dbj_BAA24440_ (AB010407) phosphoglycerate

dehydrogenase [Arabidopsis thaliana]

Seq. No. 310438

Seq. ID uC-zmroteosinte019d06b1

Method BLASTX
NCBI GI g1402918
BLAST score 221
E value 1.0e-18
Match length 127
% identity 42

NCBI Description (X98320) peroxidase [Arabidopsis thaliana]

>gi 1429215 emb CAA67310 (X98774) peroxidase ATP6a

[Arabidopsis thaliana]

Seq. No. 310439

Seq. ID uC-zmroteosinte019e04b1

Method BLASTX
NCBI GI g4426627
BLAST score 320
E value 2.0e-29
Match length 140
% identity 51

NCBI Description (AF099969) sterol-C5(6)-desaturase homolog [Nicotiana

tabacum]

Seq. No. 310440

Seq. ID uC-zmroteosinte019e06b1

Method BLASTX
NCBI GI g4217999
BLAST score 220
E value 4.0e-38
Match length 98
% identity 75

NCBI Description (AC006135) putative ubiquitin--protein ligase

(ubiquitin-conjugating enzyme) [Arabidopsis thaliana]

Seq. No. 310441

Seq. ID uC-zmroteosinte019e12b1

Method BLASTX
NCBI GI g3367534
BLAST score 241
E value 4.0e-20
Match length 67
% identity 66

NCBI Description (AC004392) Strong similarity to coatamer alpha subunit

(HEPCOP) homolog gb U24105 from Homo sapiens. [Arabidopsis

thaliana]

Seq. No. 310442

Seq. ID uC-zmroteosinte019f06b1

Method BLASTX



```
NCBI GI
                  q4314378
BLAST score
                  144
E value
                  5.0e-09
Match length
                  100
% identity
                  34
NCBI Description
                  (AC006232) putative lipase [Arabidopsis thaliana]
Seq. No.
                  310443
Seq. ID
                  uC-zmroteosinte019f09b1
Method
                  BLASTX
NCBI GI
                  g1495251
BLAST score
                  259
E value
                  2.0e-22
Match length
                  116
% identity
                  47
NCBI Description (Z70314) heat-shock protein [Arabidopsis thaliana]
Seq. No.
                  310444
Seq. ID
                  uC-zmroteosinte019g03b1
Method
                  BLASTX
NCBI GI
                  g1055130
BLAST score
                  169
E value
                  9.0e-12
Match length
                  102
% identity
                  39
NCBI Description
                  (U39998) coded for by C. elegans cDNA yk92b11.3; coded for
                  by C. elegans cDNA yk92b11.5; coded for by C. elegans cDNA
                  yk78c2.5; coded for by C. elegans cDNA cm9a8; coded for by
                  C. elegans cDNA yk66h8.3; coded for by C. elegans cDNA
                  yk78c2.3
Seq. No.
                  310445
Seq. ID
                  uC-zmroteosinte019h01b1
Method
                  BLASTX
NCBI GI
                  g3184283
BLAST score
                  304
E value
                  1.0e-27
Match length
                  161
% identity
                  43
NCBI Description
                  (AC004136) putative TBP-binding protein [Arabidopsis
                  thaliana]
Seq. No.
                  310446
Seq. ID
                  uC-zmroteosinte020g02b1
Method
                  BLASTX
NCBI GI
                  g4581856
BLAST score
                  145
E value
                  5.0e-09
Match length
                  47
% identity
                  68
NCBI Description
                  (AF116825) 1-deoxy-D-xylulose-5-phosphate reductoisomerase
                  [Mentha x piperita]
Seq. No.
                  310447
```

Seq. ID uC-zmroteosinte020g11b1

Method BLASTX NCBI GI g4587686

```
BLAST score
E value
                   6.0e-30
Match length
                  109
% identity
                  60
                  (AC007197) dynamin-like protein ADL2 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  310448
Seq. ID
                  uC-zmroteosinte020h01b1
Method
                  BLASTX
NCBI GI
                  g3800952
BLAST score
                  147
E value
                  4.0e-09
Match length
                  120
% identity
                  33
NCBI Description
                  (AF100657) No definition line found [Caenorhabditis
                  elegans]
Seq. No.
                  310449
Seq. ID
                  uC-zmroteosinte021a01b1
Method
                  BLASTX
NCBI GI
                  g1653033
BLAST score
                  240
E value
                  4.0e-20
Match length
                  123
% identity
                  51
NCBI Description
                  (D90910) hypothetical protein [Synechocystis sp.]
Seq. No.
                  310450
                  uC-zmroteosinte021a02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4572679
BLAST score
                  293
                  2.0e-26
E value
Match length
                  99
% identity
                  64
                  (AC006954) RSZp22 splicing factor; contains RNA recognition
NCBI Description
                  motif [Arabidopsis thaliana]
Seq. No. Seq. ID
                  310451
```

uC-zmroteosinte021c08b1

Method BLASTN NCBI GI g1419369 BLAST score 109 E value 2.0e-54 Match length 340 % identity 84

NCBI Description Z.mays ZmABP3 mRNA for actin depolymerizing factor

Seq. No. 310452

Seq. ID uC-zmroteosinte021d03b1

Method BLASTX NCBI GI q542185 BLAST score 304 E value 1.0e-27 Match length 93 71 % identity

NCBI Description group 3 Lea protein MGL3 - maize >gi_452560 (U05226) group



3 Lea protein MGL3 [Zea mays] >gi_45.4873_dbj_BAA05550_ (D26552) group 3 Lea protein MGL3 [Zea mays] >gi_2654379_emb_CAA82632.1_ (Z29512) Group 3 Lea protein MGL3 [Zea mays]

Seq. No. 310453

Seq. ID uC-zmroteosinte021d11b1

Method BLASTX
NCBI GI g2505874
BLAST score 242
E value 3.0e-20
Match length 99
% identity 51

NCBI Description (Y12776) putative kinase [Arabidopsis thaliana]

Seq. No. 310454

Seq. ID uC-zmroteosinte021e09b1

Method BLASTX
NCBI GI g4185507
BLAST score 265
E value 5.0e-23
Match length 101
% identity 71

NCBI Description (AF100163) EZA1 [Arabidopsis thaliana]

Seq. No. 310455

Seq. ID uC-zmroteosinte021f01b1

Method BLASTX
NCBI GI g3608479
BLAST score 242
E value 2.0e-20
Match length 133
% identity 31

NCBI Description (AF088912) ribosomal protein L15 [Petunia x hybrida]

Seq. No. 310456

Seq. ID uC-zmroteosinte021f03b1

Method BLASTX
NCBI GI 94490737
BLAST score 236
E value 1.0e-19
Match length 107
% identity 50

NCBI Description (AL035708) putative protein [Arabidopsis thaliana]

Seq. No. 310457

Seq. ID uC-zmroteosinte021g03b1

Method BLASTX
NCBI GI g3163946
BLAST score 271
E value 2.0e-44
Match length 144
% identity 74

NCBI Description (AJ005599) alpha-tubulin 1 [Eleusine indica]

Seq. No. 310458

Seq. ID uC-zmroteosinte022a06b1

```
Method
                  BLASTX
NCBI GI
                  q3132477
BLAST score
                  294
E value
                  1.0e-26
Match length
                  113
                  52
% identity
NCBI Description
                  (AC003096) unknown protein [Arabidopsis thaliana]
Seq. No.
                  310459
Seq. ID
                  uC-zmroteosinte022a10b1
Method
                  BLASTX
NCBI GI
                  q1350742
BLAST score
                  180
                  2.0e-13
E value
Match length
                  87
% identity
                  44
NCBI Description
                  PROBABLE 60S RIBOSOMAL PROTEIN L35A >gi 1086831 (U41264)
                  coded for by C. elegans cDNA yk64g10.5; coded for by C.
                  elegans cDNA yk51f3.5; coded for by C. elegans cDNA
                  yk115e7.3; coded for by C. elegans cDNA yk99d1.3; coded for
                  by C. elegans cDNA yk99d1.5; coded for by C. elegans cDNA
                  yk64g1
Seq. No.
                  310460
Seq. ID
                  uC-zmroteosinte022c06b1
```

Method BLASTX
NCBI GI g4588906
BLAST score 488
E value 3.0e-49
Match length 159
% identity 65

NCBI Description (AF118149) ribosomal protein S7 [Secale cereale]

Seq. No. 310461

Seq. ID uC-zmroteosinte022f11b1

Method BLASTN
NCBI GI g899609
BLAST score 59
E value 2.0e-24
Match length 143
% identity 88

NCBI Description Zea mays acidic ribosomal protein P2 (RPA-2A1) mRNA,

complete cds

Seq. No. 310462

Seq. ID uC-zmroteosinte022f12b1

Method BLASTX
NCBI GI g4325345
BLAST score 186
E value 2.0e-14
Match length 74
% identity 19

NCBI Description (AF128393) similar to thioredoxin-like proteins (Pfam:

PF00085, Score=42.9, E=1.4e-11, N=1); contains similarity to dihydroorotases (Pfam: PF00744, Score=154.9, E=1.4e-42,

N=1) [Arabidopsis thaliana]

Seq. No.

Seq. ID

310468

uC-zmroteosinte023c11b2



```
Seq. No.
                   310463
Seq. ID
                   uC-zmroteosinte022g01b1
Method
                   BLASTX
NCBI GI
                   g2911054
BLAST score
                   141
E value
                   8.0e-09
Match length
                   72
                   46
% identity
NCBI Description
                  (AL021961) putative protein [Arabidopsis thaliana]
Seq. No.
                   310464
Seq. ID
                   uC-zmroteosinte022g08b1
Method
                   BLASTX
NCBI GI
                   a464849
BLAST score
                   300
E value
                   7.0e-28
Match length
                   71
% identity
                   82
                   TUBULIN ALPHA CHAIN >gi_486847_pir__S36232 tubulin alpha
NCBI Description
                   chain - almond >gi 2041\overline{3} emb \overline{CAA47635} (X67162)
                   alpha-tubulin [Prunus dulcis]
Seq. No.
                   310465
Seq. ID
                   uC-zmroteosinte022h05b1
Method
                   BLASTX
NCBI GI
                   g136125
BLAST score
                   258
E value
                   4.0e-22
Match length
                   156
% identity
                   38
                  PUTATIVE AC TRANSPOSASE (ORFA) >gi 22113 emb CAA29005
NCBI Description
                   (X05424) ORFa [Zea mays]
Seq. No.
                   310466
Seq. ID
                   uC-zmroteosinte023a11b2
Method
                   BLASTX
NCBI GI
                   g2132186
BLAST score
                   261
E value
                   1.0e-22
Match length
                   146
% identity
                   39
NCBI Description
                  hypothetical protein YPL096w - yeast (Saccharomyces
                   cerevisiae) >gi 1151230 (U43281) Lpg12p [Saccharomyces
                   cerevisiae]
Seq. No.
                   310467
Seq. ID
                   uC-zmroteosinte023c02b2
Method
                   BLASTX
NCBI GI
                   q3297812
BLAST score
                   146
E value
                   6.0e-18
Match length
                   135
% identity
NCBI Description
                  (AL031032) putative protein [Arabidopsis thaliana]
```



Method BLASTX
NCBI GI g3860277
BLAST score 156
E value 1.0e-10
Match length 43
% identity 74
NCBI Description (AC00582

NCBI Description (AC005824) putative ribosomal protein L10 [Arabidopsis thaliana] >gi_4314394_gb_AAD15604_ (AC006232) putative

ribosomal protein L10A [Arabidopsis thaliana]

Seq. No. 310469

Seq. ID uC-zmroteosinte023e05b2

Method BLASTX
NCBI GI g4226152
BLAST score 174
E value 2.0e-18
Match length 120
% identity 48

NCBI Description (AF125462) contains similarity to myosin head domain

(Pfam: PF00063, Score=884.5, E=3.2e-262, N=2) and to IQ calmodulin-binding domain (Pfam: PF00612, Score=10.8,

E=1.4, N=1) [Caenorhabditis elegans]

Seq. No. 310470

Seq. ID uC-zmroteosinte023h08b2

Method BLASTX
NCBI GI g2497543
BLAST score 208
E value 1.0e-18
Match length 86
% identity 62

NCBI Description PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi 542061 pir S41379

pyruvate kinase - common tobacco >qi 444023 emb CAA82628

(Z29492) pyruvate kinase [Nicotiana tabacum]

Seq. No. 310471

Seq. ID uC-zmroteosinte024a12b1

Method BLASTX
NCBI GI g2497623
BLAST score 632
E value 6.0e-66
Match length 160
% identity 77

NCBI Description L-LACTATE DEHYDROGENASE (LDH) >gi_1519715 (U68038) lactate

dehydrogenase [Drosophila melanogaster]

Seq. No. 310472

Seq. ID uC-zmroteosinte024b05b1

Method BLASTX
NCBI GI g2493131
BLAST score 530
E value 4.0e-54
Match length 164
% identity 68

NCBI Description VACUOLAR ATP SYNTHASE SUBUNIT B ISOFORM 1 (V-ATPASE B

SUBUNIT) >gi 167108 (L11862) vacuolar ATPase B subunit

[Hordeum vulgare]



```
Seq. No.
                  310473
Seq. ID
                  uC-zmroteosinte024c11b1
Method
                  BLASTX
NCBI GI
                  g118104
BLAST score
                  304
E value
                  6.0e-48
Match length
                  121
% identity
                  77
NCBI Description
                  PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE)
                  (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN)
                  >gi_68408_pir__CSZM peptidylprolyl isomerase (EC 5.2.1.8) -
                  maize >gi 168461 (M55021) cyclophilin [Zea mays]
                  >gi_829148 emb CAA48638 (X68678) cyclophilin [Zea mays]
Seq. No.
                  310474
                  uC-zmroteosinte024q10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2459426
BLAST score
                  223
E value
                  4.0e-18
Match length
                  141
% identity
                  43
NCBI Description
                  (AC002332) putative splicing factor U2AF large chain
                  [Arabidopsis thaliana]
Seq. No.
                  310475
Seq. ID
                  uC-zmroteosinte025a09b1
Method
                  BLASTX
NCBI GI
                  q4220527
BLAST score
                  198
E value
                  3.0e-15
Match length
                  97
% identity
                  45
NCBI Description (AL035356) putative protein [Arabidopsis thaliana]
Seq. No.
                  310476
Seq. ID
                  uC-zmroteosinte025b04b1
Method
                  BLASTX
                  g730502
NCBI GI
BLAST score
                  163
E value
                  8.0e-12
Match length
                  103
% identity
                  51
NCBI Description
                  ACTIVATOR 1 41 KD SUBUNIT (REPLICATION FACTOR C 41 KD
                  SUBUNIT) >gi 626873 pir S45531 replication factor C chain
                  RFC2 - yeast (Saccharomyces cerevisiae)
                  >gi_498463_dbj_BAA05858_ (D28499) Rfc2 protein
                  [Saccharomyces cerevisiae] >gi_841464 (U26028) Rfc2p
                  [Saccharomyces cerevisiae] >gi_1015747_emb_CAA89596_
                  (Z49568) ORF YJR068w [Saccharomyces cerevisiae] >gi 1019690
                  (L47993) ORF YJR068w [Saccharomyces cerevisiae]
```

Seq. No. 310477

Seq. ID uC-zmroteosinte025b12b1

Method BLASTX NCBI GI g3860271

NCBI GI

E value

BLAST score

Match length

g2668744

4.0e-58

564

118



```
BLAST score
E value
                  6.0e-50
Match length
                  154
                  59
% identity
                  (AC005824) putative selenium-binding protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  310478
                  uC-zmroteosinte025c01b1
Seq. ID
Method
                  BLASTX
                  g4220463
NCBI GI
BLAST score
                  461
E value
                  5.0e-46
Match length
                  151
% identity
                  54
NCBI Description
                  (AC006216) This gene is cut off. [Arabidopsis thaliana]
Seq. No.
                  310479
                  uC-zmroteosinte025d01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3913811
BLAST score
                  197
                  3.0e-21
E value
Match length
                  65
% identity
                  89
                  GLUTAMYL-TRNA REDUCTASE PRECURSOR (GLUTR)
NCBI Déscription
                  >gi 2920320 dbj BAA25003 (AB011416) glutamyl-tRNA
                  reductase [Oryza sativa]
                  310480
Seq. No.
                  uC-zmroteosinte025e07b1
Seq. ID
Method
                  BLASTX
                  g4309759
NCBI GI
BLAST score
                  164
E value
                  2.0e-11
Match length
                  93
                  45
% identity
NCBI Description
                  (AC006217) unknown protein with Src homology 3 (SH3) domain
                  profile (PDOC50002) [Arabidopsis thaliana]
Seq. No.
                  310481
Seq. ID
                  uC-zmroteosinte025f12b1
Method
                  BLASTX
NCBI GI
                  q1091678
BLAST score
                  230
E value
                  6.0e-19
Match length
                  59
                  78
% identity
NCBI Description activator-like transposable element [Pennisetum glaucum]
Seq. No.
                  310482
Seq. ID
                  uC-zmroteosinte025h05b1
Method
                  BLASTX
```

```
% identity
NCBI Description
                  (AF034946) ubiquitin conjugating enzyme [Zea mays]
Seq. No.
                  310483
                  uC-zmroteosinte026b07b1
Seq. ID
                  BLASTX
Method
                  g3126967
NCBI GI
BLAST score
                  832
                  2.0e-89
E value
                  180
Match length
                  17
% identity
NCBI Description (AF061807) polyubiquitin [Elaeagnus umbellata]
```

Seq. No. 310484

uC-zmroteosinte026e10b1 Seq. ID BLASTX Method g3126967 NCBI GI 901 BLAST score 1.0e-97 E value Match length 180 % identity 18

(AF061807) polyubiquitin [Elaeagnus umbellata] NCBI Description

310485 Seq. No. uC-zmroteosinte026f08b1 Seq. ID BLASTX Method NCBI GI g548770 148 BLAST score 1.0e-09 E value

73 Match length 47 % identity

60S RIBOSOMAL PROTEIN L3 >gi_481228_pir__S38359 ribosomal NCBI Description

protein L3 - rice >gi_303853_dbj_BAA02155_ (D12630)

ribosomal protein L3 [Oryza sativa]

310486 Seq. No.

Seq. ID uC-zmroteosinte026h05b1

Method BLASTN g295845 NCBI GI BLAST score 180 E value 2.0e-96 Match length 305 % identity 91

NCBI Description T.harzianum mRNA (clone CONS)

Seq. No. 310487

Seq. ID uC-zmroteosinte027c02b1

Method BLASTX g1351129 NCBI GI BLAST score 793 E value 6.0e-85 Match length 175 % identity

NCBI Description MITOGEN-ACTIVATED PROTEIN KINASE STY1 (MAP KINASE STY1)

>gi 2130460 pir S57930 MAP kinase - fission yeast

(Schizosaccharomyces pombe) >gi 2130485 pir S62551 STY1

protein - fission yeast (Schizosaccharomyces pombe)



>gi_1488373_bbs_175803 Phh1p=Hog1-like MAP kinase
[Schizosaccharomyces pombe=fission yeast, L972, Peptide,
349 aa] >gi_897810_emb_CAA61537_ (X89262) MAP kinase
[Schizosaccharomyces pombe] >gi_1022685 (U26739) Spc1p
[Schizosaccharomyces pombe] >gi_1061294_emb_CAA91771_
(Z67757) Sty1p [Schizosaccharomyces pombe]

Seq. No. 310488
Seq. ID uC-zmroteosinte027f12b1
Method BLASTX
NCBI GI g2129652
BLAST score 200
E value 2.0e-15
Match length 140

36

NCBI Description myosin heavy chain homolog - Arabidopsis thaliana

(fragment) >gi_699495 (U19616) myosin heavy chain homolog

A.S.

[Arabidopsis thaliana]

Seq. No. 310489
Seq. ID uC-zmroteosinte028c07b1
Method BLASTX
NCBI GI g3879754
BLAST score 174
E value 2.0e-12
Match length 92

% identity

% identity 45

NCBI Description (Z72514) Similarity to Rabbit glycogenin (SW:GLYG RABIT)

[Caenorhabditis elegans]

Seq. No. 310490

Seq. ID uC-zmroteosinte028f08b1

Method BLASTX
NCBI GI g4096756
BLAST score 214
E value 4.0e-17
Match length 111
% identity 43

NCBI Description (U39394) alpha-1,3/4-fucosidase precursor [Streptomyces

sp.]

Seq. No. 310491

Seq. ID uC-zmroteosinte028g04b1

Method BLASTX
NCBI GI g3643607
BLAST score 221
E value 5.0e-18
Match length 72
% identity 58

NCBI Description (AC005395) unknown protein [Arabidopsis thaliana]

Seq. No. 310492

Seq. ID uC-zmroteosinte028h08b1

Method BLASTX
NCBI GI g2117937
BLAST score 283
E value 4.0e-25

```
Match length
                   96
                   58
% identity
NCBI Description
                  UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) -
                  barley >gi 1212996 emb CAA62689 (X91347) UDP-glucose
                  pyrophosphorylase [Hordeum vulgare]
Seq. No.
                  310493
                  uC-zmroteosinte029a11b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1181331
BLAST score
                  416
E value
                  6.0e-42
Match length
                  117
% identity
                  72
NCBI Description
                  (X77569) calnexin [Zea mays]
                  310494
Seq. No.
Seq. ID
                  uC-zmroteosinte029b03b1
Method
                  BLASTX
NCBI GI
                  q2760325
BLAST score
                  170
                  6.0e-12
E value
Match length
                  50
% identity
                  62
NCBI Description
                  (AC002130) F1N21.10 [Arabidopsis thaliana]
                  310495
Seq. No.
Seq. ID
                  uC-zmroteosinte029c07b1
Method
                  BLASTX
NCBI GI
                  q4406778
BLAST score
                  147
E value
                  3.0e-09
Match length
                  79
% identity
                  44
NCBI Description
                   (AC006532) putative brassinosteroid insensitive protein
                   [Arabidopsis thaliana]
Seq. No.
                  310496
Seq. ID
                  uC-zmroteosinte029g02b1
Method
                  BLASTX
NCBI GI
                  g3041738
BLAST score
                  305
E value
                  8.0e-28
Match length
                  127
% identity
                  50
NCBI Description
                  T-COMPLEX PROTEIN 1, ETA SUBUNIT (TCP-1-ETA) (CCT-ETA)
                   (HIV-1 NEF INTERACTING PROTEIN) >gi 2559010 (AF026292)
                  chaperonin containing t-complex polypeptide 1, eta subunit;
                  CCT-eta [Homo sapiens]
Seq. No.
                  310497
                  uC-zmroteosinte029h01b1
Seq. ID
```

Method BLASTX

Method BLASTX
NCBI GI g2335096
BLAST score 218
E value 1.0e-17
Match length 99



% identity 47
NCBI Description (AC002339) hypothetical protein [Arabidopsis thaliana]
Seq. No. 310498

Seq. ID uC-zmroteosinte030a03b1
Method BLASTX
NCBI GI g1750380
BLAST score 501
E value 8.0e-51
Match length 117

% identity 80 NCBI Description (U80912) Eucalyptus globulus NADP- isocitrate dehydrogenase

of Eucalyptus globulus bicostata [Eucalyptus globulus]

Seq. No. 310499

Seq. ID uC-zmroteosinte030a10b1

Method BLASTX
NCBI GI g266578
BLAST score 281
E value 5.0e-25
Match length 58
% identity 88

NCBI Description METALLOTHIONEIN-LIKE PROTEIN 1 >gi_100898_pir__S17560 metallothionein-like protein - maize >gi_236730 bbs 57629

(S57628) metallothionein homologue [Zea mays, Peptide, 76

aa] [Zea mays] >gi_559536 emb CAA57676 (X82186)

metallothionein- like protein [Zea mays]

>gi_228095_prf__1717215A metallothionein-like protein [Zea

mays]

Seq. No. 310500

Seq. ID uC-zmroteosinte030b06b1

Method BLASTX
NCBI GI g1363487
BLAST score 202
E value 6.0e-19
Match length 96
% identity 60

NCBI Description IAA7 protein - Arabidopsis thaliana >gi 972917 (U18409)

IAA7 [Arabidopsis thaliana]

Seq. No. 310501

Seq. ID uC-zmroteosinte030d05b1

Method BLASTX
NCBI GI g3935181
BLAST score 248
E value 7.0e-22
Match length 87
% identity 66

NCBI Description (AC004557) F17L21.24 [Arabidopsis thaliana]

Seq. No. 310502

Seq. ID uC-zmroteosinte030d12b1

Method BLASTX
NCBI GI g399854
BLAST score 243
E value 1.0e-20

Seq. No.

Seq. ID

NCBI GI

E value

BLAST score

Method



```
Match length
                  82
% identity
NCBI Description
                  HISTONE H2B.2 >gi 283042 pir S28049 histone H2B - maize
                  >gi 22325_emb CAA40565_ (X57313) H2B histone [Zea mays]
                  310503
Seq. No.
                  uC-zmroteosinte030f01b1
Seq. ID
Method
                  BLASTX
                  g2660670
NCBI GI
BLAST score
                  247
E value
                  4.0e-21
Match length
                  85
% identity
                  55
NCBI Description
                  (AC002342) putative Cu2+-transporting ATPase [Arabidopsis
                  thaliana]
Seq. No.
                  310504
Seq. ID
                  uC-zmroteosinte030f02b1
Method
                  BLASTX
NCBI GI
                  q82696
BLAST score
                  164
                  1.0e-24
E value
Match length
                  82
                  78
% identity
NCBI Description
                  glycine-rich protein - maize >gi 22293 emb CAA43431
                  (X61121) glycine-rich protein [Zea mays]
                  310505
Seq. No.
Seq. ID
                  uC-zmroteosinte030g01b1
Method
                  BLASTX
                  g3860277
NCBI GI
BLAST score
                  289
E value
                  4.0e-26
Match length
                  93
% identity
                  62
NCBI Description
                  (AC005824) putative ribosomal protein L10 [Arabidopsis
                  thaliana] >gi_4314394_gb_AAD15604_ (AC006232) putative
                  ribosomal protein L10A [Arabidopsis thaliana]
Seq. No.
                  310506
Seq. ID
                  uC-zmroteosinte031c07b1
Method
                  BLASTX
NCBI GI
                  g537404
BLAST score
                  390
E value
                  8.0e-38
Match length
                  84
% identity
                  82
NCBI Description
                  (D26537) WSI76 protein induced by water stress [Oryza
                  satival
```

3.0e-32Match length 88

72

310507

BLASTN

g312180

uC-zmroteosinte031c10b1



```
% identity
NCBI Description Z.mays GapC4 gene
                  310508
Seq. No.
                  uC-zmroteosinte031d02b1
Seq. ID
                  BLASTX
Method
                  q3738297
NCBI GI
BLAST score
                  333
                  4.0e-31
E value
Match length
                  113
                  32
% identity
NCBI Description (AC005309) unknown protein [Arabidopsis thaliana]
Seq. No.
                  310509
Seq. ID
                  uC-zmroteosinte031d09b1
                  BLASTN
Method
                                                        - 2
NCBI GI
                  g3452291
BLAST score
                  194
E value
                  1.0e-105
Match length
                  248
                  95
% identity
NCBI Description Zea mays retrotransposon Huck-2 3' LTR, partial sequence
                  310510
Seq. No.
Seq. ID
                  uC-zmroteosinte031e01b1
Method
                  BLASTX
NCBI GI
                  g4138265
BLAST score
                  362
                  4.0e-39
E value
Match length
                  91
                  82
% identity
NCBI Description (AJ006228) Avr9 elicitor response protein [Nicotiana
                  tabacum]
Seq. No.
                  310511
Seq. ID
                  uC-zmroteosinte031h01b1
Method
                  BLASTX
NCBI GI
                  q3170242
BLAST score
                  347
E value
                  9.0e-33
Match length
                  115
% identity
                  63
NCBI Description (AF042732) diphenol oxidase-A2 [Anopheles gambiae]
Seq. No.
                  310512
Seq. ID
                  uC-zmroteosinte031h11b1
Method
                  BLASTX
NCBI GI
                  q902586
BLAST score
                  582
```

E value 2.0e-60 Match length 133 % identity 20

NCBI Description (U29162) ubiquitin [Zea mays]

Seq. No. 310513

Seq. ID uC-zmroteosinte032a05b1

Method BLASTX

BLAST score

454

```
g3935181
NCBI GI
BLAST score
                  160
E value
                  2.0e-11
Match length
                  54
                  63
% identity
                  (AC004557) F17L21.24 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  310514
                  uC-zmroteosinte032c06b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1076315
BLAST score
                  196
E value
                  6.0e-15
Match length
                  72
% identity
                  60
                  cytochrome P450 - Arabidopsis thaliana
NCBI Description
                  >gi_853719 emb CAA60793 (X87367) CYP90 protein
                   [Arabidopsis thaliana] >gi 871988 emb CAA60794 (X87368)
                  CYP90 protein [Arabidopsis thaliana]
Seq. No.
                  310515
Seq. ID
                  uC-zmroteosinte032d11b1
                  BLASTX
Method
NCBI GI
                  g3522948
BLAST score
                  397
E value
                  1.0e-38
Match length
                  134
% identity
                  58
                  (AC004411) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  310516
Seq. No.
                  uC-zmroteosinte032e08b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1084336
BLAST score
                  198
E value
                  3.0e-15
Match length
                  54
% identity
                  69
NCBI Description
                  chlorophyll a/b-binding protein type II - Arabidopsis
                  thaliana >gi_541565 (U03395) PSI type II chlorophyll
                  a/b-binding protein [Arabidopsis thaliana]
Seq. No.
                  310517
Seq. ID
                  uC-zmroteosinte032q04b1
Method
                  BLASTX
NCBI GI
                  g4559327
BLAST score
                  183
E value
                  2.0e-13
Match length
                  154
                  30
% identity
NCBI Description
                  (AC007087) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  310518
Seq. ID
                  uC-zmroteosinte033a11b1
Method
                  BLASTX
NCBI GI
                  g3928758
```



E value 3.0e-45
Match length 136
% identity 61

NCBI Description (AB007987) Lipoic acid synthase [Arabidopsis thaliana]

>gi_4454462_gb_AAD20909_ (AC006234) putative lipoic acid

synthase [Arabidopsis thaliana]

Seq. No. 310519

Seq. ID uC-zmroteosinte033b01b1

Method BLASTX
NCBI GI g3041738
BLAST score 513
E value 4.0e-52
Match length 139
% identity 68

NCBI Description T-COMPLEX PROTEIN 1, ETA SUBUNIT (TCP-1-ETA) (CCT-ETA)

(HIV-1 NEF INTERACTING PROTEIN) >gi_2559010 (AF026292) chaperonin containing t-complex polypeptide 1, eta subunit;

CCT-eta [Homo sapiens]

Seq. No. 310520

Seq. ID uC-zmroteosinte033b12b1

Method BLASTX
NCBI GI g3176686
BLAST score 275
E value 2.0e-24
Match length 113
% identity 50

NCBI Description (AC003671) Similar to high affinity potassium transporter,

HAK1 protein gb U22945 from Schwanniomyces occidentalis.

[Arabidopsis thaliana]

Seq. No. 310521

Seq. ID uC-zmroteosinte033c12b1

Method BLASTX
NCBI GI g3250675
BLAST score 161
E value 7.0e-11
Match length 67
% identity 54

NCBI Description (AL024486) putative protein [Arabidopsis thaliana]

Seq. No. 310522

Seq. ID uC-zmroteosinte033d04b1

Method BLASTX
NCBI GI g3004551
BLAST score 186
E value 8.0e-14
Match length 90
% identity 43

NCBI Description (AC003673) hypothetical protein [Arabidopsis thaliana]

Seq. No. 310523

Seq. ID uC-zmroteosinte033f03b1

MethodBLASTXNCBI GIg4262245BLAST score170

```
E value
                  4.0e-12
Match length
                  71
% identity
                  52
NCBI Description
                  (AC006200) hypothetical protein [Arabidopsis thaliana]
                  310524
Seq. No.
                  uC-zmroteosinte033f11b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2493852
BLAST score
                  215
E value
                  2.0e-17
Match length
                  62
% identity
                  68
NCBI Description
                  CYTOCHROME C OXIDASE POLYPEPTIDE VC
                  >gi_1070356_emb_CAA92107 (Z68091) cytochrome c oxidase, Vc
                  subunit [Hordeum vulgare]
Seq. No.
                  310525
Seq. ID
                  uC-zmroteosinte033g05b1
Method
                  BLASTX
NCBI GI
                  g2367392
BLAST score
                  365
                  8.0e-35
E value
Match length
                  124
% identity
                  56
NCBI Description
                  (U82513) random slug cDNA25 protein [Dictyostelium
                  discoideum]
Seq. No.
                  310526
Seq. ID
                  uC-zmroteosinte033g07b1
Method
                  BLASTX
NCBI GI
                  g3236240
BLAST score
                  302
E value
                  1.0e-27
Match length
                  125
% identity
                  50
NCBI Description (AC004684) unknown protein [Arabidopsis thaliana]
Seq. No.
                  310527
Seq. ID
                  uC-zmroteosinte034b02b1
Method
                  BLASTX
NCBI GI
                  g2961377
BLAST score
                  219
```

E value 1.0e-17 Match length 155 % identity

NCBI Description (AL022141) putative receptor protein kinase [Arabidopsis thaliana] -

Seq. No. 310528 Seq. ID uC-zmroteosinte034b04b1 Method BLASTN g3747049 NCBI GI

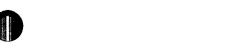
BLAST score 109 E value 2.0e-54 Match length 218 % identity 92

Match length

% identity

97

85



NCBI Description Zea mays ribosomal protein L26 mRNA, partial cds Seq. No. 310529 Seq. ID uC-zmroteosinte034b07b1 Method BLASTX NCBI GI q4508081 BLAST score 202 E value 1.0e-15 Match length 128 % identity 30 NCBI Description (AC005882) Hypothetical protein [Arabidopsis thaliana] Seq. No. 310530 Seq. ID uC-zmroteosinte034d03b1 Method BLASTN NCBI GI q22312 BLAST score 63 E value 7.0e-27 Match length 137 % identity 93 NCBI Description Maize ABA-inducible gene for glycine-rich protein (ABA = abscisic acid) Seq. No. 310531 Seq. ID uC-zmroteosinte034f08b1 Method BLASTX NCBI GI g3894178 BLAST score 142 4.0e-11 E value Match length 47 % identity 68 NCBI Description (AC005312) putative nucleic acid binding protein [Arabidopsis thaliana] Seq. No. 310532 Seq. ID uC-zmroteosinte034g07b1 Method BLASTX NCBI GI q3041738 BLAST score 189 E value 4.0e-16 Match length 146 % identity 34 T-COMPLEX PROTEIN 1, ETA SUBUNIT (TCP-1-ETA) (CCT-ETA) NCBI Description (HIV-1 NEF INTERACTING PROTEIN) >gi 2559010 (AF026292) chaperonin containing t-complex polypeptide 1, eta subunit; CCT-eta [Homo sapiens] Seq. No. 310533 Seq. ID uC-zmroteosinte034h07b1 Method BLASTN NCBI GI g3341647 BLAST score 37 E value 3.0e-11

NCBI Description Zea mays Ama gene encoding single-subunit RNA polymerase



Seq. No. 310534

Seq. ID uC-zmroteosinte035b07b2

Method BLASTX
NCBI GI g730606
BLAST score 150
E value 2.0e-09
Match length 79
% identity 43

NCBI Description DNA-DIRECTED RNA POLYMERASES I, II, AND III 7.7 KD POLYPEPTIDE (ABC10-ALPHA) >gi 1363863 pir S58932

DNA-directed RNA polymerase (EC 2.7.7.6) chain ABC10 alpha - yeast (Saccharomyces cerevisiae) >gi_733518 (U23378) RNA polymerase I, II and III subunit ABC10 alpha [Saccharomyces cerevisiae] >gi_2358017 (U10397) Rpb12p: RNA polymerase II

subunit [Saccharomyces cerevisiae]

Seq. No. 310535

Seq. ID uC-zmroteosinte035b10b2

Method BLASTX
NCBI GI g115679
BLAST score 317
E value 5.0e-29
Match length 82
% identity 76

NCBI Description CATALASE ISOZYME

Seq. No. 310536

Seq. ID uC-zmroteosinte035c07b2

Method BLASTN
NCBI GI g22314
BLAST score 57
E value 7.0e-24
Match length 113
% identity 88

NCBI Description Maize mRNA for GSH gluthathione S-transferase I (GST; EC

2.5.1.18)

Seq. No. 310537

Seq. ID uC-zmroteosinte035c11b2

Method BLASTN
NCBI GI g998429
BLAST score 40
E value 5.0e-13
Match length 64
% identity 91

NCBI Description GRF1=general regulatory factor [Zea mays, XL80, Genomic,

5348 nt]

Seq. No. 310538

Seq. ID uC-zmroteosinte035g03b2

Method BLASTX
NCBI GI g2827630
BLAST score 354
E value 2.0e-33
Match length 159
% identity 46

NCBI Description (AL021636) putative protein [Arabidopsis thaliana]

% identity

NCBI Description

51

sapiens]



```
Seq. No.
                   310539
Seq. ID
                   uC-zmroteosinte035q05b2
Method
                   BLASTX
NCBI GI
                   q3548810
BLAST score
                   283
E value
                   4.0e-25
Match length
                   136
% identity
                   40
NCBI Description
                   (AC005313) putative chloroplast nucleoid DNA binding
                  protein [Arabidopsis thaliana]
Seq. No.
                   310540
Seq. ID
                  uC-zmroteosinte035h02b2
Method
                   BLASTX
NCBI GI
                   q2190992
BLAST score
                   220
E value
                   9.0e-18
Match length
                   120
% identity
                   42
NCBI Description
                   (AF004358) glutathione S-transferase TSI-1 [Aegilops
                  tauschii]
Seq. No.
                   310541
Seq. ID
                  uC-zmroteosinte036a06b1
Method
                  BLASTX
                  g1705735
NCBI GI
BLAST score
                  194
                  1.0e-19
E value
Match length
                   67
                   79
% identity
NCBI Description
                  CALCIUM-DEPENDENT PROTEIN KINASE, ISOFORM 11 (CDPK 11)
                  >gi_1362175_pir__S56651 probable calcium-dependent protein
                   kinase (clone OSCPK11) - rice >gi_587500_emb_CAA57156
                   (X81393) calcium-dependent protein kinase [Oryza sativa]
Seq. No.
                   310542
Seq. ID
                  uC-zmroteosinte036a11b1
Method
                  BLASTN
NCBI GI
                  q2944384
BLAST score
                   63
E value
                  3.0e-27
Match length
                  111
% identity
                  90
                  Oryza sativa calcium dependent protein kinase (CDPK12)
NCBI Description
                  mRNA, complete cds
Seq. No.
                  310543
Seq. ID
                  uC-zmroteosinte036b01b1
Method
                  BLASTX
NCBI GI
                  g189422
BLAST score
                  233
E value
                  7.0e-28
Match length
                  142
```

(M32110) proliferating cell nuclear protein P120 [Homo

% identity

64

```
Seq. No.
                  310544
Seq. ID
                  uC-zmroteosinte036c04b1
Method
                  BLASTX
NCBI GI
                  q3668171
                  286
BLAST score
E value
                  2.0e-25
                  168
Match length
% identity
                  43
                  (AB006052) RNA polymerase I second-largest subunit
NCBI Description
                  [Neurospora crassa]
Seq. No.
                  310545
                  uC-zmroteosinte036e10b1
Seq. ID
Method
                  BLASTX
                  a2499610
NCBI GI
                  225
BLAST score
E value
                  3.0e-18
Match length
                  46
                  96
% identity
                  MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG 6 (MAP KINASE 6)
NCBI Description
                   (ATMPK6) >gi_629547_pir__S40472 mitogen-activated protein
                  kinase 6 (EC 2.7.1.-) - Arabidopsis thaliana
                  >gi_457404_dbj_BAA04869_ (D21842) MAP kinase [Arabidopsis
                  thaliana] >gi_2281091 (AC002333) MAP Kinase 6 [Arabidopsis
                  thaliana]
Seq. No.
                  310546
Seq. ID
                  uC-zmroteosinte036f01b1
                  BLASTN
Method
                  g3004949
NCBI GI
                  82
BLAST score
                  2.0e-38
E value
Match length
                  178
% identity
NCBI Description
                  Zea mays tonoplast intrinsic protein (ZmTIP1) mRNA,
                  complete cds
Seq. No.
                  310547
Seq. ID
                  uC-zmroteosinte036f02b1
Method
                  BLASTX
NCBI GI
                  g3873821
BLAST score
                  234
E value
                  2.0e-19
Match length
                  72
% identity
NCBI Description
                  (Z68213) cDNA EST yk266c4.5 comes from this gene; cDNA EST
                  yk266c4.3 comes from this gene [Caenorhabditis elegans]
Seq. No.
                  310548
Seq. ID
                  uC-zmroteosinte036h08b1
Method
                  BLASTX
NCBI GI
                  g1632831
BLAST score
                  288
                  7.0e-26
E value
Match length
                  91
```



```
NCBI Description (Z49698) orf [Ricinus communis]
```

Seq. No. 310549

Seq. ID uC-zmroteosinte037a02b1

Method BLASTX
NCBI GI g3023816
BLAST score 159
E value 9.0e-11
Match length 73
% identity 52

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC

>gi 968996 (U31676) glyceraldehyde-3-phosphate

dehydrogenase [Oryza sativa]

Seq. No. 310550

Seq. ID uC-zmroteosinte037a10b1

Method BLASTX
NCBI GI g1346073
BLAST score 390
E value 6.0e-38
Match length 112
% identity 66

NCBI Description GLUCOSE-6-PHOSPHATE ISOMERASE, CYTOSOLIC (GPI)

(PHOSPHOGLUCOSE ISOMERASE) (PGI) (PHOSPHOHEXOSE ISOMERASE) (PHI) >gi_596023 (U17225) glucose-6 phosphate isomerase

[Zea mays]

Seq. No. 310551

Seq. ID uC-zmroteosinte037b04b1

Method BLASTX
NCBI GI g3695389
BLAST score 401
E value 5.0e-39
Match length 150
% identity 26

NCBI Description (AF096371) contains similarity to D-isomer specific

2-hydroxyacid dehydrogenases (Pfam: 2-Hacid_DH.hmm, score:

19.11) [Arabidopsis thaliana]

Seq. No. 310552

Seq. ID uC-zmroteosinte037c10b1

Method BLASTX
NCBI GI g4587533
BLAST score 210
E value 1.0e-16
Match length 64
% identity 62

NCBI Description (AC007060) EST gb AA721821 comes from this gene.

[Arabidopsis thaliana]

Seq. No. 310553

Seq. ID uC-zmroteosinte037f07b1

Method BLASTX
NCBI GI g3033399
BLAST score 254
E value 7.0e-22
Match length 134



```
% identity
NCBI Description
                  (AC004238) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   310554
                  uC-zmroteosinte037g04b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2979554
BLAST score
                   171
E value
                   4.0e-12
Match length
                   91
                   47
% identity
                  (AC003680) CDC4 like protein [Arabidopsis thaliana]
NCBI Description
                  310555
Seq. No.
Seq. ID
                  uC-zmroteosinte037g08b1
Method
                  BLASTX
NCBI GI
                   g4126809
BLAST score
                   232
E value
                   3.0e-19
Match length
                   46
% identity
                   93
NCBI Description
                  (AB017042) glyoxalase I [Oryza sativa]
Seq. No.
                   310556
Seq. ID
                   uC-zmroteosinte037h06b1
Method
                  BLASTX
NCBI GI
                   g3540190
BLAST score
                  235
E value
                   1.0e-19
Match length
                   80
% identity
                   53
NCBI Description
                  (AC004122) Hypothetical protein [Arabidopsis thaliana]
                  310557
Seq. No.
                  uC-zmroteosinte037h11b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g129021
BLAST score
                  286
E value
                   1.0e-25
Match length
                  123
                  50
% identity
NCBI Description
                  SPOOB-ASSOCIATED GTP-BINDING PROTEIN >gi 98326 pir B32804
                  GTP-binding protein, spo0B 3'-region - Bacillus subtilis
                  >gi 508979 (M24537) GTP-binding protein [Bacillus subtilis]
                  >gi 2635257 emb CAB14752 (Z99118) GTPase activity
                   [Bacillus subtilis]
Seq. No.
                  310558
Seq. ID
                  uC-zmroteosinte037h12b1
Method
                  BLASTX
NCBI GI
                  g4586116
BLAST score
                  372
E value
                  1.0e-35
Match length
                  151
% identity
                   46
NCBI Description
                  (ALO49638) putative C-4 sterol methyl oxidase [Arabidopsis
```

44251

thaliana]

```
Seq. No.
                   310559
Seq. ID
                   uC-zmroteosinte038a01b1
Method
                   BLASTN
NCBI GI
                   q2832242
BLAST score
                   66
E value
                   1.0e-28
Match length
                   260
% identity
                   87
NCBI Description
                  Zea mays 22-kDa alpha zein gene cluster, complete sequence
Seq. No.
                   310560
Seq. ID
                   uC-zmroteosinte038a08b1
Method
                   BLASTN
NCBI GI
                   g1181330
BLAST score
                   53
E value
                   3.0e-21
Match length
                   105
% identity
                   89
NCBI Description Z.mays CNX mRNA
Seq. No.
                   310561
Seq. ID
                   uC-zmroteosinte038c01b1
Method
                   BLASTX
NCBI GI
                   g417494
BLAST score
                   189
                   2.0e-14
E value
Match length
                   87
% identity
                   48
NCBI Description
                  18 KD SEED MATURATION PROTEIN >gi 170008 (M80666)
                   maturation polypeptide [Glycine max]
                   >gi_444332_prf__1906381A 18kD late embryogenesis abundant
                   protein [Glycine max]
Seq. No.
                   310562
Seq. ID
                   uC-zmroteosinte038c10b1
                   BLASTX
Method
NCBI GI
                   g1905998
BLAST score
                   175
E value
                   1.0e-12
Match length
                   60
% identity
                   65
NCBI Description
                  (U90426) nuclear RNA helicase [Homo sapiens]
Seq. No.
                   310563
Seq. ID
                  uC-zmroteosinte038d06b1
Method
                  BLASTX
NCBI GI
                  g464621
BLAST score
                  267
E value
                  2.0e-23
Match length
                  100
% identity
                  57
NCBI Description
                  60S RIBOSOMAL PROTEIN L6 (YL16-LIKE) >gi_280374 pir S28586
                  ribosomal protein ML16 - common ice plant
```

[Mesembryanthemum crystallinum]

>gi_19539_emb_CAA49175_ (X69378) ribosomal protein YL16

```
Seq. No.
                   310564
Seq. ID
                  uC-zmroteosinte038e09b1
Method
                  BLASTX
NCBI GI
                   g2584860
BLAST score
                   312
E value
                   1.0e-28
Match length
                  131
% identity
                   46
NCBI Description
                  (U97665) subunit III precursor [Erwinia cypripedii]
Seq. No.
                  310565
Seq. ID
                  uC-zmroteosinte038f02b1
Method
                  BLASTX
NCBI GI
                   g3913427
BLAST score
                  396
E value
                   1.0e-38
Match length
                  109
% identity
                  72
                  S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC)
NCBI Description
                   (SAMDC) >gi_1532073_emb_CAA69075_ (Y07767)
                   S-adenosylmethionine decarboxylase [Zea mays]
Seq. No.
                  310566
Seq. ID
                  uC-zmroteosinte038f03b1
Method
                  BLASTX
NCBI GI
                  g974782
BLAST score
                   631
E value
                  5.0e-66
Match length
                  135
% identity
                  90
NCBI Description
                  (Z49150) cobalamine-independent methionine synthase
                   [Solenostemon scutellarioides]
Seq. No.
                  310567
Seq. ID
                  uC-zmroteosinte038g01b1
Method
                  BLASTX
NCBI GI
                  g4587550
BLAST score
                  461
E value
                  4.0e-46
Match length
                  138
% identity
NCBI Description
                  (AC006577) EST gb R64848 comes from this gene. [Arabidopsis
                  thaliana]
Seq. No.
                  310568
Seq. ID
                  uC-zmroteosinte038h02b1
Method
                  BLASTX
```

Method BLASTX
NCBI GI g118104
BLAST score 325
E value 2.0e-30
Match length 89
% identity 73

NCBI Description PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE)

(CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN)

>gi_68408_pir__CSZM peptidylprolyl isomerase (EC 5.2.1.8) -

maize >gi_168461 (M55021) cyclophilin [Zea mays]

>gi_829148_emb_CAA48638 (X68678) cyclophilin [Zea mays]

BLAST score

E value

47 2.0e-17

```
310569
Seq. No.
Seq. ID
                  uC-zmroteosinte039a07b1
                  BLASTX
Method
NCBI GI
                  g3892056
BLAST score
                  278
                  7.0e-25
E value
                  102
Match length
% identity
                  56
NCBI Description
                  (AC002330) putative vacuolar ATPase [Arabidopsis thaliana]
Seq. No.
                  310570
                  uC-zmroteosinte039a10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2905643
BLAST score
                  354
                  1.0e-33
E value
Match length
                  132
% identity
                  52
NCBI Description
                  (AF045244) ribitol kinase [Klebsiella pneumoniae]
                  310571
Seq. No.
                  uC-zmroteosinte039c08b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3881976
BLAST score
                  143
E value
                  8.0e-09
Match length
                  36
                  75
% identity
NCBI Description
                  (AJ012409) hypothetical protein [Homo sapiens]
Seq. No.
                  310572
Seq. ID
                  uC-zmroteosinte039d04b1
Method
                  BLASTX
NCBI GI
                  g3757522
BLAST score
                  167
E value
                  1.0e-11
                  143
Match length
% identity
                  36
NCBI Description
                  (AC005167) putative splicing factor [Arabidopsis thaliana]
                  310573
Seq. No.
Seq. ID
                  uC-zmroteosinte039e12b1
Method
                  BLASTX
NCBI GI
                  g4454477
BLAST score
                  152
E value
                  7.0e-10
Match length
                  82
% identity
                  43
NCBI Description
                  (AC006234) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  310574
Seq. ID
                  uC-zmroteosinte039f07b1
Method
                  BLASTN
NCBI GI
                  g22324
```



Match length 59 % identity 95 NCBI Description Z.

NCBI Description Z.mays mRNA for H2B histone (clone cH2B221)

Seq. No.

310575

Seq. ID

uC-zmroteosinte039g02b1

Method BLASTX
NCBI GI g3759177
BLAST score 261
E value 1.0e-22
Match length 72
% identity 71

NCBI Description (AB018408) 3-phosphoserine phosphatase [Arabidopsis thaliana] >qi 3759179 dbj BAA33807.1 (AB018409)

3-phosphoserin phosphatase [Arabidopsis thaliana]

Seq. No. 310576

Seq. ID uC-zmroteosinte039g12b1

Method BLASTX
NCBI GI g2370493
BLAST score 166
E value 2.0e-11
Match length 104
% identity 37

NCBI Description (298944) hypothetical protein [Schizosaccharomyces pombe]

Seq. No. 310577

Seq. ID uC-zmroteosinte040a09b1

Method BLASTX
NCBI GI g2213597
BLAST score 155
E value 3.0e-10
Match length 108
% identity 31

NCBI Description (ACO00348) T7N9.17 [Arabidopsis thaliana]

Seq. No.

310578

Seq. ID uC-zmroteosinte040b03b1

Method BLASTX
NCBI GI g3341678
BLAST score 403
E value 3.0e-39
Match length 162
% identity 52

NCBI Description (AC003672) putative zinc finger protein [Arabidopsis

thaliana]

Seq. No.

310579

Seq. ID

uC-zmroteosinte040g09b1

Method BLASTX
NCBI GI g4455250
BLAST score 393
E value 6.0e-38
Match length 173
% identity 49

NCBI Description (AL035523) putative protein [Arabidopsis thaliana]

BLAST score

Match length

E value

68

120

4.0e-30



```
310580
Seq. No.
                  uC-zmroteosinte041a07b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4567197
BLAST score
                  309
                  3.0e-28
E value
                  171
Match length
% identity
                  42
                  (AC007168) unknown protein [Arabidopsis thaliana]
NCBI Description
                  310581
Seq. No.
                  uC-zmroteosinte041a10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3702329
BLAST score
                  174
                  2.0e-12
E value
                  96
Match length
% identity
                  39
                  (AC005397) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  310582
                  uC-zmroteosinte041c12b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3236248
BLAST score
                  234
                  2.0e-19
E value
Match length
                  76
% identity
                  66
                  (AC004684) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  310583
                  uC-zmroteosinte041d08b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1870214
BLAST score
                  250
E value
                  3.0e-21
Match length
                  153
% identity
                  45
                  (AC000133) G4P04 [Emericella nidulans]
NCBI Description
Seq. No.
                  310584
                  uC-zmroteosinte041e06b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1709970
BLAST score
                   400
                  5.0e-39
E value
Match length
                  118
% identity
                   68
NCBI Description 60S RIBOSOMAL PROTEIN L10A
Seq. No.
                  310585
Seq. ID
                  uC-zmroteosinte041f12b1
Method
                  BLASTN
NCBI GI
                  q2668747
```

```
% identity
                  Zea mays ribosomal protein L17 (rpl17) mRNA, complete cds
NCBI Description
                  310586
Seq. No.
Seq. ID
                  uC-zmroteosinte041q12b1
Method
                  BLASTN
NCBI GI
                  q467995
BLAST score
                  218
                  1.0e-119
E value
                  438
Match length
% identity
                  93
NCBI Description
                  Zea mays flavanone 3-beta-hydroxylase (fht) mRNA, complete
                  310587
Seq. No.
                  uC-zmroteosinte042b03b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4454474
BLAST score
                  272
E value
                  7.0e-24
Match length
                  116
                  43
% identity
NCBI Description
                  (AC006234) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  310588
                  uC-zmroteosinte042c04b1
Seq. ID
Method
                  BLASTX
                  a4503363
NCBI GI
BLAST score
                  372
                  1.0e-35
E value
Match length
                  149
% identity
                  49
                  UNKNOWN >gi_3062806_dbj_BAA25646_ (D86198)
NCBI Description
                  dolichol-phosphate-mannose synthase [Homo sapiens]
Seq. No.
                  310589
Seq. ID
                  uC-zmroteosinte042d02b1
Method
                  BLASTX
NCBI GI
                  q135104
BLAST score
                  331
E value
                  9.0e-31
Match length
                  117
% identity
                  53
NCBI Description
                  MULTIFUNCTIONAL AMINOACYL-TRNA SYNTHETASE (CONTAINS:
                  GLUTAMYL-TRNA SYNTHETASE (GLUTAMATE--TRNA LIGASE), AND
                  PROLYL-TRNA SYNTHETASE (PROLINE--TRNA LIGASE))
                  >gi_68554_pir__SYHUQT glutamyl-prolyl-tRNA synthetase -
                  human >gi_31958_emb_CAA38224_ (X54326) glutaminyl-tRNA
                  synthetase [Homo sapiens]
Seq. No.
                  310590
Seq. ID
                  uC-zmroteosinte042d05b1
Method
                  BLASTN
NCBI GI
                  g2773153
BLAST score
                  83
                  7.0e-39
E value
Match length
                  155
```



% identity 89

NCBI Description Oryza sativa abscisic acid- and stress-inducible protein

(Asr1) mRNA, complete cds

Seq. No. 310591

Seq. ID uC-zmroteosinte042e03b1

Method BLASTX
NCBI GI g3549672
BLAST score 232
E value 6.0e-33
Match length 121
% identity 67

NCBI Description (AL031394) putative protein [Arabidopsis thaliana]

Seq. No. 310592

Seq. ID uC-zmroteosinte042e11b1

Method BLASTX
NCBI GI g3928084
BLAST score 306
E value 6.0e-28
Match length 105
% identity 61

NCBI Description (AC005770) retrotransposon-like protein [Arabidopsis

thaliana]

Seq. No. 310593

Seq. ID uC-zmroteosinte042g05b1

Method BLASTX
NCBI GI g403318
BLAST score 180
E value 5.0e-13
Match length 102
% identity 37

NCBI Description (Z26494) hexaprenyl pyrophosphate synthetase [Saccharomyces

cerevisiae] >gi_1582566_prf__2118405G hexaprenyl pyrophosphate synthetase [Saccharomyces cerevisiae]

Seq. No. 310594

Seq. ID uC-zmroteosinte042h02b1

Method BLASTX
NCBI GI g3482967
BLAST score 255
E value 4.0e-22
Match length 102
% identity 53

NCBI Description (AL031369) Protein phosphatase 2C-like protein [Arabidopsis

thaliana] >gi 4559345 gb AAD23006.1 AC006585 1 (AC006585)

protein phosphatase 2C [Arabidopsis thaliana]

Seq. No. 310595

Seq. ID uC-zmroteosinte042h08b1

Method BLASTX
NCBI GI g4584525
BLAST score 341
E value 4.0e-32
Match length 101
% identity 65



NCBI Description (AL049607) protein phosphatase 2C-like protein [Arabidopsis thaliana]

Seq. No. 310596

Seq. ID uC-zmroteosinte043b11b2

Method BLASTX
NCBI GI g2499542
BLAST score 210
E value 8.0e-17
Match length 76
% identity 57

NCBI Description IRON(III)-ZINC(II) PURPLE ACID PHOSPHATASE PRECURSOR (PAP)

>gi_1218042 (U48448) secreted purple acid phosphatase

precursor [Arabidopsis thaliana]

Seq. No. 310597

Seq. ID uC-zmroteosinte043c07b2

Method BLASTN
NCBI GI g4140643
BLAST score 62
E value 4.0e-26
Match length 121
% identity 97

NCBI Description Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster,

complete sequence

Seq. No. 310598

Seq. ID uC-zmroteosinte043c09b2

Method BLASTX
NCBI GI g4249382
BLAST score 288
E value 9.0e-26
Match length 69
% identity 71

NCBI Description (AC005966) Strong similarity to gi_3337350 F13P17.3

putative permease from Arabidopsis thaliana BAC

gb_AC004481. [Arabidopsis thaliana]

Seq. No. 310599

Seq. ID uC-zmroteosinte043f06b2

Method BLASTX
NCBI GI g2854190
BLAST score 259
E value 1.0e-23
Match length 94
% identity 56

NCBI Description (AF045645) similar to purine nucleoside phosphorylases

[Caenorhabditis elegans]

Seq. No. 310600

Seq. ID uC-zmroteosinte043g08b2

85

Method BLASTN
NCBI GI g2832242
BLAST score 43
E value 6.0e-15
Match length 219

% identity

```
NCBI Description Zea mays 22-kDa alpha zein gene cluster, complete sequence
                    310601
 Seq. No.
 Seq. ID
                    uC-zmroteosinte043h01b2
 Method
                    BLASTX
 NCBI GI
                    g3850139
 BLAST score
                    154
 E value
                    2.0e-10
 Match length
                    56
 % identity
                    52
 NCBI Description
                   (AL033391) potential membrane protein [Candida albicans]
 Seq. No.
                    310602
 Seq. ID
                    uC-zmroteosinte044b05b2
 Method
                    BLASTX
 NCBI GI
                    g1076791
 BLAST score
                   336
 E value
                    1.0e-31
 Match length
                   79
 % identity
                   76
 NCBI Description
                   calcium-binding protein - maize >gi 2119370 pir $58170
                    Calreticulin precursor - maize >gi 577612_emb_CAA86728
                    (Z46772) calcium-binding protein [Zea mays]
                    >gi 927572 emb CAA61939 (X89813) Calreticulin precursor
                    [Zea mays] >gi_1587033_prf 2205314A calreticulin [Zea
 Seq. No.
                    310603
 Seq. ID
                   uC-zmroteosinte044b11b2
 Method
                   BLASTN
 NCBI GI
                   q4733890
 BLAST score
                    40
 E value
                   3.0e-13
 Match length
                   120
 % identity
                   83
 NCBI Description
                   Zea mays unconventional myosin heavy chain (MYO1) mRNA,
                   partial cds
 Seq. No.
                   310604
 Seq. ID
                   uC-zmroteosinte044d05b2
 Method
                   BLASTX
 NCBI GI
                   q2129550
 BLAST score
                   164
 E value
                   9.0e-12
 Match length
                   65
 % identity
                   52
 NCBI Description
                   calcium-dependent protein kinase (EC 2.7.1.-) CDPK6 -
                   Arabidopsis thaliana >gi_2129554_pir__S71901
                   calcium-dependent protein kinase 6 - Arabidopsis thaliana
                   >gi 836940 (U20623) calcium-dependent protein kinase
                    [Arabidopsis thaliana] >gi_836944 (U20625)
```

Seq. No. 310605

Seq. ID

uC-zmroteosinte044e12b2

protein kinase (CDPK6) [Arabidopsis thaliana]

calcium-dependent protein kinase [Arabidopsis thaliana] >gi_4454034 emb CAA23031.1 (AL035394) calcium-dependent

NCBI GI

BLAST score

```
Method
                   BLASTX
NCBI GI
                   q1703378
BLAST score
                   209
E value
                   7.0e-17
Match length
                   85
% identity
                   53
                   ADP-RIBOSYLATION FACTOR 4 >gi_967251 (U31460) Arf4 [Xenopus
NCBI Description
Seq. No.
                   310606
Seq. ID
                   uC-zmroteosinte044f03b2
Method
                   BLASTN
NCBI GI
                   q1532072
BLAST score
                   46
E value
                   7.0e-17
Match length
                   163
% identity
                   88
NCBI Description Z.mays mRNA for S-adenosylmethionine decarboxylase
Seq. No.
                   310607
Seq. ID
                   uC-zmroteosinte044f11b2
Method
                   BLASTX
NCBI GI
                   g2564249
BLAST score
                   224
                   3.0e-18
E value
Match length
                   96
% identity
                   47
NCBI Description
                   (Y08686) serine palmitoyltransferase, subunit II [Homo
                   sapiens] >gi_3043576_dbj_BAA25452 (AB011098) KIAA0526
                   protein [Homo sapiens] >gi_4186182 (AF111168) serine
                   palmitoyl transferase, subunit II [Homo sapiens]
Seq. No.
                   310608
Seq. ID
                   uC-zmroteosinte044q08b2
Method
                   BLASTX
NCBI GI
                   q4539401
BLAST score
                   310
E value
                   1.0e-28
Match length
                   94
% identity
                   59
NCBI Description (AL035526) putative protein [Arabidopsis thaliana]
Seq. No.
                   310609
Seq. ID
                  uC-zmroteosinte045a03b2
Method
                  BLASTN
NCBI GI
                  g2832242
BLAST score
                  41
E value
                  9.0e-14
Match length
                  177
% identity
NCBI Description Zea mays 22-kDa alpha zein gene cluster, complete sequence
Seq. No.
                  310610
Seq. ID
                  uC-zmroteosinte045a07b2
Method
                  BLASTX
```

44261

g3377820



E value 7.0e-09 Match length 70

% identity 43

NCBI Description (AF076275) contains similarity to coatomer zeta chains

[Arabidopsis thaliana]

Seq. No. 310611

Seq. ID uC-zmroteosinte045a09b2

Method BLASTX
NCBI GI g4454452
BLAST score 221
E value 3.0e-18
Match length 77
% identity 57

NCBI Description (AC006234) unknown protein [Arabidopsis thaliana]

Seq. No. 310612

Seq. ID uC-zmroteosinte045a10b2

Method BLASTN
NCBI GI g1532072
BLAST score 47
E value 2.0e-17
Match length 217
% identity 81

NCBI Description Z.mays mRNA for S-adenosylmethionine decarboxylase

Seq. No. 310613

Seq. ID uC-zmroteosinte045b05b2

Method BLASTX
NCBI GI g312179
BLAST score 200
E value 6.0e-33
Match length 111
% identity 77

NCBI Description (X73151) glyceraldehyde 3-phosphate dehydrogenase

(phosphorylating) [Zea mays] >gi_1184772 (U45855) cytosolic glyceroldehyde-3-phosphate dehydrogenase GAPC2 [Zea mays]

>gi_1185554 (U45858) glyceraldehyde-3-phosphate

dehydrogenase [Zea mays]

Seq. No. 310614

Seq. ID uC-zmroteosinte045b07b2

Method BLASTX
NCBI GI g3377820
BLAST score 161
E value 3.0e-11
Match length 53
% identity 62

NCBI Description (AF076275) contains similarity to coatomer zeta chains

[Arabidopsis thaliana]

Seq. No. 310615

Seq. ID uC-zmroteosinte045b08b2

MethodBLASTNNCBI GIg2921303BLAST score126E value1.0e-64

Match length % identity 91 NCBI Description Zea mays herbicide safener binding protein (SBP1) mRNA, 310616 Seq. No. Seq. ID uC-zmroteosinte045c04b2 Method BLASTX NCBI GI g312179 472 BLAST score E value 2.0e-47 Match length 115 % identity 79 NCBI Description (X73151) glyceraldehyde 3-phosphate dehydrogenase (phosphorylating) [Zea mays] >gi 1184772 (U45855) cytosolic glyceroldehyde-3-phosphate dehydrogenase GAPC2 [Zea mays] >gi 1185554 (U45858) glyceraldehyde-3-phosphate dehydrogenase [Zea mays] 310617 Seq. No. Seq. ID uC-zmroteosinte045c05b2 Method BLASTX NCBI GI g312179 BLAST score 527 E value 7.0e-54Match length 117 % identity 88 NCBI Description (X73151) glyceraldehyde 3-phosphate dehydrogenase (phosphorylating) [Zea mays] >gi 1184772 (U45855) cytosolic glyceroldehyde-3-phosphate dehydrogenase GAPC2 [Zea mays] >gi_1185554 (U45858) glyceraldehyde-3-phosphate dehydrogenase [Zea mays] Seq. No. 310618 uC-zmroteosinte045c06b2 Seq. ID Method BLASTX NCBI GI q1076809 BLAST score 395 E value 2.0e-38 Match length 115

% identity

NCBI Description H+-transporting ATPase (EC 3.6.1.35) - maize

>gi_758355 emb CAA59800 (X85805) H(+)-transporting ATPase

, š.-

[Zea mays]

Seq. No. 310619

Seq. ID uC-zmroteosinte045c10b2

Method BLASTX NCBI GI g229953 BLAST score 151 E value 3.0e-10 Match length 86 % identity 40

NCBI Description Homarus americanus >gi 229954 pdb 1GPD R Homarus americanus

310620 Seq. No.

Seq. ID uC-zmroteosinte045f10b2



```
BLASTX
Method
                  g113460
NCBI GI
BLAST score
                  195
                  9.0e-18
E value
Match length
                  91
                  62
% identity
                  ADP, ATP CARRIER PROTEIN 2 PRECURSOR (ADP/ATP TRANSLOCASE 2)
NCBI Description
                  (ADENINE NUCLEOTIDE TRANSLOCATOR 2) (ANT 2)
                  >gi 100851 pir S16568 ADP, ATP carrier protein precursor -
                  maize >gi_22164_emb_CAA41812_ (X59086) adenine nucleotide
                  translocator [Zea mays]
                  310621
Seq. No.
                  uC-zmroteosinte045g07b2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4588906
                  200
BLAST score
                  7.0e-16
E value
                  90
Match length
                  53
% identity
                   (AF118149) ribosomal protein S7 [Secale cereale]
NCBI Description
                  310622
Seq. No.
                  uC-zmroteosinte045h05b2
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1483150
BLAST score
                  419
E value
                  3.0e-41
Match length
                  115
                  71
% identity
                   (D84417) monodehydroascorbate reductase [Arabidopsis
NCBI Description
                  thaliana]
                   310623
Seq. No.
                  uC-zmroteosinte046b06b1
Seq. ID
                  BLASTX
Method
                   g2960216
NCBI GI
BLAST score
                   229
E value
                   4.0e-32
Match length
                   109
% identity
                   70
                   (AJ223384) 26S proteasome regulatory ATPase subunit 10b
NCBI Description
                   (S10b) [Manduca sexta]
                   310624
Seq. No.
Seq. ID
                   uC-zmroteosinte046c02b1
Method
                   BLASTX
                   g4508069
NCBI GI
BLAST score
                   152
                   2.0e-10
E value
Match length
                   78
% identity
                   44
```

NCBI Description (AC005882) 12246 [Arabidopsis thaliana]

Seq. No. 310625

Seq. ID uC-zmroteosinte046g05b1

Method BLASTX

NCBI GI

E value

BLAST score

Match length

q453670

3.0e-47

472

114

```
q4263821
NCBI GI
BLAST score
                  273
                  4.0e-24
E value
Match length
                  121
% identity
                  47
                  (AC006067) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  310626
Seq. No.
                  uC-zmroteosinte046h02b1
Seq. ID
Method
                  BLASTN
                  g559535
NCBI GI
BLAST score
                  42
                  1.0e-14
E value
Match length
                  78
% identity
                  88
NCBI Description
                  Z.mays mRNA for metallothionein
                  310627
Seq. No.
                  uC-zmroteosinte047b04b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2226331
BLAST score
                  213
E value
                  2.0e-32
Match length
                  163
% identity
                  59
NCBI Description
                  (AF001635) physical impedance induced protein [Zea mays]
Seq. No.
                  310628
Seq. ID
                  uC-zmroteosinte047d04b2
Method
                  BLASTX
NCBI GI
                  q4544412
BLAST score
                  153
                  3.0e-10
E value
                  50
Match length
% identity
                  54
NCBI Description
                  (AC006955) hypothetical protein [Arabidopsis thaliana]
                  310629
Seq. No.
                  uC-zmroteosinte047e09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3702632
BLAST score
                  141
                  6.0e-09
E value
Match length
                  72
% identity
                  42
NCBI Description
                  (AL031824) putative transcriptional regulator
                  [Schizosaccharomyces pombe] >gi_3859080_emb_CAA21957
                   (AL033406) putative alcohol dehydrogenase repressor protein
                  [Schizosaccharomyces pombe]
Seq. No.
                  310630
Seq. ID
                  uC-zmroteosinte047f09b1
Method
                  BLASTX
```

```
% identity
                  (L28712) heat shock protein 26 [Zea mays]
NCBI Description
                  >gi 227776_prf 1710350A heat shock protein 26 [Zea mays]
Seq. No.
                  310631
                  uC-zmroteosinte047h07b1
Seq. ID
                  BLASTN
Method
                  q1808687
NCBI GI
BLAST score
                  41
E value
                  1.0e-13
Match length
                  73
                  89
% identity
NCBI Description S.stapfianus pSD.13 mRNA
Seg. No.
                  310632
Seq. ID
                  uC-zmroteosinte047h10b1
                  BLASTX
Method
                  q3834310
NCBI GI
                  290
BLAST score
                  4.0e-26
E value
Match length
                  69
% identity
                  81
                  (AC005679) Similar to Ubiquitin-conjugating enzyme E2-17 KD
NCBI Description
                  gb D83004 from Homo sapiens. ESTs gb T88233, gb_Z24464,
                  gb N37265, gb H36151, gb Z34711, gb AA040983, and gb T22122
                  come from this gene. [Arabidopsis thaliana]
Seq. No.
                  310633
Seq. ID
                  uC-zmroteosinte047h11b1
                  BLASTX
Method
                  q2668744
NCBI GI
                  708
BLAST score
                  5.0e-75
E value
Match length
                  130
                  100
% identity
                  (AF034946) ubiquitin conjugating enzyme [Zea mays]
NCBI Description
                  310634
Seq. No.
                  uC-zmroteosinte048b12b1
Seq. ID
                  BLASTX
Method
                  g4585988
NCBI GI
                  496
BLAST score
                  5.0e-50
E value
                  190
Match length
```

52 % identity

(AC005287) Similar to phosphoprotein phosphatase 2A NCBI Description

regulatory subunit [Arabidopsis thaliana]

310635 Seq. No.

Seq. ID uC-zmroteosinte048e03b1

Method BLASTX NCBI GI g2829688 230 BLAST score 7.0e-19 E value Match length 53 89 % identity

NCBI Description CYSTEINE SYNTHASE (O-ACETYLSERINE SULFHYDRYLASE)



(O-ACETYLSERINE (THIOL)-LYASE) (CSASE)

>gi_1076798_pir__S52738 cysteine synthase (EC 4.2.99.8)
precursor - maize >gi 758353 emb CAA59798 (X85803)

cysteine synthase [Zea mays]

Seq. No. 310636

Seq. ID uC-zmroteosinte048f05b1

Method BLASTX
NCBI GI g3915186
BLAST score 189
E value 2.0e-25
Match length 124
% identity 49

NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-21 KD (UBIQUITIN-PROTEIN

LIGASE) (UBIQUITIN CARRIER PROTEIN) (PEROXIN-4) >gi_3128447 (AF061604) ubiquitin-conjugating enzyme homolog peroxin 4

[Pichia angusta]

Seq. No. 310637

Seq. ID uC-zmroteosinte049c03b1

Method BLASTX
NCBI GI 94239889
BLAST score 521
E value 5.0e-53
Match length 102
% identity 98

NCBI Description (AB016802) MAP kinase 5 [Zea mays]

Seq. No. 310638

Seq. ID uC-zmroteosinte049d05b1

Method BLASTX
NCBI GI 94512682
BLAST score 159
E value 1.0e-13
Match length 106
% identity 47

NCBI Description (AC006931) unknown protein [Arabidopsis thaliana]

Seq. No. 310639

Seq. ID uC-zmroteosinte049e06b1

Method BLASTX
NCBI GI g321029
BLAST score 519
E value 6.0e-53
Match length 112
% identity 91

NCBI Description potassium channel protein Slo - fruit fly (Drosophila

melanogaster) $>gi_157776$ (M96840) calcium activated

potassium channel [Drosophila melanogaster]

Seq. No. 310640

Seq. ID uC-zmroteosinte049g07b1

Method BLASTX
NCBI GI g1170711
BLAST score 300
E value 3.0e-27
Match length 94



% identity NCBI Description

SHAGGY RELATED PROTEIN KINASE ASK-ALPHA >gi 541901 pir S41596 protein kinase ASK-alpha (EC 2.7.1.-) - Arabidopsis thaliana >gi_460832_emb_CAA53181_ (X75432) shaggy related kinase [Arabidopsis thaliana] >gi 1769889 emb CAA48538_ (X68525) serine /threonine protein kinase [Arabidopsis thaliana]

Seq. No. 310641

uC-zmroteosinte051a01b2 Seq. ID

Method BLASTX NCBI GI g1814403 BLAST score 548 E value 4.0e-66 Match length 173 % identity 81

(U84889) methionine synthase [Mesembryanthemum NCBI Description

crystallinum]

Seq. No. 310642

uC-zmroteosinte051c01b2 Seq. ID

Method BLASTN g1155264 NCBI GI BLAST score 58 3.0e-24 E value Match length 134 % identity 87

Pennisetum ciliare possible apospory-associated protein NCBI Description

mRNA, complete cds

Seq. No. 310643

uC-zmroteosinte051e09b2 Seq. ID

Method BLASTX NCBI GI g4504279 609 BLAST score E value 3.0e-63 Match length 122 % identity 100 NCBI Description

 ${\tt H3}$ histone, family ${\tt 3A} > {\tt gi_122075_sp_P06351} {\tt H33} {\tt HUMAN}$ HISTONE H3.3 (H3.B) (H3.3 \overline{Q}) >gi $\overline{9}00\overline{4}3$ _pir $\underline{}$ S10168 histone H3.3A - rabbit >gi_90624_pir__S04186 histone H3.3 - mouse

>gi_423678_pir__\$334185 histone H3 - rat
>gi_476852_pir__\$A45941 histone H3 - Atlantic surf clam

>gi_1070596_pir_ HSHU33 histone H3.3 - human >gi_2119006_pir__S61220 histone H3.3 - fruit fly

(Drosophila melanogaster) >gi_2119007_pir__S61215 histone

H3.3 - fruit fly (Drosophila melanogaster)

>gi_2119008_pir__S20109 histone H3.3Q - fruit fly

(Drosophila melanogaster) >gi_2119022_pir__I50245 histone H3.3B - chicken >gi_2119023_pir__S61218 histone H3.3 - fruit fly (Drosophila hydei) >gi_2119024_pir__S61214

histone H3.3 - fruit fly (Drosophila hydei)

>gi_1568_emb_CAA36179_ (X51897) H3.3A histone (AA 1-136)
[Oryctolagus cuniculus] >gi_8046_emb_CAA37819_ (X53822)

Histone H3.3Q [Drosophila melanogaster]

>gi 51198 emb CAA31940 (X13605) Histone H3.3 (AA 1 - 136) [Mus musculus] >gi 63480 emb CAA68458 (Y00392) histone

% identity

57

```
H3.3B (AA 1 - 136) [Gallus gallus] >gi 161190 (M17876)
histone H3 [Spisula solidissima] >gi_211853 (M11393)
histone 3.3 [Gallus gallus] >gi_306848 (M11354) H3.3 histone [Homo sapiens] >gi_306849 (M11353) H3.3 histone
[Homo sapiens] >gi_313319_emb_CAA52035_ (X73683) histon H3
[Rattus norvegicus] >gi_761716_emb_CAA88778 (Z48950)
histone H3.3 [Homo sapiens] >gi 963024 emb CAA57078
(X81206) histone H3.3 [Drosophila hydei]
>gi_963026_emb CAA57081 (X81208) histone H3.3 [Drosophila
```

hydei] >gi_963029_emb_CAA57080_ (X81207) histone H3.3 [Drosophila melanogaster] >gi_963031_emb_CAA57077_ (X81205)

histone H3.3 [Drosophila melanogaster]

>gi_1006654_emb_CAA57712_ (X82257) histone H3.3A variant
[Drosophila melanogaster] >gi_1838986_emb_CAB06625_

(Z85979) histone H3.3A [Mus musculus]

```
Seq. No.
                   310644
Seq. ID
                   uC-zmroteosinte051f01b2
Method
                   BLASTX
NCBI GI
                   g2194143
BLAST score
                   185
E value
                   1.0e-13
Match length
                   75
% identity
                   52
NCBI Description (AC002062) No definition line found [Arabidopsis thaliana]
Seq. No.
                   310645
Seq. ID
                   uC-zmroteosinte051f11b2
Method
                   BLASTX
NCBI GI
                   q2662343
BLAST score
                   178
E value
                   2.0e-16
Match length
                   128
% identity
                   50
NCBI Description (D63581) EF-1 alpha [Oryza sativa]
Seq. No.
                   310646
Seq. ID
                   uC-zmroteosinte053a04b2
Method
                   BLASTX
NCBI GI
                   q1620753
BLAST score
                   190
E value
                   3.0e-14
Match length
                   61
% identity
                   (U72942) proteinase inhibitor [Oryza sativa]
NCBI Description
                   >gi_2829212_gb_AAC00503_ (AF044059) proteinase inhibitor
                   [Oryza sativa]
Seq. No.
                   310647
Seq. ID
                   uC-zmroteosinte053b01b2
Method
                   BLASTX
NCBI GI
                   q4587584
BLAST score
                   153
E value
                   5.0e-10
Match length
                   60
```

44269

NCBI Description (AC007232) unknown protein [Arabidopsis thaliana]

```
310648
Seq. No.
                  uC-zmroteosinte053b10b2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3183237
                  295
BLAST score
                  1.0e-26
E value
                  120
Match length
% identity
                  54
                  HYPOTHETICAL 103.4 KD TRP-ASP REPEATS CONTAINING PROTEIN
NCBI Description
                  C3D6.12 IN CHROMOSOME II >gi 2117308 emb CAB09121.1
                  (Z95620) trp asp repeat protein [Schizosaccharomyces pombe]
Seq. No.
                  310649
Seq. ID
                  uC-zmroteosinte053c04b2
Method
                  BLASTX
                  g3746069
NCBI GI
BLAST score
                  171
                  5.0e-12
E value
                  104
Match length
% identity
                  38
                  (AC005311) putative reverse transcriptase [Arabidopsis
NCBI Description
                  thaliana]
                  310650
Seq. No.
Seq. ID
                  uC-zmroteosinte053c08b2
                  BLASTX
Method
                  g4650844
NCBI GI
BLAST score
                  169
E value
                  9.0e-12
Match length
                  153
% identity
                  12
NCBI Description (AB026190) Kelch motif containing protein [Homo sapiens]
Seq. No.
                  310651
Seq. ID
                  uC-zmroteosinte053e10b2
                  BLASTX
Method
NCBI GI
                  g2781345
BLAST score
                  357
                  9.0e-34
E value
Match length
                  178
% identity
                  46
NCBI Description (AC003113) F2401.2 [Arabidopsis thaliana]
                  310652
Seq. No.
Seq. ID
                  uC-zmroteosinte057a08b1
Method
                  BLASTX
NCBI GI
                  g2367392
BLAST score
                  149
E value
                  2.0e-09
Match length
                  56
% identity
                  54
                  (U82513) random slug cDNA25 protein [Dictyostelium
NCBI Description
                  discoideum]
Seq. No.
                  310653
                  uC-zmroteosinte057b06b1
Seq. ID
```

```
BLASTX
Method
                  g1707011
NCBI GI
BLAST score
                  179
                  3.0e-13
E value
Match length
                  40
% identity
                  80
                  (U78721) auxin-repressed protein isolog [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  310654
                  uC-zmroteosinte057d09b1
Seq. ID
Method
                  BLASTX
                  g2760349
NCBI GI
BLAST score
                  780
E value
                  2.0e-83
Match length
                  158
% identity
                  22
NCBI Description (U84969) ubiquitin [Arabidopsis thaliana]
Seq. No.
                  310655
Seq. ID
                  uC-zmroteosinte058b03b2
Method
                  BLASTN
NCBI GI
                  g22275
BLAST score
                  289
E value
                  1.0e-161
Match length
                  451
% identity
                  97
NCBI Description Maize mRNA for ferritin (clone FM1)
Seq. No.
                  310656
                  uC-zmroteosinte058e04b2
Seq. ID
Method
                  BLASTN
NCBI GI
                  q342676
BLAST score
                  295
E value
                   1.0e-165
Match length
                   327
% identity
                   97
                  Maize (cms-T) mitochondrial TURF 2H3 sequence containing 2
NCBI Description
                  ORFs
                   310657
Seq. No.
                   uC-zmroteosinte058f06b2
Seq. ID
Method
                  BLASTX
                   q1655637
NCBI GI
BLAST score
                   187
                   1.0e-14
E value
                   56
Match length
% identity
                   62
NCBI Description (Z54179) orf [Mus musculus]
```

Seq. No.

310658

Seq. ID

uC-zmroteosinte058g09b2

BLASTX Method g1483230 NCBI GI BLAST score 192 1.0e-14 E value Match length 128

```
% identity
NCBI Description (X99654) MADS4 protein [Betula pendula]
                  310659
Seq. No.
                  uC-zmroteosinte058g10b2
Seq. ID
Method
                  BLASTN
NCBI GI
                  g736358
BLAST score
                  34
                  1.0e-09
E value
                  58
Match length
                  90
% identity
NCBI Description Zea mays cell wall invertase mRNA, complete cds
Seq. No.
                  310660
                  uC-zmroteosinte058h06b2
Seq. ID
                  BLASTX
Method
                  g2464880
NCBI GI
BLAST score
                  154
                  3.0e-10
E value
Match length
                  107
% identity
                  35
                  (Z99707) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  310661
                  uC-zmroteosinte059b04b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q902584
BLAST score
                  765
                  1.0e-81
E value
Match length
                  155
% identity
                  17
                  (U29159) polyubiquitin containing 7 ubiquitin monomers [Zea
NCBI Description
                  mays]
                  310662
Seq. No.
                  uC-zmroteosinte059c04b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3695404
BLAST score
                  307
E value
                  6.0e-28
Match length
                  150
                  47
% identity
                  (AF096373) contains similarity to DnaJ domains (Pfam:
NCBI Description
                  PF00226, E=5.8e-13) [Arabidopsis thaliana]
                  >gi 4538977 emb CAB39765.1 (AL049487) putative protein
                   [Arabidopsis thaliana]
                  310663
Seq. No.
Seq. ID
                  uC-zmroteosinte059c11b1
Method
                  BLASTX
NCBI GI
                  g119355
BLAST score
                  585
                  1.0e-60
E value
Match length
                  144
% identity
                  82
NCBI Description
                  ENOLASE 1 (2-PHOSPHOGLYCERATE DEHYDRATASE 1)
                   (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE 1)
```



>gi_100869_pir__S16257 phosphopyruvate hydratase (EC
4.2.1.11) - maize >gi_22273_emb_CAA39454_ (X55981) enolase
[Zea mays]

Seq. No. 310664

Seq. ID uC-zmroteosinte059e03b1

Method BLASTX
NCBI GI g4557565
BLAST score 176
E value 4.0e-21
Match length 113
% identity 49

NCBI Description excision repair cross-complementing rodent repair

deficiency, complementation group 6

>gi_416959_sp_Q03468_ERC6_HUMAN EXCISION REPAIR PROTEIN

ERCC-6 (COCKAYNE SYNDROME PROTEIN CSB)

>gi_345826_pir__A44224 DNA repair helicase ERCC6 - human >gi_182181 (L04791) excision repair protein [Homo sapiens]

Seq. No. 310665

Seq. ID uC-zmroteosinte059e07b1

Method BLASTX
NCBI GI g1362108
BLAST score 493
E value 7.0e-50
Match length 119
% identity 84

NCBI Description histone H3 homolog - common tobacco

Seq. No. 310666

Seq. ID uC-zmroteosinte059f04b1

Method BLASTX
NCBI GI g2809324
BLAST score 170
E value 7.0e-12
Match length 160
% identity 32

NCBI Description (U67280) calumenin [Homo sapiens]

Seq. No. 310667

Seq. ID uC-zmroteosinte059f06b1

Method BLASTX
NCBI GI g2429467
BLAST score 158
E value 2.0e-10
Match length 85
% identity 39

NCBI Description (AF025462) contains similarity to glutathione S

transferases [Çaenorhabditis elegans]

Seq. No. 310668

Seq. ID uC-zmroteosinte059f08b1

Method BLASTX
NCBI GI g960289
BLAST score 141
E value 9.0e-09
Match length 101



```
% identity
                  (L34343) anthranilate synthase alpha subunit [Ruta
NCBI Description
                  graveolens]
                  310669
Seq. No.
                  uC-zmroteosinte059g10b1
Seq. ID
Method
                  BLASTX
                  g3402722
NCBI GI
BLAST score
                  338
                  1.0e-31
E value
                  125
Match length
                  50
% identity
                  (AC004261) CPDK-related protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  310670
                  uC-zmroteosinte059h09b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4371280
                  208
BLAST score
                  2.0e-16
E value
Match length
                  119
                  41
% identity
                  (AC006260) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  310671
                  uC-zmroteosinte060c07b1
Seq. ID
Method
                  BLASTX
                  g312179
NCBI GI
                  507
BLAST score
                  2.0e-58
E value
Match length
                  118
                  98
% identity
                  (X73151) glyceraldehyde 3-phosphate dehydrogenase
NCBI Description
                   (phosphorylating) [Zea mays] >gi_1184772 (U45855) cytosolic
                  glyceroldehyde-3-phosphate dehydrogenase GAPC2 [Zea mays]
                  >gi_1185554 (U45858) glyceraldehyde-3-phosphate
                  dehydrogenase [Zea mays]
                  310672
Seq. No.
                  uC-zmroteosinte060c08b1
Seq. ID
Method
                  BLASTX
                  g170354
NCBI GI
BLAST score
                  612
E value
                  7.0e-64
Match length
                  127
% identity
                  21
                  (M74156) pentameric polyubiquitin [Nicotiana sylvestris]
NCBI Description
Seq. No.
                  310673
                  uC-zmroteosinte060e08b1
Seq. ID
Method
                  BLASTX
```

Method BLASTX
NCBI GI 9719291
BLAST score 437
E value 3.0e-43
Match length 155
% identity 63

NCBI Description (U19134) unknown [Arabidopsis thaliana]



>gi 1095007_prf _2107236A SABRE gene [Arabidopsis thaliana]

Seq. No. 310674

Seq. ID uC-zmroteosinte060e11b1

Method BLASTX
NCBI GI g1175468
BLAST score 144
E value 8.0e-12
Match length 146
% identity 30

NCBI Description HYPOTHETICAL 47.3 KD PROTEIN C22G7.07C IN CHROMOSOME I

>gi 2130328_pir__S62451 hypothetical protein SPAC22G7.07c -

fission yeast (Schizosaccharomyces pombe)

>gi_1009457_emb_CAA91131.1_ (Z54328) hypothetical protein

[Schizosaccharomyces pombe]

Seq. No. 310675

Seq. ID uC-zmroteosinte060f06b1

Method BLASTX
NCBI GI g3668151
BLAST score 150
E value 8.0e-10
Match length 53
% identity 60

NCBI Description (AL031764) putative FAD synthetase [Schizosaccharomyces

pombe]

Seq. No. 310676

Seq. ID uC-zmroteosinte060f08b1

Method BLASTX
NCBI GI g2827552
BLAST score 147
E value 3.0e-09
Match length 59
% identity 42

NCBI Description (AL021635) predicted protein [Arabidopsis thaliana]

Seq. No. 310677

Seq. ID uC-zmroteosinte060h10b1

Method BLASTX
NCBI GI g2384956
BLAST score 153
E value 5.0e-10
Match length 99
% identity 37

NCBI Description (AF022985) No definition line found [Caenorhabditis

elegans]

Seq. No. 310678

Seq. ID uC-zmroteosinte061e12b2

Method BLASTX
NCBI GI g2464914
BLAST score 262
E value 8.0e-23
Match length 96
% identity 54

NCBI Description (Z99708) hypothetical protein [Arabidopsis thaliana]



```
310679
Seq. No.
                  uC\text{-}zmroteosinte061f03b2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2058273
BLAST score
                  342
                  5.0e-32
E value
Match length
                  142
% identity
                   49
                  (D83527) YK426 [Oryza sativa]
NCBI Description
                  310680
Seq. No.
                  uC-zmroteosinte061h04b2
Seq. ID
                  BLASTX
Method
NCBI GI
                   g4512653
BLAST score
                   155
E value
                   1.0e-21
Match length
                   97
% identity
                  (AC007048) unknown protein [Arabidopsis thaliana]
NCBI Description
                   310681
Seq. No.
                   uC-zmroteosinte062e05b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4510377
BLAST score
                   169
E value
                   6.0e-12
Match length
                   103
% identity
                   36
                  (AC007017) putative RNA helicase A [Arabidopsis thaliana]
NCBI Description
                   310682
Seq. No.
                   uC-zmroteosinte062g08b1
Seq. ID
                   BLASTX
Method
                   g1122317
NCBI GI
BLAST score
                   242
                   4.0e-22
E value
Match length
                   111
% identity
                   58
                  (X94193) heat shock protein 17.9 [Pennisetum glaucum]
NCBI Description
                   310683
Seq. No.
                   uC-zmroteosinte062g11b1
Seq. ID
                   BLASTX
Method
                   g3445397
NCBI GI
BLAST score
                   512
                   6.0e-52
E value
                   153
Match length
% identity
                   66
                  (AJ010166) S-domain receptor-like protein kinase [Zea mays]
NCBI Description
Seq. No.
                   310684
                   uC-zmroteosinte063b01b1
Seq. ID
Method
                   BLASTX
```

44276

q1813595

398 1.0e-38

NCBI GI BLAST score

E value

```
Match length
                  113
% identity
                   65
                  (U73749) xylan endohydrolase isoenzyme X-I [Hordeum
NCBI Description
                  vulgare]
                  310685
Seq. No.
                  uC-zmroteosinte063b04b1
Seq. ID
                  BLASTN
Method
                                                               3000
NCBI GI
                  g2623247
BLAST score
                  69
                  2.0e-30
E value
Match length
                  125
% identity
                  89
                  Zea mays SU1 isoamylase (sugary1) gene, complete cds
NCBI Description
Seq. No.
                   310686
                  uC-zmroteosinte063e02b1
Seq. ID
                  BLASTX
Method
                   q899608
NCBI GI
BLAST score
                   768
E value
                   4.0e-82
Match length
                   158
% identity
                   22
                  (U29158) polyubiquitin [Zea mays]
NCBI Description
Seq. No.
                   310687
                   uC-zmroteosinte063h08b1
Seq. ID
                  BLASTX
Method
NCBI GI
                   g2582193
BLAST score
                   242
                   9.0e-21
E value
Match length
                   91
                   56
% identity
                   (AF017443) NAD-malic enzyme; diphosphopyridine nucleotide
NCBI Description
                   (NAD+)-dependent-malic enzyme [Sinorhizobium meliloti]
                   310688
Seq. No.
                   uC-zmroteosinte064f05b1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4138912
BLAST score
                   344
E value
                   6.0e-33
Match length
                   77
                   73
% identity
                  (AF059487) expansin precursor [Lycopersicon esculentum]
NCBI Description
Seq. No.
                   310689
                   uC-zmroteosinte066b08b1
Seq. ID
Method
                   BLASTX
```

NCBI GI g2662310
BLAST score 317
E value 2.0e-29
Match length 106
% identity 61

NCBI Description (AB009307) bpwl [Hordeum vulgare]

Seq. No. 310690

```
uC-zmroteosinte066e01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q433970
BLAST score
                  230
E value
                  4.0e-19
Match length
                  101
% identity
NCBI Description (Z28649) polyubiquitin [Acetabularia cliftonii]
Seq. No.
                  310691
                  uC-zmroteosinte066e04b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g22161
BLAST score
                  37
E value
                  2.0e-11
Match length
                  85
% identity
                  86
NCBI Description Z.mays MANT1 mRNA for adenine nucleotide translocator (also
                  called ADP/ATP translocase)
Seq. No.
                  310692
Seq. ID
                  uC-zmroteosinte066f12b1
Method
                  BLASTX
NCBI GI
                  q3914423
BLAST score
                  341
E value
                  3.0e-32
Match length
                  89
% identity
                  71
NCBI Description PROFILIN 4 > gi 2642324 (AF032370) profilin [Zea mays]
Seq. No.
                  310693
Seq. ID
                  uC-zmroteosinte066q07b1
Method
                  BLASTX
NCBI GI
                  g2851538
BLAST score
                  373
E value
                  7.0e-36
Match length
                  107
% identity
                  67
NCBI Description TRYPTOPHANYL-TRNA SYNTHETASE (TRYPTOPHAN--TRNA LIGASE)
                  (TRPRS)
                  310694
Seq. No.
                  uC-zmroteosinte066h12b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1841354
BLAST score
                  47
                  3.0e-17
E value
Match length
                  63
% identity
                  94
NCBI Description
                  Oryza sativa mitochondrial DNA for cytochrome c oxidase
                  subunit Vb precursor, complete cds
                  310695
Seq. No.
Seq. ID
                  uC-zmroteosinte067a02b1
Method
                  BLASTX
NCBI GI
                  g2326188
BLAST score
                  282
```

```
4.0e-25
E value
Match length
                  156
                  41
% identity
                  (U81606) mixed-linked glucanase precursor [Cochliobolus
NCBI Description
                  carbonum]
                  310696
Seq. No.
                  uC-zmroteosinte067a06b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2982451
BLAST score
                  592
E value
                  2.0e-61
                  173
Match length
                  73
% identity
NCBI Description (AL022223) putative protein [Arabidopsis thaliana]
                  310697
Seq. No.
                  uC-zmroteosinte067c05b1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g4204371
BLAST score
                  151
                  2.0e-79
E value
                  243
Match length
                  91
% identity
NCBI Description Zea mays acidic ribosomal protein P2a-2 (rpp2a-2) mRNA,
                  complete cds
                  310698
Seq. No.
Seq. ID
                  uC-zmroteosinte067c08b1
Method
                  BLASTN
NCBI GI
                  g575425
BLAST score
                  122
                   6.0e-62
E value
                   399
Match length
                   95
% identity
                  Z.mays mRNA for sugar-starvation induced protein
NCBI Description
Seq. No.
                   310699
                   uC-zmroteosinte067d02b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3063471
BLAST score
                   206
E value
                   3.0e-16
Match length
                   121
                   37
% identity
                  (AC003981) F22013.33 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   310700
                   uC-zmroteosinte067d11b1
Seq. ID
                   BLASTX
Method
```

Method BLASTX
NCBI GI g3935168
BLAST score 344
E value 3.0e-32
Match length 153
% identity 57

NCBI Description (AC004557) F17L21.11 [Arabidopsis thaliana]

Method

NCBI GI

BLASTX

g2492519

```
310701
Seq. No.
                  uC-zmroteosinte067f02b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q465008
                  390
BLAST score
                  5.0e-41
E value
                  106
Match length
                  79
% identity
                  UREASE (UREA AMIDOHYDROLASE) >gi 418642 pir_URJB urease
NCBI Description
                  (EC 3.5.1.5) - jack bean
Seq. No.
                  310702
                  uC-zmroteosinte068b05b1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2196672
BLAST score
                  419
                  4.0e-41
E value
                  119
Match length
% identity
                  73
NCBI Description
                  (Y08807) HMGd1 [Zea mays]
                  310703
Seq. No.
                  uC-zmroteosinte068b11b1
Seq. ID
Method
                  BLASTX
                  g284587
NCBI GI
BLAST score
                  224
                   3.0e-18
E value
Match length
                  109
% identity
                   43
                  Ca2+-transporting ATPase (EC 3.6.1.38) PMCA4b - bovine
NCBI Description
                   (fragment) >gi 163550 (M83364) plasma membrane calcium
                  ATPase [Bos taurus]
                   310704
Seq. No.
                  uC-zmroteosinte068c03b1
Seq. ID
Method
                  BLASTX
                   g746401
NCBI GI
BLAST score
                   233
                   3.0e-19
E value
Match length
                   77
% identity
                   57
                  (U01376) ATP-binding protein [Escherichia coli]
NCBI Description
                   310705
Seq. No.
                   uC-zmroteosinte068d08b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3415009
BLAST score
                   221
E value
                   8.0e-18
                   93
Match length
% identity
                   48
                  (AF080245) sesquiterpene synthase [Elaeis oleifera]
NCBI Description
                   310706
Seq. No.
                   uC-zmroteosinte068d10b1
Seq. ID
```



```
BLAST score
                  774
                  1.0e-82
E value
Match length
                  151
% identity
                  99
                  26S PROTEASE REGULATORY SUBUNIT 7 (26S PROTEASOME SUBUNIT
NCBI Description
                  7) >gi 1395191 dbj BAA13021 (D86121) 26S proteasome ATPase
                  subunit [Spinacia oleracea]
Seq. No.
                  310707
                  uC-zmroteosinte068h10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3169883
BLAST score
                  463
                  3.0e-46
E value
Match length
                  161
% identity
                  57
                  (AF033194) dehydroquinate dehydratase/shikimate:NADP
NCBI Description
                  oxidoreductase [Lycopersicon esculentum] >gi 3169888
                  (AF034411) dehydroquinate dehydratase/shikimate:NADP
                  oxidoreductase [Lycopersicon esculentum]
Seq. No.
                  310708
                  uC-zmroteosinte069a06b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2662310
BLAST score
                  415
E value
                  6.0e-41
Match length
                  105
% identity
                  79
NCBI Description
                  (AB009307) bpw1 [Hordeum vulgare]
                  310709
Seq. No.
                  uC-zmroteosinte069b12b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4416300
BLAST score
                  109
                  3.0e-54
E value
Match length
                  197
% identity
                  45
NCBI Description
                  Zea mays chromosome 4 22 kDa zein-associated intercluster
                  region, complete sequence
Seq. No.
                  310710
                  uC-zmroteosinte069c08b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3927830
BLAST score
                  411
E value
                  4.0e-40
Match length
                  166
% identity
                  53
NCBI Description (AC005727) hypothetical protein [Arabidopsis thaliana]
```

Seq. No. 310711

Seq. ID uC-zmroteosinte069c10b1

Method BLASTX
NCBI GI g322752
BLAST score 456

Seq. ID Method

```
7.0e-61
E value
Match length
                  154
                  77
% identity
                  auxin-independent growth promoter - Nicotiana tabacum
NCBI Description
                  >gi 559921_emb_CAA56570_ (X80301) axi 1 [Nicotiana tabacum]
                  310712
Seq. No.
                  uC-zmroteosinte069d05b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2914706
BLAST score
                  299
E value
                  3.0e-27
                  107
Match length
                  56
% identity
NCBI Description (AC003974) putative homeobox protein [Arabidopsis thaliana]
Seq. No.
                  310713
Seq. ID
                  uC-zmroteosinte069e01b1
Method
                  BLASTX
NCBI GI
                  g266578
BLAST score .
                  177
                  5.0e-13
E value
Match length
                  56
% identity
                  METALLOTHIONEIN-LIKE PROTEIN 1 >gi_100898_pir__S17560
NCBI Description
                  metallothionein-like protein - maize >gi 236730 bbs 57629
                  (S57628) metallothionein homologue [Zea mays, Peptide, 76
                  aa] [Zea mays] >gi_559536_emb_CAA57676 (X82186)
                  metallothionein- like protein [Zea mays]
                  >gi 228095 prf 1717215A metallothionein-like protein [Zea
                  mays]
Seq. No.
                  310714
                  uC-zmroteosinte069h02b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g293885
BLAST score
                  253
E value
                  1.0e-140
Match length
                  308
                  96
% identity
                  Zea diploperennis alcohol dehydrogenase 1 (Adhl) gene,
NCBI Description
                  exons 4 through 10
Seq. No.
                  310715
                  uC-zmroteosinte069h04b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q729051
BLAST score
                  454
E value
                  3.0e-45
Match length
                  127
% identity
                  71
                  CALTRACTIN (CENTRIN) >gi 444342 prf 1906390A
NCBI Description
                  caltractin-like protein [Atriplex nummularia]
                  310716
Seq. No.
```

44282

uC-zmroteosinte070c12b1

BLASTX

```
q4099148
NCBI GI
BLAST score
                  297
E value
                  1.0e-36
Match length
                  150
% identity
NCBI Description (U84268) YLP [Hordeum vulgare]
Seq. No.
                  310717
                  uC-zmroteosinte070e02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4584255
BLAST score
                  188
E value
                  2.0e-14
Match length
                  70
% identity
NCBI Description (Y18471) SINAlp [Vitis vinifera]
Seq. No.
                  310718
Seq. ID
                  uC-zmroteosinte070e10b1
Method
                  BLASTX
NCBI GI
                  q1709927
BLAST score
                  433
E value
                  9.0e-43
Match length
                  147
% identity
                  57
NCBI Description
                  PROBABLE MULTIFUNCTIONAL PROTEIN ADE2
                   (PHOSPHORIBOSYLAMINOIMIDAZOLE-SUCCINOCARBOXAMIDE SYNTHASE
                   (SAICAR SYNTHETASE) / PHOSPHORIBOSYLAMINOIMIDAZOLE
                  CARBOXYLASE (AIR CARBOXYLASE) (AIRC)) >gi 1053219 (U39848)
                  coded for by C. elegans cDNA yk92a5.5; coded for by C.
                  elegans cDNA yk58q5.5; coded for by C. elegans cDNA
                  yk55a3.5; coded for by C. elegans cDNA yk70b1.5; coded for
                  by C. elegans cDNA yk58g5.5; coded for by C. elegans cDNA
                  yk124e4
Seq. No.
                  310719
Seq. ID
                  uC-zmroteosinte070e11b1
Method
                  BLASTN
NCBI GI
                  q498772
BLAST score
                  59
                  2.0e-24
E value
                  95
Match length
% identity
                  91
NCBI Description Z.mays (cv DH5xDH7) hsp70-4 mRNA for heat shock protein
Seq. No.
                  310720
Seq. ID
                  uC-zmroteosinte070e12b1
                  BLASTX
Method
NCBI GI
                  g3378495
BLAST score
                  191
E value
                  2.0e-14
```

Match length 76

(AJ007580) Mitochondrial carrier protein [Ribes nigrum] NCBI Description

310721 Seq. No.

% identity

uC-zmroteosinte070f02b1 Seq. ID

```
Method
                  BLASTX
                  g2244740
NCBI GI
BLAST score
                  156
                  1.0e-10
E value
                  78
Match length
                  41
% identity
                  (D88417) endo-1,4-beta-glucanase [Gossypium hirsutum]
NCBI Description
Seq. No.
                  310722
                  uC-zmroteosinte070f12b1
Seq. ID
                  BLASTX
Method
                  g2978452
NCBI GI
                  415
BLAST score
                  1.0e-40
E value
Match length
                  119
% identity
                  71
                  (AE001274) MCAK; L549.3 [Leishmania major]
NCBI Description
                  310723
Seq. No.
                  uC-zmroteosinte070g01b1
Seq. ID
                  BLASTX
Method
                   g2129742
NCBI GI
                   205
BLAST score
                   3.0e-16
E value
Match length
                   60
                   65
% identity
                  stress-induced protein OZI1 precursor - Arabidopsis
NCBI Description
                   thaliana >gi_790583 (U20347) mRNA corresponding to this
                   gene accumulates in response to ozone stress and pathogen
                   (bacterial) infection; putative pathogenesis-related
                   protein [Arabidopsis thaliana] >gi_2252869 (AF013294) No
                   definition line found [Arabidopsis thaliana]
                   310724
Seq. No.
                   uC-zmroteosinte072a06b2
Seq. ID
                   BLASTX
Method
                   g3461814
NCBI GI
BLAST score
                   145
E value
                   3.0e-09
Match length
                   94
% identity
                   41
                  (AC004138) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   310725
Seq. No.
Seq. ID
                   uC-zmroteosinte072a11b2
                   BLASTX
Method
                   q3461814
NCBI GI
                   179
BLAST score
E value
                   5.0e-13
                   112
Match length
% identity
                   (AC004138) hypothetical protein [Arabidopsis thaliana]
NCBI Description
```

Seq. No. 310726

Seq. ID uC-zmroteosinte072e12b2

Method BLASTX NCBI GI g1848225

```
BLAST score
E value
                  3.0e-14
Match length
                  56
                  59
% identity
                  (U88090) nonspecific lipid transfer protein [Hordeum
NCBI Description
                  vulgare]
                  310727
Seq. No.
Seq. ID
                  uC-zmroteosinte072f02b2
Method
                  BLASTX
```

Method BLASTX
NCBI GI g3850108
BLAST score 320
E value 2.0e-29
Match length 174
% identity 41

NCBI Description (AL033388) putative calcium-transporting atpase

[Schizosaccharomyces pombe]

Seq. No. 310728 uC-zmroteosinte072f12b2 Seq. ID Method BLASTN g473602 NCBI GI BLAST score 53 E value 7.0e-21 93 Match length % identity ∴ 89

NCBI Description Zea mays W-22 histone H2A mRNA, complete cds

Seq. No. 310729
Seq. ID uC-zmroteosinte073a01b1
Method BLASTX
NCBI GI g1173237
BLAST score 191
E value 8.0e-15

BLAST score 191 E value 8.0e-15 Match length 65 % identity 66

NCBI Description 40S RIBOSOMAL PROTEIN S28 >gi_629860_pir__S49035 ribosomal protein S28 - maize >gi_557682_emb_CAA57636_ (X82124) small

subunit ribosomal protein S28 [Zea mays]

Seq. No. 310730

Seq. ID uC-zmroteosinte073a02b1

Method BLASTX
NCBI GI g1332579
BLAST score 205
E value 6.0e-19
Match length 82
% identity 7

NCBI Description (X98063) polyubiquitin [Pinus sylvestris]

Seq. No. 310731

Seq. ID uC-zmroteosinte073a06b1

Method BLASTX
NCBI GI g3004950
BLAST score 327
E value 1.0e-30
Match length 103

% identity (AF037061) tonoplast intrinsic protein; ZmTIP1 [Zea mays] NCBI Description Seq. No. 310732 uC-zmroteosinte073b06b1 Seq. ID BLASTX Method q4206208 NCBI GI BLAST score 242 2.0e-20 E value Match length 79 % identity 54 (AF071527) hypothetical protein [Arabidopsis thaliana]

NCBI Description >gi 4263041 gb AAD15310 (AC005142) hypothetical protein [Arabidopsis thaliana]

Seq. No. 310733 uC-zmroteosinte073c01b1 Seq. ID

Method BLASTX NCBI GI g309557 BLAST score 498 E value 2.0e-50

Match length 154 % identity 70

(L21007) chaperonin 60 [Zea mays] NCBI Description

Seq. No. 310734

uC-zmroteosinte073c04b1 Seq. ID

BLASTX Method g4586058 NCBI GI BLAST score 270 7.0e-24 E value 100 Match length % identity 53

(AC007020) unknown protein [Arabidopsis thaliana] NCBI Description

Seq. No. 310735

uC-zmroteosinte073f02b1 Seq. ID

Method BLASTX g322525 NCBI GI BLAST score 641 E value 3.0e-67 Match length 144 83 % identity

omnipotent suppressor protein SUP1 homolog (clone A18) -NCBI Description

> Arabidopsis thaliana (fragment) >gi_16512_emb_CAA49171 (X69374) similar to yeast omnipotent suppressor protein

SUP1 (SUP45); ORF [Arabidopsis thaliana]

Seq. No. 310736

uC-zmroteosinte073g02b1 Seq. ID

Method BLASTX q4558669 NCBI GI BLAST score 573 4.0e-59 E value 180 Match length % identity 61

NCBI Description (AC007063) putative vanadate resistance protein

Seq. ID



[Arabidopsis thaliana]

```
310737
  Seq. No.
                    uC-zmroteosinte073h06b1
  Seq. ID
  Method
                    BLASTX
                    q82684
  NCBI GI
                    203
  BLAST score
                    2.0e-16
- E value
                    68
  Match length
                    59
  % identity
                    dehydrin 3 - maize >gi_18964_emb_CAA33364_ (X15290)
  NCBI Description
                    dehydrin (AA 1-167) [Zea mays]
                    310738
  Seq. No.
  Seq. ID
                    uC-zmroteosinte073h08b1
  Method
                    BLASTX
                    g2911044
  NCBI GI
  BLAST score
                    387
                    4.0e-39
  E value
                    140
  Match length
  % identity
                    63
                    (AL021961) putative protein [Arabidopsis thaliana]
  NCBI Description
                    310739
  Seq. No.
                    uC-zmroteosinte073h12b1
  Seq. ID
  Method
                    BLASTN
                     g18963
  NCBI GI
  BLAST score
                    167
                     4.0e-89
  E value
                     231
  Match length
                     93
  % identity
  NCBI Description Z.mays mRNA for dehydrin (dhn3)
                     310740
  Seq. No.
                    uC-zmroteosinte074c04b1
  Seq. ID
  Method
                    BLASTX
                     g2772934
  NCBI GI
                     222
  BLAST score
                     3.0e-18
  E value
  Match length
                     119
  % identity
                     (AF030357) C-8,7 sterol isomerase; aSI1 [Arabidopsis
  NCBI Description
                     thaliana]
                     310741
  Seq. No.
                     uC-zmroteosinte074e03b1
  Seq. ID
                     BLASTX
  Method
                     g1912395
  NCBI GI
  BLAST score
                     676
                     3.0e-71
  E value
  Match length
                     174
  % identity
                     68
                     (U49169) vacuolar H+-ATPase A subunit [Dictyostelium
  NCBI Description
                     discoideum]
  Seq. No.
                     310742
```

44287

uC-zmroteosinte074f04b1



Method BLASTX
NCBI GI g126938
BLAST score 695
E value 2.0e-73
Match length 176
% identity 78

NCBI Description PUTATIVE ATP-DEPENDENT RNA HELICASE >gi_157594 (M59926) RNA

helicase [Drosophila melanogaster]

Seq. No. 310743

Seq. ID uC-zmroteosinte074h02b1

Method BLASTX
NCBI GI g3287693
BLAST score 360
E value 3.0e-34
Match length 121
% identity 60

NCBI Description (AC003979) Similar to LIM17 gene product gb_1653769 from

the genome of Synechocystis sp. gb D90916. [Arabidopsis

thaliana]

Seq. No. 310744

Seq. ID uC-zmroteosinte074h09b1

Method BLASTX
NCBI GI g4455327
BLAST score 166
E value 2.0e-11
Match length 80
% identity 47

NCBI Description (AL035525) hypothetical protein [Arabidopsis thaliana]

Seq. No. 310745

Seq. ID uC-zmroteosinte075a03b1

Method BLASTN
NCBI GI g4587641
BLAST score 34
E value 1.0e-09
Match length 50
% identity 92

NCBI Description Arabidopsis thaliana chromosome I BAC F20D21 genomic

sequence, complete sequence

Seq. No. 310746

Seq. ID uC-zmroteosinte075a04b1

Method BLASTX
NCBI GI g2654870
BLAST score 418
E value 8.0e-50
Match length 144
% identity 75

NCBI Description (AF015302) RbohAOsp [Oryza sativa]

Seq. No. 310747

Seq. ID uC-zmroteosinte075a05b1

Method BLASTX NCBI GI g626042 BLAST score 453

```
4.0e-45°
E value
Match length
                  161
% identity
                  57
                  beta-glucosidase, root meristem (EC 3.2.1.-) precursor -
NCBI Description
                  maize >gi_435313_emb_CAA52293_ (X74217) beta-glucosidase
                  [Zea mays]
                  310748
Seq. No.
                  uC-zmroteosinte075a06b1
Seq. ID
Method
                  BLASTX
                  g2961378
NCBI GI
                  291
BLAST score
                  2.0e-26
E value
                  94
Match length
% identity
                  30
                  (AL022141) putative protein [Arabidopsis thaliana]
NCBI Description
                  310749
Seq. No.
                  uC-zmroteosinte075b03b1
Seq. ID
Method
                  BLASTX
                  g2702268
NCBI GI
BLAST score
                  243
                                              100
                  1.0e-20
E value
Match length
                  69
% identity
                   62
NCBI Description (AC003033) putative cellulase [Arabidopsis thaliana]
Seq. No.
                   310750
                  uC-zmroteosinte075b06b1
Seq. ID
                  BLASTN
Method
NCBI GI
                   q559535
BLAST score
                   345
                   0.0e + 00
E value
                   388
Match length
                   97
% identity
NCBI Description Z.mays mRNA for metallothionein
Seq. No.
                   310751
                   uC-zmroteosinte075c09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g4191789
BLAST score
                   160
                   7.0e-11
E value
Match length
                   56
                   62
% identity
                   (AC005917) putative transmembrane transport protein
NCBI Description
                   [Arabidopsis thaliana]
```

Seq. No. 310752

Seq. ID uC-zmroteosinte075e08b1

Method BLASTX NCBI GI q4103635 BLAST score 290 E value 5.0e-26 Match length 98 % identity 53

NCBI Description (AF026538) ABA-responsive protein [Hordeum vulgare]

Seq. ID

```
310753
Seq. No.
                  uC-zmroteosinte076a04b2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q312179
BLAST score
                  297
                  4.0e-27
E value
                  109
Match length
% identity
NCBI Description
                  (X73151) glyceraldehyde 3-phosphate dehydrogenase
                  (phosphorylating) [Zea mays] >gi 1184772 (U45855) cytosolic
                  glyceroldehyde-3-phosphate dehydrogenase GAPC2 [Zea mays]
                  >gi 1185554 (U45858) glyceraldehyde-3-phosphate
                  dehydrogenase [Zea mays]
Seq. No.
                  310754
Seq. ID
                  uC-zmroteosinte076b04b2
Method
                  BLASTX
NCBI GI
                  q2760349
BLAST score
                  186
E value
                  3.0e-14
Match length
                  103
% identity
NCBI Description (U84969) ubiquitin [Arabidopsis thaliana]
                  310755
Seq. No.
Seq. ID
                  uC-zmroteosinte076b09b2
Method
                  BLASTX
NCBI GI
                  q2660674
BLAST score
                  331
                  9.0e-31
E value
Match length
                  171
% identity
                  (AC002342) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  310756
Seq. No.
                  uC-zmroteosinte076d06b2
Seq. ID
                  BLASTN
Method
                  g4574239
NCBI GI
BLAST score
                  36
                  7.0e-11
E value
Match length
                  64
                  89
% identity
                  Tortula ruralis ribosomal protein S14 mRNA, complete cds
NCBI Description
                  310757
Seq. No.
                  uC-zmroteosinte076h02b2
Seq. ID
                  BLASTX
Method
                  g3451069
NCBI GI
BLAST score
                  387
E value
                  2.0e-37
Match length
                  154
% identity
                  54
                  (AL031326) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   310758
Seq. No.
```

44290

uC-zmroteosinte076h06b2

E value

3.0e-12

```
BLASTX
Method
                   g2462762
NCBI GI
BLAST score
                   154
E value
                   3.0e-10
Match length
                   112
% identity
                   41
                   (AC002292) Highly similar to auxin-induced protein
NCBI Description
                   (aldo/keto reductase family) [Arabidopsis thaliana]
                   310759
Seq. No.
                   uC\text{-}zmroteosinte076h10b2\\
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1363487
BLAST score
                   186
                   8.0e-14
E value
Match length
                   90
% identity
                   IAA7 protein - Arabidopsis thaliana >gi_972917 (U18409)
NCBI Description
                   IAA7 [Arabidopsis thaliana]
                   310760
Seq. No.
Seq. ID
                   uC-zmroteosinte077a12b1
                   BLASTX
Method
                   q3413704
NCBI GI
BLAST score
                   255
                   3.0e €22
E value
Match length
                   72
% identity
                   64
                   (AC004747) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   310761
Seq. No.
                   uC-zmroteosinte077b08b1
Seq. ID
Method
                   BLASTN
NCBI GI
                   q218130
BLAST score
                   32
                   5.0e-09
E value
Match length
                   44
                   93
% identity
NCBI Description Rice mRNA for Ribosomal protein S15
Seq. No.
                   310762
                   uC-zmroteosinte077c10b1
Seq. ID
Method
                   BLASTN
                   q3290003
NCBI GI
                   49
BLAST score
                   4.0e-19
E value
Match length
                   53
                   98
% identity
                   Zea mays pathogenesis related protein-1 (PR-1) mRNA,
NCBI Description
                   complete cds
                   310763
Seq. No.
                   uC-zmroteosinte077d06b1
Seq. ID
                   BLASTX
Method
                   g2392056
NCBI GI
                   170
BLAST score
```

```
52
Match length
                  69
% identity
                  Chain A, Class 3 Aldehyde Dehydrogenase Complex With
NCBI Description
                  Nicotinamide-Adenine-Dinucleotide >gi_2392057_pdb_1AD3_B
                  Chain B, Class 3 Aldehyde Dehydrogenase Complex With
                  Nicotinamide-Adenine-Dinucleotide
                  310764
Seq. No.
                  uC-zmroteosinte077e06b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3746071
BLAST score
                  174
                  7.0e-13
E value
Match length
                  46
% identity
                  (AC005311) putative GTP-binding protein [Arabidopsis
NCBI Description
                  thaliana]
                  310765
Seq. No.
                  uC-zmroteosinte077e10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q549986
BLAST score
                  194
E value
                  6.0e-15
Match length
                  46
                  80
% identity
                  (U13149) possible apospory-associated protein [Pennisetum
NCBI Description
                  ciliare]
                   310766
Seq. No.
                  uC-zmroteosinte077f12b1
Seq. ID
Method
                  BLASTX
                  q66009
NCBI GI
                   182
BLAST score
                   5.0e-14
E value
                   55
Match length
                   71
% identity
                  glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) C,
NCBI Description
                   cytosolic - maize >gi_22238_emb_CAA30151_ (X07156) GADPH
                   (AA 1-337) [Zea mays]
                   310767
Seq. No.
                   uC-zmroteosinte077h11b1
Seq. ID
                   BLASTX
Method
                   g3482974
NCBI GI
BLAST score
                   190
                   6.0e-15
E value
                   58
Match length
                   71
% identity
                   (AL031369) ATP-dependent Clp proteinase-like protein
NCBI Description
                   [Arabidopsis thaliana]
                   310768
Seq. No.
                   uC-zmroteosinte078g10b1
Seq. ID
```

44292

BLASTX

294

q2160144

Method NCBI GI

BLAST score

```
E value 5.0e-27

Match length 74
% identity 68
NCBI Description (AC000375) Strong similarity to Arabidopsis oligopeptide transporter (gb_X77503). [Arabidopsis thaliana]

Seq. No. 310769
```

Seq. ID uC-zmroteosinte080a09b1
Method BLASTX
NCBI GI g4589974
BLAST score 314
E value 6.0e-29
Match length 119
% identity 50

NCBI Description (AC007195) unknown protein [Arabidopsis thaliana]

Seq. ID uC-zmroteosinte080c02b1
Method BLASTX
NCBI GI g3320104
BLAST score 301
E value 1.0e-39

E value 1.0e-3
Match length 100
% identity 85

Seq. No.

NCBI Description (AJ007366) calcium-dependent protein kinase [Zea mays]

Seq. No. 310771

Seq. ID uC-zmroteosinte080d08b1

310770

Method BLASTX
NCBI GI g3702317
BLAST score 165
E value 1.0e-11
Match length 38
% identity 84

NCBI Description (AC005397) unknown protein [Arabidopsis thaliana]

>gi 4559376 gb AAD23036.1_AC006526_1 (AC006526) unknown

protein [Arabidopsis thaliana]

Seq. No. 310772

Seq. ID uC-zmroteosinte080d10b1

Method BLASTX
NCBI GI g2497486
BLAST score 424
E value 2.0e-44
Match length 118
% identity 77

NCBI Description URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP

KINASE) >gi 2121275 (AF000147) UMP/CMP kinase [Arabidopsis

thaliana]

Seq. No. 310773

Seq. ID uC-zmroteosinte080g01b1

Method BLASTX
NCBI GI g1370603
BLAST score 169
E value 6.0e-12
Match length 35

```
% identity
                  (X98245) annexin p35 [Zea mays]
NCBI Description
                  310774
Seq. No.
Seq. ID
                  uC-zmroteosinte080g06b1
```

Method BLASTX NCBI GI q3970880 BLAST score 172 4.0e-12 E value 69 Match length % identity

(AB015724) nuclear receptor binding factor-1 [Rattus NCBI Description

norvegicus]

310775 Seq. No. Seq. ID uC-zmroteosinte080h06b1 Method BLASTX NCBI GI q4588002

BLAST score 323 6.0e-30 E value 135 Match length % identity

(AF085279) hypothetical ankyrin-like protein [Arabidopsis NCBI Description

thaliana]

310776 Seq. No.

Seq. ID uC-zmroteosinte082b01b2

Method BLASTX NCBI GI q3142292 BLAST score 194 E value 4.0e-25 Match length 88 % identity 68

(AC002411) Contains similarity to tetratricopeptide repeat NCBI Description

protein gb_U46571 from home sapiens. EST gb_Z47802 and gb Z48402 come from this gene. [Arabidopsis thaliana]

310777 Seq. No.

uC-zmroteosinte082d03b2 Seq. ID

BLASTX Method NCBI GI q1350969 BLAST score 374 1.0e-35 E value Match length 104 72 % identity

40S RIBOSOMAL PROTEIN S26 (S31) >gi_971284_dbj_BAA07208_ NCBI Description

(D38011) ribosomal protein S31 [Oryza sativa]

310778 Seq. No.

uC-zmroteosinte082g12b1 Seq. ID

BLASTX Method NCBI GI g3548802 BLAST score 335 2.0e-31 E value 138 Match length 48 % identity

(AC005313) axi 1-like protein [Arabidopsis thaliana] NCBI Description



>qi 4335769 gb AAD17446 (AC006284) putative axi1 protein [Nicotiana tabacum] [Arabidopsis thaliana]

Seq. No. 310779

uC-zmroteosinte083c03b1 Seq. ID

Method BLASTX NCBI GI q4539660 BLAST score 441 4.0e-57 E value Match length 187 % identity

(AF061282) polyprotein [Sorghum bicolor] NCBI Description

310780 Seq. No.

Seq. ID uC-zmroteosinte083c06b1

Method BLASTN q4321977 NCBI GI BLAST score 71 2.0e-31 E value 163 Match length % identity 86

NCBI Description Zea mays beta-amylase (Amy2) gene, complete cds

310781 Seq. No.

uC-zmroteosinte083f07b1 Seq. ID

Method BLASTX NCBI GI g1168493 BLAST score 286 E value 2.0e-25 Match length 75 75 % identity

NCBI Description ARGINASE >gi 602422 (U15019) arginase [Arabidopsis

> thaliana] >qi 4325373 qb AAD17369 (AF128396) Arabidopsis thaliana arginase (SW:P46637) (Pfam: PF00491, Score=419.6,

E=3.7e-142 N=1) [Arabidopsis thaliana]

Seq. No. 310782

uC-zmroteosinte084a03b1 Seq. ID

BLASTX Method NCBI GI g3522929 BLAST score 163 E value 8.0e-12 57 Match length 58 % identity

(AC002535) putative dTDP-glucose 4-6-dehydratase NCBI Description

[Arabidopsis thaliana] >gi_3738279 (AC005309) putative

dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana]

310783 Seq. No.

uC-zmroteosinte084c08b1 Seq. ID

Method BLASTX NCBI GI g3169170 BLAST score 229 7.0e-19 E value Match length 59 76 % identity

(AC004401) putative chloroplast envelope Ca2+-ATPase, 5' NCBI Description



partial [Arabidopsis thaliana]

```
Seq. No.
                  310784
                  uC-zmroteosinte084c11b1
Seq. ID
Method
                  BLASTX
                  g3377819
NCBI GI
BLAST score
                  213
                  3.0e-17 ·
E value
Match length
                  76
% identity
                  59
                  (AF076275) No definition line found [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  310785
Seq. ID
                  uC-zmroteosinte084d05b1
Method
                  BLASTX
NCBI GI
                  q3859597
BLAST score
                  173
E value
                  1.0e-12
Match length
                  83
% identity
                  46
NCBI Description
                  (AF104919) No definition line found [Arabidopsis thaliana]
Seq. No.
                  310786
                  uC-zmroteosinte084d09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2661179
BLAST score
                  266
E value
                  4.0e-23
Match length
                  135
% identity
                  39
                  (U80984) AtZW10 [Arabidopsis thaliana]
NCBI Description
                  310787
Seq. No.
                  uC-zmroteosinte084e04b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1184771
BLAST score
                  41
E value
                  4.0e-14
                  93
Match length
% identity
                  86
NCBI Description
                  Zea mays glyceraldehyde-3-phosphate dehydrogenase GAPC2
                   (gpc2) mRNA, complete cds
                  310788
Seq. No.
                  uC-zmroteosinte084e10b1
Seq. ID
Method
                  BLASTX
                  g486849
NCBI GI
BLAST score
                  424
E value
                  8.0e-47
Match length
                  116
% identity
                  80
NCBI Description
                  licheninase (EC 3.2.1.73) precursor - wheat
                  >gi_311764 emb CAA80493_ (Z22874) (1,3;1,4) beta glucanase
                  [Triticum aestivum]
Seq. No.
                  310789
Seq. ID
                  uC-zmroteosinte084e11b1
```

Match length

```
BLASTX
Method
                  g4531444
NCBI GI
                  323
BLAST score
                   6.0e-30
E value
                  140
Match length
                  51
% identity
NCBI Description (AC006224) putative protein kinase [Arabidopsis thaliana]
                  310790
Seq. No.
                  uC-zmroteosinte084f04b1
Seq. ID
                  BLASTX
Method
                   g2811226
NCBI GI
                   296
BLAST score
                   1.0e-26
E value
Match length
                   153
% identity
                   41
                  (AF042669) fimbrin 2 [Arabidopsis thaliana] >gi_2811232
NCBI Description
                   (AF042671) fimbrin 2 [Arabidopsis thaliana]
Seq. No.
                   310791
                   uC-zmroteosinte084h02b1
Seq. ID
                   BLASTX
Method
                   g4539370
NCBI GI
BLAST score
                   222
                   1.0e-18
E value
Match length
                   76
% identity
                   66
                   (AL049525) UDP-galactose 4-epimerase-like protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   310792
                   uC-zmroteosinte084h12b1
Seq. ID
                   BLASTX
Method
                   g4587993
NCBI GI
                   187
BLAST score
                   5.0e-14
E value
                   99
Match length
                   41
% identity
                  (AF085279) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   310793
                   uC-zmroteosinte085c09b1
Seq. ID
Method
                   BLASTX
                   g3776027
NCBI GI
BLAST score
                   138
E value
                   7.0e-09
                   49
Match length
                   59
% identity
NCBI Description (AJ010475) RNA helicase [Arabidopsis thaliana]
Seq. No.
                   310794
                   uC-zmroteosinte085e02b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1658315
BLAST score
                   325
E value
                   4.0e-30
```

```
% identity
NCBI Description (Y08988) osr40g3 [Oryza sativa]
                  310795
Seq. No.
Seq. ID
                  uC-zmroteosinte085e08b1
Method
                  BLASTX
NCBI GI
                  g119150
                  178
BLAST score
                  2.0e-13
E value
                  77
Match length
                  55
% identity
                  ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)
NCBI Description
                  >qi 82081 pir S10507 translation elongation factor eEF-1
                  alpha chain - tomato >gi 19273 emb CAA32618 (X14449) EF
                  1-alpha (AA 1-448) [Lycopersicon esculentum]
                  >gi 295810 emb CAA37212 (X53043) elongation factor 1-alpha
                  [Lycopersicon esculentum]
                  310796
Seq. No.
                  uC-zmroteosinte086b01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4210451
BLAST score
                  154
                  5.0e-10
E value
                  107
Match length
                  40
% identity
NCBI Description (AB016472) ARR2 protein [Arabidopsis thaliana]
                  310797
Seq. No.
Seq. ID
                  uC-zmroteosinte086d06b1
                  BLASTX
Method
NCBI GI
                  q1172809
BLAST score
                  203
                  9.0e-16
E value
Match length
                  60
                  70
% identity
                  60S RIBOSOMAL PROTEIN L10 (QM PROTEIN HOMOLOG) >gi_468056
NCBI Description
                   (U06108) QM protein [Zea mays]
                   310798
Seq. No.
                  uC-zmroteosinte086e09b1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g945021
BLAST score
                  137
                   6.0e-71
E value
Match length
                   141
                   99
% identity
NCBI Description
                  Z.mays DNA for tbp1 gene
                   310799
Seq. No.
                   uC-zmroteosinte086e11b1
Seq. ID
Method
                  {\tt BLASTX}
NCBI GI
                  g3047114
                   175
BLAST score
```

2.0e-12

59

58

E value

Match length % identity



72

% identity

NCBI Description

```
(AF058919) No definition line found [Arabidopsis thaliana]
NCBI Description
                  310800
Seq. No.
                  uC-zmroteosinte086f01b1
Seq. ID
                  BLASTX
Method
                  g2501555
NCBI GI
                  186
BLAST score
                  6.0e-20
E value
                  91
Match length
                  71
% identity
                  POSSIBLE APOSPORY-ASSOCIATED PROTEIN C >gi 549984 (U13148)
NCBI Description
                  possible apospory-associated protein [Pennisetum ciliare]
                   310801
Seq. No.
                  uC-zmroteosinte086g05b1
Seq. ID
Method
                  BLASTX
                   g4220511
NCBI GI
BLAST score
                   325
                   4.0e-30
E value
                   140
Match length
                   51
% identity
                   (AL035356) DNA polymerase III like protein [Arabidopsis
NCBI Description
                   thaliana]
                   310802
Seq. No.
                   uC-zmroteosinte086g07b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3645899
BLAST score
                   171
                   2.0e-12
E value
                   82
Match length
% identity
                   54
                  (U68408) 5' end not determined experimentally [Zea mays]
NCBI Description
                   310803
Seq. No.
                   uC\text{-}zmroteosinte086h09b1\\
Seq. ID
                   BLASTX
Method
                   g232282
NCBI GI
                   344
BLAST score
                   2.0e-32
E value
                   143
Match length
                   50
% identity
                   22.0 KD CLASS IV HEAT SHOCK PROTEIN PRECURSOR
NCBI Description
                   >gi_477760_pir__B48113 heat shock protein HSP22.0 - soybean
                   >gi_18661_emb_CAA44882_ (X63198) heat shock protein
                   [Glycine max]
                   310804
Seq. No.
                   uC-zmroteosinte087a04b2
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2982451
BLAST score
                   551
                   2.0e-56
E value
                   174
Match length
```

(AL022223) putative protein [Arabidopsis thaliana]

```
310805
Seq. No.
                  uC-zmroteosinte087a06b2
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4582445
BLAST score
                  169
                  5.0e-12
E value
                  40
Match length
                  72
% identity
                   (AC007071) unknown protein [Arabidopsis thaliana]
NCBI Description
                  >gi 4589952 gb AAD26470.1 AC007169 2 (AC007169) unknown
                  protein [Arabidopsis thaliana]
                  310806
Seq. No.
                  uC-zmroteosinte087b03b2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1381154
BLAST score
                  200
                  2.0e-15
E value
Match length
                  61
                  57
% identity
                  (U58278) WCOR719 [Triticum aestivum]
NCBI Description
                  310807
Seq. No.
                  uC-zmroteosinte087b06b2
Seq. ID
                  BLASTX
Method
                   q4206195
NCBI GI
BLAST score
                   224
                   3.0e-18
E value
                   56
Match length
                   68
% identity
                   (AF071527) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   >gi_4262169_gb_AAD14469_ (AC005275) hypothetical protein
                   [Arabidopsis thaliana]
Seq. No.
                   310808
                   uC-zmroteosinte087e02b2
Seq. ID
Method
                   BLASTX
                   g3318615
NCBI GI
BLAST score
                   742
E value
                   6.0e-79
Match length
                   186
% identity
                   74
                   (AB016065) mitochondrial phosphate transporter [Oryza
NCBI Description
                   sativa]
                   310809
Seq. No.
                   uC-zmroteosinte087e11b2
Seq. ID
Method
                   BLASTX
```

Method BLASTX
NCBI GI g3935157
BLAST score 145
E value 1.0e-16
Match length 85
% identity 60

NCBI Description (AC005106) T25N20.21 [Arabidopsis thaliana]

Seq. No. 310810

Seq. ID uC-zmroteosinte087h06b2

Seq. ID

Method

```
BLASTX
Method
                  g136140
NCBI GI
                  225
BLAST score
E value
                  2.0e-18
                  140
Match length
                  35
% identity
NCBI Description PUTATIVE AC9 TRANSPOSASE >gi_72973_pir__TQZMCA probable
                  transposase - maize transposon Ac9
                  310811
Seq. No.
                  uC-zmroteosinte088g06b1
Seq. ID
                  BLASTX
Method
                  g82696
NCBI GI
                  366
BLAST score
E value
                  3.0e-35
Match length
                  86
% identity
                  81
                  glycine-rich protein - maize >gi_22293_emb_CAA43431_
NCBI Description
                   (X61121) glycine-rich protein [Zea mays]
Seq. No.
                  310812
                  uC-zmroteosinte090a11b2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g82696
BLAST score
                  180
E value
                   4.0e-21
Match length
                  79
% identity
                  71
                  glycine-rich protein - maize >gi_22293_emb_CAA43431_
NCBI Description
                   (X61121) glycine-rich protein [Zea mays]
                   310813
Seq. No.
                   uC-zmroteosinte090c12b2
Seq. ID
                   BLASTX
Method
                   g4510349
NCBI GI
BLAST score
                   166
                   2.0e-11
E value
                   96
Match length
% identity
                   54
                  (AC006921) putative bZIP transcription factor [Arabidopsis
NCBI Description
                   thaliana]
                   310814
Seq. No.
                   uC-zmroteosinte090e05b2
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1168518
                   232
BLAST score
                   4.0e-19
E value
                   88
Match length
% identity
                   56
                   APURINIC ENDONUCLEASE-REDOX PROTEIN (DNA-(APURINIC OR
NCBI Description
                   APYRIMIDINIC SITE) LYASE) >gi_472869_emb_CAA54234_ (X76912)
                   ARP protein [Arabidopsis thaliana]
                   310815
Seq. No.
```

44301

uC-zmroteosinte090f08b2

BLASTN

BLAST score

Match length

E value

166

117

4.0e-16



```
q2226328
NCBI GI
BLAST score
                  41
                  8.0e-14
E value
Match length
                  200
% identity
                  80
                  Zea mays physical impedance induced protein (IIG1) mRNA,
NCBI Description
                  complete cds
                  310816
Seq. No.
                  uC-zmroteosinte090h10b2
Seq. ID
                  BLASTX
Method
                  g4580462
NCBI GI
                  279
BLAST score
                  1.0e-24
E value
Match length
                  112
% identity
                   54
                  (AC006081) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  310817
Seq. No.
                  uC-zmroteosinte091a09b2
Seq. ID
Method
                  BLASTX
                   g4512715
NCBI GI
                   191
BLAST score
                   3.0e-14
E value
Match length
                   117
% identity
                   41
                  (AC006569) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   310818
                   uC-zmroteosinte091c04b2
Seq. ID
Method
                   BLASTX
                   g4587514
NCBI GI
BLAST score
                   146
                   3.0e-09
E value
                   102
Match length
% identity
                   38
                   (AC007060) Similar to WO8E3.3 gi_3880615 putative
NCBI Description
                   GTP-binding protein from C. elegans cosmid gb_Z92773.
                   gb AA597331 comes from this gene. [Arabidopsis thaliana]
Seq. No.
                   310819
                   uC-zmroteosinte091d03b2
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3461852
BLAST score
                   285
                   4.0e-26
E value
                   70
Match length
                   66
% identity
                   (AC005315) putative laccase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   310820
                   uC-zmroteosinte091e05b2
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3560166
```

E value

Match length

% identity

2.0e-25

NCBI Description HIGH AFFINITY AMMONIUM TRANSPORTER

61

74



```
% identity
                  (AL031525) ubiquitin carboxyl-terminal hydrolase
NCBI Description
                  [Schizosaccharomyces pombe]
                  310821
Seq. No.
                  uC-zmroteosinte091h08b2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4586251
BLAST score
                  328
                  2.0e-32
E value
                  137
Match length
% identity
                  51
NCBI Description (AL049640) putative protein [Arabidopsis thaliana]
                  310822
Seq. No.
                  uC-zmroteosinte091h09b2
Seq. ID
Method
                  BLASTX
                                           -
NCBI GI
                  g3641837
BLAST score
                  519
                  6.0e-53
E value
                  137
Match length
                  75
% identity
NCBI Description (AL023094) Nonclathrin coat protein gamma - like protein
                  [Arabidopsis thaliana]
Seq. No.
                  310823
                  uC-zmroteosinte092d05b2
Seq. ID
                  BLASTX
Method
                  g4512615
NCBI GI
BLAST score
                  566
E value
                  2.0e-58
Match length
                  159
                  70
% identity
NCBI Description
                  (AC004793) Strong similarity to gb_X59970 3-isopropylmalate
                  dehydrogenase (IMDH) from Brassica napus. EST gb F14478
                  comes from this gene. [Arabidopsis thaliana]
                  310824
Seq. No.
                  uC-zmroteosinte092d08b2
Seq. ID
Method
                  BLASTX
                  a532822
NCBI GI
                  189
BLAST score
                  4.0e-14
E value
Match length
                  82
% identity
                  44
                  (U13876) similar to 4-hydroxybenzoate octaprenyltransferase
NCBI Description
                   [Caenorhabditis elegans]
Seq. No.
                  310825
Seq. ID
                  uC-zmroteosinte092e11b2
Method
                  BLASTX
NCBI GI
                  q3023281
BLAST score
                  282
```



>gi_2065194_emb_CAA64475_ (X95098) ammonium transporter [Lycopersicon esculentum]

Seq. No. 310826

Seq. ID uC-zmroteosinte092f04b2

Method BLASTX
NCBI GI g3881189
BLAST score 345
E value 8.0e-33
Match length 103
% identity 69

NCBI Description (Z99281) similar to ADP-ribosylation factor; cDNA EST

EMBL:C08179 comes from this gene; cDNA EST EMBL:C08337 comes from this gene; cDNA EST EMBL:C09829 comes from this gene; cDNA EST yk291b4.5 comes from this gene; cDNA EST yk4

Seq. No. 310827

Seq. ID uC-zmroteosinte092f07b2

Method BLASTX
NCBI GI g4218010
BLAST score 234
E value 4.0e-25
Match length 104
% identity 62

NCBI Description (AC006135) putative sugar transporter [Arabidopsis

thaliana] >gi 4309720 gb AAD15490 (AC006439) putative

sugar transporter [Arabidopsis thaliana]

Seq. No. 310828

Seq. ID uC-zmroteosinte092h04b2

Method BLASTX
NCBI GI g2506139
BLAST score 312
E value 1.0e-28
Match length 87
% identity 77

NCBI Description COATOMER DELTA SUBUNIT (DELTA-COAT PROTEIN) (DELTA-COP)

(ARCHAIN) >gi_1314049_emb_CAA91901_ (Z67962)

archain/delta-COP [Oryza sativa]

Seq. No. 310829

Seq. ID uC-zmroteosinte093b06b2

Method BLASTX
NCBI GI 94206210
BLAST score 278
E value 2.0e-24
Match length 166
% identity 37

NCBI Description (AF071527) putative calcium channel [Arabidopsis thaliana]

>gi_4263043_gb_AAD15312_ (AC005142) putative calcium

channel [Arabidopsis thaliana]

Seq. No. 310830

Seq. ID uC-zmroteosinte093g01b2

Method BLASTX
NCBI GI g1362008
BLAST score 266

Match length

50

```
1.0e-23
E value
Match length
                  92
% identity
                  15
NCBI Description ubiquitin-like protein 12 - Arabidopsis thaliana
                  310831
Seq. No.
                  uC-zmroteosinte094b09b2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2088826
BLAST score
                  170
                  8.0e-12
E value
Match length
                  50
% identity
                  52
                  (AF003385) R08F11.1 gene product [Caenorhabditis elegans]
NCBI Description
                  310832
Seq. No.
                  uC-zmroteosinte094f02b2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g118104
BLAST score
                  313
                  6.0e-29
E value
Match length
                  81
                  75
% identity
                  PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE)
NCBI Description
                  (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN)
                  >gi_68408_pir__CSZM peptidylprolyl isomerase (EC 5.2.1.8) -
                  maize >gi_168461 (M55021) cyclophilin [Zea mays]
                  >gi 829148 emb CAA48638 (X68678) cyclophilin [Zea mays]
Seq. No.
                  310833
                  uC-zmroteosinte094f03b2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2462911
BLAST score
                  196
                  7.0e-25
E value
Match length
                  91
% identity
                  (Z83832) UDP-glucose:sterol glucosyltransferase [Avena
NCBI Description
                  sativa]
                  310834
Seq. No.
                  uC-zmroteosinte094f04b2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2494129
BLAST score
                  147
E value
                  1.0e-09
                  143
Match length
% identity
NCBI Description (AC002376) T1G11.3 [Arabidopsis thaliana]
Seq. No.
                  310835
Seq. ID
                  uC-zmroteosinte094q06b2
Method
                  BLASTX
NCBI GI
                  g168570
BLAST score
                  216
                  1.0e-17
E value
```

```
% identity
                  (M95077) phenylalanine ammonia lyase [Zea mays]
NCBI Description
Seq. No.
                  310836
Seq. ID
                  uC-zmroteosinte094g10b2
                  BLASTX
Method
                  q2499967
NCBI GI
BLAST score
                  166
                  1.0e-11
E value
Match length
                  35
% identity
                  94
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV B PRECURSOR (PSI-E
NCBI Description
                  B) >gi 632724 bbs 151002 (S72358) photosystem I subunit
                  PSI-E [Nicotiana sylvestris, leaves, Peptide Chloroplast,
                  143 aa] [Nicotiana sylvestris]
Seq. No.
                  310837
                  uC-zmroteosinte095a05b2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4432840
BLAST score
                   409
E value
                   6.0e-40
Match length
                  134
% identity
                  57
```

(AC006283) unknown protein [Arabidopsis thaliana] NCBI Description

Seq. No. 310838 Seq. ID uC-zmroteosinte095d11b2 Method BLASTX q730680 NCBI GI BLAST score 691 6.0e-73 E value 170 Match length

76 % identity

40S RIBOSOMAL PROTEIN SA (P40) (STUBARISTA PROTEIN) NCBI Description (LAMININ RECEPTOR HOMOLOG) (K14) >gi_158031 (M90422) p40 [Drosophila melanogaster] >gi_3292889_emb_CAA19839_ (AL031027) EG:80H7.6 [Drosophila melanogaster]

Seq. No. 310839

uC-zmroteosinte095h08b2 Seq. ID

Method BLASTX NCBI GI g36796 BLAST score 327 1.0e-30 E value Match length 110 % identity 64

(X52882) t-complex polypeptide 1 (AA 1-556) [Homo sapiens] NCBI Description

310840 Seq. No.

uC-zmroteosinte096c03b2 Seq. ID

Method BLASTX g3860271 NCBI GI BLAST score 448 E value 2.0e-44 Match length 192 % identity 44



NCBI Description (AC005824) putative selenium-binding protein [Arabidopsis thaliana]

Seq. No. 310841

Seq. ID uC-zmroteosinte096c09b2

Method BLASTX
NCBI GI g3128195
BLAST score 152
E value 1.0e-09
Match length 60
% identity 53

NCBI Description (AC004521) putative phosphoribosyl pyrophosphate synthetase

[Arabidopsis thaliana] >gi_3341673 (AC003672) putative phosphoribosyl pyrophosphate synthetase [Arabidopsis

thaliana]

Seq. No. 310842

Seq. ID uC-zmroteosinte096d01b2

Method BLASTX
NCBI GI g4539460
BLAST score 269
E value 2.0e-23
Match length 162
% identity 8

NCBI Description (AL049500) putative protein [Arabidopsis thaliana]

Seq. No. 310843

Seq. ID uC-zmroteosinte096d06b2

Method BLASTX
NCBI GI g2497953
BLAST score 165
E value 1.0e-11
Match length 45
% identity 82

NCBI Description MOLYBDOPTERIN BIOSYNTHESIS CNX1 PROTEIN (MOLYBDENUM

COFACTOR BIOSYNTHESIS ENZYME CNX1) >gi_1263314 (L47323) molybdenum cofactor biosynthesis enzyme [Arabidopsis thaliana] >gi_4469123_emb_CAB38312_ (AJ236870) molybdenum cofactor biosynthesis enzyme [Arabidopsis thaliana]

Seq. No. 310844

Seq. ID uC-zmroteosinte096e07b2

Method BLASTX
NCBI GI g2072990
BLAST score 160
E value 1.0e-10
Match length 36
% identity 81

NCBI Description (U95144) putative G-protein-coupled receptor [Brassica

napus]

Seq. No. 310845

Seq. ID uC-zmroteosinte096f02b2

Method BLASTX
NCBI GI g4105798
BLAST score 357
E value 2.0e-62

```
Match length
% identity
                  67
                  (AF049930) PGP237-11 [Petunia x hybrida]
NCBI Description
Seq. No.
                  310846
                  uC-zmroteosinte096f11b2
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3885968
BLAST score
                  613
                  8.0e-64
E value
                  160
Match length
                  73
% identity
                  (AF100985) phosphopyruvate hydratase [Penaeus monodon]
NCBI Description
Seq. No.
                  310847
                  uC-zmroteosinte096h09b2
Seq. ID
                  BLASTX
Method
NCBI GI
                  g115492
BLAST score
                  455
                  2.0e-45
E value
                  96
Match length
                  93
% identity
                  CALMODULIN-RELATED PROTEIN >gi 169205 (M80831)
NCBI Description
                  calmodulin-related protein [Petunia hybrida]
Seq. No.
                  310848
                  uC-zmroteosinte097b02b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3641836
BLAST score
                  269
E value
                  1.0e-29
                  118
Match length
% identity
                  54
                   (AL023094) putative serine/threonine protein kinase
NCBI Description
                   [Arabidopsis thaliana]
                  310849
Seq. No.
Seq. ID
                  uC-zmroteosinte098b12b2
Method
                  BLASTX
                  g310587
NCBI GI
BLAST score
                  170
E value
                  7.0e-12
Match length
                  113
                  42
% identity
NCBI Description
                  (L20864) ascorbate peroxidase [Spinacia oleracea]
                  >gi 1384110 dbj BAA12890 (D85864) cytosolic ascorbate
                  peroxidase [Spinacia oleracea]
```

Seq. No. 310850

Seq. ID uC-zmroteosinte098e10b2

Method BLASTX
NCBI GI g2618701
BLAST score 208
E value 3.0e-16
Match length 102
% identity 48

NCBI Description (AC002510) hypothetical protein [Arabidopsis thaliana]

```
310851
Seq. No.
                  uC-zmroteosinte098h06b2
Seq. ID
Method
                  BLASTX
                  g2961358
NCBI GI
                  258
BLAST score
                  3.0e-22
E value
                  106
Match length
% identity
                  47
                  (AL022140) serine/threonine protein kinase like protein
NCBI Description
                  [Arabidopsis thaliana]
                  310852
Seq. No.
                  uC-zmroteosinte099b03b2
Seq. ID
Method
                  BLASTX
                  q4249402
NCBI GI
BLAST score
                  244
                  4.0e-30
E value
                  123
Match length
                  59
% identity
                  (AC006072) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  310853
                  uC-zmroteosinte099g08b2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g122022
BLAST score
                  287
E value
                  1.0e-25
Match length
                  67
                  88
% identity
                  HISTONE H2B >gi 283025_pir__S22323 histone H2B - wheat
NCBI Description
                  >qi 21801 emb CAA42530 (X59873) histone H2B [Triticum
                  aestivum]
Seq. No.
                   310854
                  uC-zmroteosinte099g12b2
Seq. ID
Method
                  BLASTX
                   g4098319
NCBI GI
BLAST score
                   148
                   1.0e-11
E value
Match length
                   61
% identity
                   64
                  (U76744) beta-tubulin 1 [Triticum aestivum]
NCBI Description
                   310855
Seq. No.
Seq. ID
                   uC-zmroteosinte100d05b2
Method
                   BLASTX
                   g3334349
NCBI GI
BLAST score
                   189
E value
                   2.0e-14
Match length
                   75
% identity
                   60
                  GLYCYL-TRNA SYNTHETASE (GLYCINE--TRNA LIGASE) (GLYRS)
NCBI Description
                   >gi_2564215_emb_CAA05162_ (AJ002062) glycyl-tRNA synthetase
                   [Arabidopsis thaliana]
```

44309

310856

Seq. No.

```
uC-zmroteosinte100d07b2
Seq. ID
                  BLASTX
Method
                  q3023522
NCBI GI
BLAST score
                   349
                  1.0e-35
E value
                  163
Match length
% identity
                   47
                  COATOMER BETA' SUBUNIT (BETA'-COAT PROTEIN) (BETA'-COP)
NCBI Description
                   (P102) >gi 2454309 (AF002705) beta prime COP [Rattus
                   norvegicus]
                   310857
Seq. No.
                   uC-zmroteosinte100g08b2
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3859659
BLAST score
                   185
                   6.0e-14
E value
Match length
                   66
% identity
                   56
                   (AL031394) putative potassium transporter AtKT5p (AtKT5)
NCBI Description
                   [Arabidopsis thaliana]
                   310858
Seq. No.
                   uC-zmroteosinte100h04b2
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2114046
BLAST score
                   150
E value
                   3.0e-09
Match length
                   36
                   75
% identity
                   (AB002147) water channel protein [Nicotiana excelsior]
NCBI Description
                   310859
Seq. No.
                   uC-zmroteosinte101a03b2
Seq. ID
                   BLASTX
Method
                   g3024126
NCBI GI
BLAST score
                   212
                   6.0e-17
E value
                   52
Match length
                   79
% identity
                   S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
NCBI Description
                   ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                   >gi 1655576_emb_CAA95856_ (Z71271) S-adenosyl-L-methionine
                   synthetase 1 [Catharanthus roseus]
                   310860
Seq. No.
                   uC-zmroteosinte101a05b2
Seq. ID
                   BLASTX
Method
                   g587564
NCBI GI
BLAST score
                   406
                   1.0e-39
E value
Match length
                   131
% identity
                   62
                   (X80235) mitochondrial processing peptidase [Solanum
NCBI Description
```

Seq. No. 310861

tuberosum]

BLAST score E value

Match length

6.0e-30

67



```
uC-zmroteosinte101a11b2
Seq. ID
                  BLASTX
Method
                  q100490
NCBI GI
                  743
BLAST score
                  5.0e-79
E value
                  150
Match length
% identity
                  polyubiquitin - garden snapdragon (fragment)
NCBI Description
                  >gi 16071_emb_CAA48140_ (X67957) ubiquitin [Antirrhinum
                  310862
Seq. No.
                  uC-zmroteosinte101f06b2
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4557867
BLAST score
                  144
                  4.0e-09
E value
                  94
Match length
                  39
% identity
                  sulfite oxidase >gi_1711606_sp_P51687 SUOX HUMAN SULFITE
NCBI Description
                  OXIDASE PRECURSOR >gi_1362942_pir__S55874 sulfite oxidase
                   (EC 1.8.3.1) precursor, mitochondrial - human >gi_508502
                   (L31573) sulfite oxidase [Homo sapiens]
                  >gi 1098062 prf _2115221A sulfide oxidase [Homo sapiens]
                  310863
Seq. No.
                  uC-zmroteosinte101f09b2
Seq. ID
Method
                  BLASTN
                   g168606
NCBI GI
BLAST score
                  122
                   8.0e-62
E value
Match length
                   206
                   90
% identity
                  Zea mays mitochondrial Rieske Fe-S protein mRNA, complete
NCBI Description
Seq. No.
                   310864
                   uC-zmroteosinte101h12b2
Seq. ID
                   BLASTX
Method
                   g312179
NCBI GI
                   269
BLAST score
                   1.0e-23
E value
                   90
Match length
                   64
% identity
                   (X73151) glyceraldehyde 3-phosphate dehydrogenase
NCBI Description
                   (phosphorylating) [Zea mays] >gi_1184772 (U45855) cytosolic
                   glyceroldehyde-3-phosphate dehydrogenase GAPC2 [Zea mays]
                   >gi_1185554 (U45858) glyceraldehyde-3-phosphate
                   dehydrogenase [Zea mays]
                   310865
Seq. No.
                   uC-zmroteosinte102a04b2
Seq. ID
                   BLASTX
Method
                   q224293
NCBI GI
                   323
```

NCBI Description



```
% identity
NCBI Description histone H4 [Triticum aestivum]
                  310866
Seq. No.
Seq. ID
                  uC-zmroteosinte102a05b2
Method
                  BLASTX
NCBI GI
                  g2198853
BLAST score
                  234
E value
                  2.0e-25
Match length
                  109
% identity
                  61
NCBI Description
                  (AF007786) cystathionine gamma-synthase [Zea mays]
Seq. No.
                  310867
Seq. ID
                  uC-zmroteosinte102c01b2
Method
                  BLASTX
NCBI GI
                  q832876
BLAST score
                  147
E value
                  3.0e-09
Match length
                  85
% identity
                  42
NCBI Description
                  (L41345) ascorbate free radical reductase [Solanum
                  lycopersicum] >gi_1097368_prf__2113407A ascorbate free
                  radical reductase [Lycopersicon esculentum]
Seq. No.
                  310868
Seq. ID
                  uC-zmroteosinte102c08b2
Method
                  BLASTN
NCBI GI
                  g927571
BLAST score
                  59
                  9.0e-25
E value
Match length
                  67
                  97
% identity
NCBI Description
                  Z.mays mRNA for calreticulin precursor
Seq. No.
                  310869
Seq. ID
                  uC-zmroteosinte102c09b2
Method
                  BLASTX
NCBI GI
                  q1169528
BLAST score
                  292
E value
                  5.0e-26
Match length
                  67
% identity
                  90
NCBI Description
                  ENOLASE 2 (2-PHOSPHOGLYCERATE DEHYDRATASE 2)
                  (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE 2) >gi 602253 (U17973)
                  enolase [Zea mays]
Seq. No.
                  310870
Seq. ID
                  uC-zmroteosinte102h01b2
Method
                  BLASTX
NCBI GI
                  g122022
BLAST score
                  316
E value
                  4.0e-29
Match length
                  69
% identity
                  94
```

HISTONE H2B >gi_283025_pir__S22323 histone H2B - wheat >gi_21801_emb_CAA42530_ (X59873) histone H2B [Triticum



aestivum]

Seq. No. 310871
Seq. ID uC-zmroteosinte103f02b2
Method BLASTX
NCBI GI g122022
BLAST score 294

E value 2.0e-27.
Match length 95
% identity 76

NCBI Description HISTONE H2B >gi_283025_pir_ S22323 histone H2B - wheat >gi_21801 emb CAA42530 (X59873) histone H2B [Triticum

>g1_21001_enb_CAA42550_ (X5507

aestivum]

Seq. No. 310872

Seq. ID uC-zmroteosinte103f04b2

Method BLASTX
NCBI GI g547901
BLAST score 376
E value 3.0e-36
Match length 122
% identity 57

NCBI Description MALATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR

>gi_65933_pir__DEBYMM malate dehydrogenase (EC 1.1.1.37)
precursor, mitochondrial - yeast (Saccharomyces cerevisiae)
>gi_171892 (J02841) malate dehydrogenase [Saccharomyces cerevisiae] >gi_486125_emb_CAA81923_ (Z28085) ORF YKL085w

erected in a

[Saccharomyces cerevisiae]

Seq. No. 310873

Seq. ID uC-zmroteosinte103f10b2

Method BLASTX
NCBI GI g3548810
BLAST score 337
E value 3.0e-31
Match length 175
% identity 39

NCBI Description (AC005313) putative chloroplast nucleoid DNA binding

protein [Arabidopsis thaliana]

Seq. No. 310874

Seq. ID uC-zmroteosinte103h09b2

Method BLASTX
NCBI GI g4558672
BLAST score 209
E value 1.0e-16
Match length 113
% identity 42

NCBI Description (AC007063) putative 1,3-beta-D-glucan synthase [Arabidopsis

thaliana]

Seq. No. 310875

Seq. ID uC-zmroteosinte104a11b2

Method BLASTX
NCBI GI g3236259
BLAST score 585
E value 1.0e-60



```
160
Match length
% identity
                  70
                  (AC004684) putative alcohol dehydrogenase [Arabidopsis
NCBI Description
                  thaliana]
                  310876
Seq. No.
                  uC-zmroteosinte104c11b2
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4586105
BLAST score
                  233
E value
                  2.0e-19
Match length
                  133
% identity
                  35
                  (AL049638) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  310877
                  uC-zmroteosinte104e05b2
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1749676
BLAST score
                  224
E value
                  3.0e-18
Match length
                  124
% identity
                  41
NCBI Description
                  (D89234) similar to Saccharomyces cerevisiae ORF YGR205W,
                  EMBL Accession Number Z72990 [Schizosaccharomyces pombe]
Seq. No.
                  310878
                  uC-zmroteosinte104e08b2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3367596
BLAST score
                  287
                  1.0e-25
E value
                  79
Match length
                  67
% identity
                  (AL031135) putative protein [Arabidopsis thaliana]
NCBI Description
                  310879
Seq. No.
Seq. ID
                  uC-zmroteosinte104g12b2
Method
                  BLASTX
NCBI GI
                  g1076668
BLAST score
                  173
E value
                  4.0e-19
Match length
                  68
                  76
% identity
                  NADH dehydrogenase (EC 1.6.99.3) - potato
NCBI Description
                  >gi_639834_emb_CAA58823_ (X83999) NADH dehydrogenase
                  [Solanum tuberosum]
                  310880
Seq. No.
Seq. ID
                  uC-zmroteosinte105b09b1
Method
                  BLASTN
```

Method BLASTN
NCBI GI g1420923
BLAST score 164
E value 4.0e-87
Match length 192
% identity 82

NCBI Description Zea mays repressor-like protein (in1) gene, complete cds

NCBI GI

g4455331

```
310881
Seq. No.
                  uC-zmroteosinte105b12b1
Seq. ID
Method
                  BLASTN
                  g758352
NCBI GI
BLAST score
                  84
                  1.0e-39
E value
Match length
                  124
                  92
% identity
NCBI Description Z.mays mRNA for cysteine synthase
                  310882
Seq. No.
Seq. ID
                  uC-zmroteosinte105d04b1
Method
                  BLASTX
                  g2244749
NCBI GI
BLAST score
                  150
                  1.0e-17
E value
                  123
Match length
% identity
                  46
                  (Z97335) hydroxymethyltransferase [Arabidopsis thaliana]
NCBI Description
                  310883
Seq. No.
                  uC-zmroteosinte105d07b1
Seq. ID
Method
                  BLASTX
                  g3212851
NCBI GI
BLAST score
                  187
                  8.0e-16
E value
Match length
                  64
                  70
% identity
NCBI Description
                  (AC004005) unknown protein [Arabidopsis thaliana]
                  310884
Seq. No.
                  uC-zmroteosinte105h08b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3128206
BLAST score
                  327
E value
                  3.0e-30
Match length
                  184
% identity
                  40
                  (AC004077) unknown protein [Arabidopsis thaliana]
NCBI Description
                  310885
Seq. No.
                  uC-zmroteosinte105h10b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3122762
BLAST score
                  210
                  1.0e-16
E value
Match length
                  106
% identity
                  39
NCBI Description
                  RIBOSOME RECYCLING FACTOR (RIBOSOME RELEASING FACTOR) (RRF)
                  (VEGETATIVE PROTEIN 12B) (VEG12B) >gi 2634024 emb CAB13525
                  (Z99112) ribosome recycling factor [Bacillus subtilis]
                  310886
Seq. No.
Seq. ID
                  uC-zmroteosinte106a11b2
Method
                  BLASTX
```



```
BLAST score
E value
                  1.0e-20
Match length
                  149
                  10
% identity
NCBI Description (AL035525) putative protein [Arabidopsis thaliana]
                  310887
Seq. No.
                  uC-zmroteosinte106c05b2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2462911
BLAST score
                  260
E value
                  4.0e-26
Match length
                  83
% identity
                  75
                  (Z83832) UDP-glucose:sterol glucosyltransferase [Avena
NCBI Description
                  sativa]
Seq. No.
                  310888
Seq. ID
                  uC-zmroteosinte106c08b2
Method
                  BLASTX
NCBI GI
                  g1353673
BLAST score
                  489
E value
                  3.0e-49
Match length
                  137
% identity
                  61
NCBI Description (U42349) 39 kDa encoded by N33 [Homo sapiens]
                  310889
Seq. No.
                  uC-zmroteosinte106e02b2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2130145
BLAST score
                  595
                  9.0e-62
E value
Match length
                  152
                  80
% identity
NCBI Description
                  seed storage protein opaque-2 - maize >gi_1144536 (U35063)
                  opaque-2 heterodimerizing protein 1b [Zea mays]
Seq. No.
                  310890
Seq. ID
                  uC-zmroteosinte107a05b2
Method
                  BLASTX
NCBI GI
                  q4033421
BLAST score
                  235
E value
                  8.0e-20
Match length
                  74
% identity
                   65
```

NCBI Description SOLUBLE INORGANIC PYROPHOSPHATASE (PYROPHOSPHATE

PHOSPHO-HYDROLASE) (PPASE) >gi_2570501 (AF022733) inorganic

pyrophosphatase [Oryza sativa]

Seq. No. 310891

uC-zmroteosinte107b01b2 Seq. ID

BLASTN Method NCBI GI g4416300 99 BLAST score 2.0e-48 E value Match length 180

```
% identity
NCBI Description
                  Zea mays chromosome 4 22 kDa zein-associated intercluster
                  region, complete sequence
                  310892
Seq. No.
                  uC-zmroteosinte107d12b2
Seq. ID
Method
                  BLASTX
                  g3600061
NCBI GI
BLAST score
                  186
                  9.0e-14
E value
Match length
                  66
                  52
% identity
                  (AF080120) contains similarity to DNA binding proteins
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  310893
Seq. ID
                  uC-zmroteosinte107g09b2
Method
                  BLASTX
                  g2801442
NCBI GI
BLAST score
                  174
                  4.0e-13
E value
Match length
                  48
                  71
% identity
```

NCBI Description (AF028338) ubiquitin-conjugating enzyme 15 [Arabidopsis thaliana]

Seq. No. 310894
Seq. ID uC-zmroteosinte108e03b3
Method BLASTX
NCBI GI q4056502

NCBI GI g4056502 BLAST score 271 E value 2.0e-24 Match length 138 % identity 51

NCBI Description (AC005896) 40S ribosomal protein S5 [Arabidopsis thaliana]

Seq. No. 310895

Seq. ID uC-zmroteosinte108f02b3

Method BLASTN
NCBI GI 94240538
BLAST score 68
E value 7.0e-30
Match length 140
% identity 88

NCBI Description Zea mays knotted class 1 homeodomain protein liguleless3

(1g3) mRNA, complete cds

Seq. No. 310896

Seq. ID uC-zmroteosinte108h04b3

Method BLASTX
NCBI GI g421960
BLAST score 184
E value 8.0e-14
Match length 93
% identity 44

NCBI Description small nuclear ribonucleoprotein U2B'' - potato >gi 169589

(M72892) spliceosomal protein [Solanum tuberosum]

Seq. No. 310897

Seq. ID uC-zmroteosinte109c01b3

Method BLASTX
NCBI GI g2497486
BLAST score 500
E value 1.0e-50
Match length 115
% identity 83

NCBI Description URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP

KINASE) >gi 2121275 (AF000147) UMP/CMP kinase [Arabidopsis

thaliana]

Seq. No. 310898

Seq. ID uC-zmroteosinte109d11b3

Method BLASTX
NCBI GI g3289002
BLAST score 272
E value 9.0e-24
Match length 175
% identity 6

NCBI Description (AF073522) CRP1 [Zea mays]

Seq. No. 310899

Seq. ID uC-zmroteosinte109e09b3

Method BLASTX
NCBI GI g3183237
BLAST score 149
E value 2.0e-09
Match length 102
% identity 28

NCBI Description HYPOTHETICAL 103.4 KD TRP-ASP REPEATS CONTAINING PROTEIN

C3D6.12 IN CHROMOSOME II >gi 2117308 emb CAB09121.1

(Z95620) trp asp repeat protein [Schizosaccharomyces pombe]

Seq. No. 310900

Seq. ID uC-zmroteosinte109h03b3

Method BLASTX
NCBI GI g1370194
BLAST score 241
E value 1.0e-28
Match length 112
% identity 70

NCBI Description (Z73946) RAB8C [Lotus japonicus]

Seq. No. 310901

Seq. ID uC-zmroteosintel15c05b1

Method BLASTN
NCBI GI g1177368
BLAST score 52
E value 3.0e-20

Match length 68 % identity 94

NCBI Description Z.mays mRNA for ribosomal protein L39

Seq. No. 310902

Seq. ID uC-zmroteosintel15c12b1

E value

Match length

% identity

7.0e-09

81

41



```
Method
                  BLASTX
NCBI GI
                  g294845
BLAST score
                  266
                  2.0e-23
E value
Match length
                  99
                  56
% identity
NCBI Description
                  (L13655) membrane protein [Saccharum hybrid cultivar
                  H65-7052]
                  310903
Seq. No.
Seq. ID
                  uC-zmroteosinte115d01b1
Method
                  BLASTX
NCBI GI
                  g112994
BLAST score
                  417
E value
                  5.0e-41
Match length
                  88
% identity
                  94
NCBI Description
                  GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN
                  >gi_82685_pir__S04536 embryonic abundant protein,
                  glycine-rich - maize >gi 22313 emb CAA31077 (X12564)
                  ABA-inducible gene protein [Zea mays]
                  >gi_226091_prf__1410284A abscisic acid inducible gene [Zea
                  mays]
Seq. No.
                  310904
Seq. ID
                  uC-zmroteosinte115e05b1
Method
                  BLASTX
NCBI GI
                  g114420
BLAST score
                  147
E value
                  2.0e-09
Match length
                  95
% identity
                  43
NCBI Description
                  ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR
                  >gi_100882_pir__S11491 H+-transporting ATP synthase (EC
                  3.6.1.34) beta chain, mitochondrial - maize
                  >gi_22173_emb_CAA38140 (X54233) ATPase F1 subunit protein
                  [Zea mays] >gi 897618 (M36087) F-1-ATPase subunit 2 [Zea
                  mays]
Seq. No.
                  310905
Seq. ID
                  uC-zmroteosinte115q02b1
Method
                  BLASTX
                  g2213626
NCBI GI
BLAST score
                  170
E value
                  5.0e-12
Match length
                  68
% identity
                  43
NCBI Description
                  (AC000103) F21J9.18 [Arabidopsis thaliana]
Seq. No.
                  310906
Seq. ID
                  uC-zmroteosinte115q09b1
Method
                  BLASTX
NCBI GI
                  q2529677
BLAST score
                  144
```





```
NCBI Description
                  (AC002535) kinesin-like protein, heavy chain [Arabidopsis
                  thaliana]
                  310907
Seq. No.
                  uC-zmroteosintel15h09b1
Seq. ID
                  BLASTN
Method
NCBI GI
                  q532622
BLAST score
                  66
                  2.0e-28
E value
                  197
Match length
% identity
                  88
NCBI Description Zea mays lipase (LIP) mRNA, complete cds
Seq. No.
                  310908
Seq. ID
                  uC-zmroteosintel16b01b2
                  BLASTX
Method
NCBI GI
                  g3935178
BLAST score
                  185
                  6.0e-14
E value
Match length
                  67
% identity
                  54
NCBI Description (AC004557) F17L21.21 [Arabidopsis thaliana]
Seq. No.
                  310909
Seq. ID
                  uC-zmroteosinte116c08b2
Method
                  BLASTX
NCBI GI
                  g3953479
BLAST score
                  336
E value
                  4.0e-32
Match length
                  71
% identity
                  92
NCBI Description (AC002328) F2202.24 [Arabidopsis thaliana]
                  310910
Seq. No.
Seq. ID
                  uC-zmroteosintel16f05b2
Method
                  BLASTN
NCBI GI
                  g498772
BLAST score
                  36
E value
                  3.0e-11
Match length
                  52
% identity
                  92
NCBI Description Z.mays (cv DH5xDH7) hsp70-4 mRNA for heat shock protein
Seq. No.
                  310911
Seq. ID
                  uC-zmroteosintel16f06b2
Method
                  BLASTX
NCBI GI
                  g2129553
                  314
```

BLAST score 8.0e-29 E value

Match length 83 % identity

NCBI Description calcium-dependent protein kinase 6 - Arabidopsis thaliana

Seq. No.

310912

Seq. ID

uC-zmroteosintel16h07b2

Method NCBI GI BLASTX g2668742

```
BLAST score
E value
                   2.0e-34
                   80
Match length
                   88
% identity
NCBI Description
                   (AF034945) glycine-rich RNA binding protein [Zea mays]
Seq. No.
                   310913
                   uC-zmroteosinte117a02b1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3288821
BLAST score
                   488
E value
                   3.0e-49
Match length
                   122
% identity
                   76
                   (AF063901) alanine:glyoxylate aminotransferase;
NCBI Description
                   transaminase [Arabidopsis thaliana]
                   310914
Seq. No.
Seq. ID
                   uC-zmroteosinte117a05b1
Method
                   BLASTX
                   g1184776
NCBI GI
BLAST score
                   559
E value
                   1.0e-57
Match length
                   132
% identity
                   81
NCBI Description
                   (U45857) cytosolic glyceroldehyde-3-phosphate dehydrogenase
                   GAPC4 [Zea mays]
Seq. No.
                   310915
Seq. ID
                   uC-zmroteosinte117a06b1
Method
                   BLASTX
NCBI GI
                   q4455335
BLAST score
                   189
E value
                   1.0e-14
                   88
Match length
% identity
                   48
NCBI Description
                   (AL035525) putative protein [Arabidopsis thaliana]
Seq. No.
                   310916
Seq. ID
                   uC-zmroteosintel17a08b1
Method
                   BLASTX
NCBI GI
                   g3138799
BLAST score
                   775
E value
                   7.0e-83
Match length
                   146
                   99
% identity
NCBI Description
                  (AB014058) beta 6 subunit of 20S proteasome [Oryza sativa]
Seq. No.
                   310917
Seq. ID
                   uC-zmroteosintel17a08b2
Method
                   BLASTN
NCBI GI
                   g3341647
```

Method BLASTN
NCBI GI g3341647
BLAST score 39
E value 2.0e-12
Match length 145
% identity 88

NCBI Description Zea mays Ama gene encoding single-subunit RNA polymerase



```
310918
Seq. No.
Seq. ID
                  uC-zmroteosintel17a09b1
Method
                  BLASTX
NCBI GI
                  g2104681
BLAST score
                  182
E value
                  2.0e-13
Match length
                  120
% identity
                  44
NCBI Description (X97907) transcription factor [Vicia faba]
                  310919
Seq. No.
                  uC-zmroteosinte117a10b1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g409782
BLAST score
                  351
                  0.0e+00
E value
Match length
                  417
                  96
% identity
NCBI Description Rice mRNA for ferredoxin-NADP+ reductase, complete cds
Seq. No.
                  310920
Seq. ID
                  uC-zmroteosintel17a12b1
Method
                  BLASTX
NCBI GI
                  g4455335
BLAST score
                  254
                  9.0e-22
E value
Match length
                  79
                  58
% identity
NCBI Description (AL035525) putative protein [Arabidopsis thaliana]
                  310921
Seq. No.
Seq. ID
                  uC-zmroteosintel17b01b1
Method
                  BLASTX
NCBI GI
                  g4249382
BLAST score
                  454
E value
                  2.0e-45
Match length
                  122
% identity
                  72
NCBI Description
                  (AC005966) Strong similarity to gi 3337350 F13P17.3
                  putative permease from Arabidopsis thaliana BAC
                  gb_AC004481. [Arabidopsis thaliana]
Seq. No.
                  310922
Seq. ID
                  uC-zmroteosinte117b03b1
Method
                  BLASTN
NCBI GI
                  g414704
BLAST score
                  235
E value
                  1.0e-129
Match length
                  255
% identity
                  98
```

NCBI Description O.sativa mRNA for cytochrome b5

Seq. No.

310923 Seq. ID uC-zmroteosintel17b06b1

Method BLASTX NCBI GI g4210332



BLAST score 481 E value 1.0e-48 Match length 108 % identity 85

NCBI Description (AJ223803) 2-oxoglutarate dehydrogenase E2 subunit

[Arabidopsis thaliana]

Seq. No. 310924

Seq. ID uC-zmroteosintel17b07b1

Method BLASTX
NCBI GI g1778095
BLAST score 235
E value 1.0e-19
Match length 70
% identity 66

NCBI Description (U64903) putative sugar transporter; member of major

facilitative superfamily; integral membrane protein [Beta

vulgaris]

Seq. No. 310925

Seq. ID uC-zmroteosinte117b09b1

Method BLASTX
NCBI GI g4104976
BLAST score 200
E value 2.0e-15
Match length 117
% identity 38

NCBI Description (AF043117) ubiquitin-fusion degradation protein 2 [Homo

sapiens]

Seq. No. 310926

Seq. ID uC-zmroteosintel17c01b1

Method BLASTX
NCBI GI g1351014
BLAST score 455
E value 2.0e-45
Match length 112
% identity 85

NCBI Description 40S RIBOSOMAL PROTEIN S8 >gi 968902 dbj BAA07207 (D38010)

ribosomal protein S8 [Oryza sativa]

Seq. No. 310927

Seq. ID uC-zmroteosintel17c02b1

Method BLASTX
NCBI GI g1167836
BLAST score 363
E value 1.0e-34
Match length 101
% identity 61

NCBI Description (Z68893) protein with incomplete signal sequence [Holcus

lanatus]

Seq. No. 310928

Seq. ID uC-zmroteosintel17c04b1

Method BLASTX NCBI GI g2306811 BLAST score 179



E value 2.0e-13
Match length 32
% identity 81
NCBI Description (U97521) class IV endochitinase [Vitis vinifera]

Seq. No. 310929

Seq. ID uC-zmroteosintel17c06b1

Method BLASTX
NCBI GI g4006848
BLAST score 555
E value 5.0e-57
Match length 158
% identity 63

NCBI Description (AJ131433) selenocysteine methyltransferase [Astragalus

bisulcatus]

Seq. No. 310930

Seq. ID uC-zmroteosinte117c12b2

Method BLASTX
NCBI GI g4455287
BLAST score 334
E value 3.0e-31
Match length 95
% identity 71

NCBI Description (AL035527) putative protein [Arabidopsis thaliana]

Seq. No. 310931

Seq. ID uC-zmroteosinte117d01b1

Method BLASTX
NCBI GI g401190
BLAST score 528
E value 6.0e-54
Match length 115
% identity 86

NCBI Description THAUMATIN-LIKE PROTEIN PRECURSOR >gi_100715 pir S25551

thaumatin-like protein - rice >gi 20376 emb CAA48278

(X68197) thaumatin-like protein [Oryza sativa]

Seq. No. 310932

Seq. ID uC-zmroteosinte117d02b1

Method BLASTX
NCBI GI g1907270
BLAST score 190
E value 6.0e-15
Match length 40
% identity 80

NCBI Description (X96761) sulphate transporter protein [Sporobolus

stapfianus]

Seq. No. 310933

Seq. ID uC-zmroteosintel17d04b1

Method BLASTX
NCBI GI g3367517
BLAST score 202
E value 8.0e-16
Match length 79
% identity 47



NCBI Description (AC004392) Similar to F4I1.26 putative beta-glucosidase

gi_3128187 from A. thaliana BAC gb_AC004521. ESTs gb_N97083, gb_F19868 and gb_F15482 come from this gene.

[Arabidopsis thaliana]

Seq. No. 310934

Seq. ID uC-zmroteosinte117d05b1

Method BLASTX
NCBI GI g3482979
BLAST score 199
E value 2.0e-15
Match length 90

% identity 44

NCBI Description (AL031369) putative protein [Arabidopsis thaliana]

>gi_4567258_gb_AAD23672.1_AC007070_21 (AC007070)

hypothetical protein [Arabidopsis thaliana]

Seq. No. 310935

Seq. ID uC-zmroteosinte117d12b1

Method BLASTX
NCBI GI g1854378
BLAST score 842
E value 1.0e-90
Match length 170
% identity 96

NCBI Description (AB001338) Sucrose-Phosphate Synthase [Saccharum

officinarum]

Seq. No. 310936

Seq. ID uC-zmroteosintel17e04b1

Method BLASTX
NCBI GI g2625084
BLAST score 240
E value 4.0e-20
Match length 52
% identity 90

NCBI Description (AF030382) ADP-glucose pyrophosphorylase small subunit

[Cucumis melo var. markuwa Markino]

Seq. No. 310937

Seq. ID uC-zmroteosintel17e09b1

Method BLASTX
NCBI GI g631978
BLAST score 217
E value 1.0e-17
Match length 114
% identity 39

NCBI Description cytochrome P-450 oxidase - Mentha piperita

>gi_493475_emb_CAA83941 (Z33875) cytochrome P-450 oxidase

[Mentha x piperita]

Seq. No. 310938

Seq. ID uC-zmroteosintel17e10b1

Method BLASTX
NCBI GI g1778147
BLAST score 366
E value 5.0e-35



Match length 85 % identity 86 NCBI Description (U

(U66403) phosphate/phosphoenolpyruvate translocator

precursor [Zea mays]

Seq. No. 310939

Seq. ID uC-zmroteosintel17e12b1

Method BLASTN
NCBI GI g3885891
BLAST score 162
E value 5.0e-86
Match length 298
% identity 93

NCBI Description Oryza sativa photosystem-1 F subunit precursor (PSI-F)

mRNA, complete cds

Seq. No. 310940

Seq. ID uC-zmroteosinte117f07b1

Method BLASTX
NCBI GI g2293480
BLAST score 380
E value 6.0e-37
Match length 83
% identity 89

NCBI Description (AF011331) glycine-rich protein [Oryza sativa]

Seq. No. 310941

Seq. ID uC-zmroteosinte117f09b1

Method BLASTX
NCBI GI g1351014
BLAST score 571
E value 5.0e-59
Match length 127
% identity 89

NCBI Description 40S RIBOSOMAL PROTEIN S8 >gi_968902_dbj_BAA07207_ (D38010)

ribosomal protein S8 [Oryza sativa]

Seq. No. 310942

Seq. ID uC-zmroteosintel17f10b1

Method BLASTX
NCBI GI g3785989
BLAST score 465
E value 1.0e-46
Match length 116
% identity 75

NCBI Description (AC005560) unknown protein [Arabidopsis thaliana]

Seq. No. 310943

Seq. ID uC-zmroteosintel17f12b1

Method BLASTX
NCBI GI g1174199
BLAST score 149
E value 2.0e-09
Match length 103
% identity 40

NCBI Description (U44760) S25-PR6 [Nicotiana tabacum]



```
310944
Seq. No.
Seq. ID
                   uC-zmroteosintel17g04b1
                  BLASTX
Method
                   g3395423
NCBI GI
BLAST score
                   275
                   2.0e-24
E value
Match length
                   91
% identity
                   57
                   (AC004683) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                   >gi 3786023 (AC005499) putative protein kinase [Arabidopsis
                   thaliana]
                   310945
Seq. No.
Seq. ID
                   uC-zmroteosinte117q06b1
Method
                   BLASTX
NCBI GI
                   q4406132
BLAST score
                   239
E value
                   1.0e-20
Match length
                   50
                   90
% identity
NCBI Description
                  (AF077760) MADS box protein [Oryza sativa]
Seq. No.
                   310946
Seq. ID
                   uC-zmroteosintel17g07b1
Method
                   BLASTX
NCBI GI
                   q2791278
BLAST score
                   168
E value
                   7.0e-12
Match length
                   100
% identity
                   44
NCBI Description
                  (Z69257) beta-xylosidase [Hypocrea jecorina]
Seq. No.
                   310947
Seq. ID
                   uC-zmroteosintel17g09b1
Method
                   BLASTX
                   q4587611
NCBI GI
BLAST score
                   386
                   2.0e-37
E value
Match length
                   100
                   73
% identity
                   (AC006951) putative 40S ribosomal protein S17 [Arabidopsis
NCBI Description
                   thaliana]
                   310948
Seq. No.
Seq. ID
                   uC\text{-}zmroteosintell7gl1bl\\
```

Method BLASTX
NCBI GI g1170503
BLAST score 158
E value 8.0e-11
Match length 53
% identity 68

NCBI Description EUKARYOTIC INITIATION FACTOR 4A-1 (EIF-4A-1)

>gi_322503_pir__JC1452 translation initiation factor eIF-4A1 - Arabidopsis thaliana >gi_16554_emb_CAA46188_ (X65052) eukaryotic translation initiation factor 4A-1

[Arabidopsis thaliana]

NCBI Description

mays]



```
Seq. No.
Seq. ID
                  uC-zmroteosintel17h06b1
Method
                  BLASTX
NCBI GI
                  q1321661
BLAST score
                  158
E value
                  3.0e-11
Match length
                  54
                  65
% identity
NCBI Description
                  (D45423) ascorbate peroxidase [Oryza sativa]
Seq. No.
                  310950
Seq. ID
                  uC-zmroteosintel18a11b1
Method
                  BLASTX
NCBI GI
                  q465873
BLAST score
                  315
E value
                  6.0e-29
Match length
                  153
% identity
                  HYPOTHETICAL 59.1 KD PROTEIN F22B7.6 IN CHROMOSOME III
NCBI Description
                  >gi_1078846_pir__S44637 f22b7.6 protein - Caenorhabditis
                  elegans >gi_156308 (L12018) putative [Caenorhabditis
                  elegans]
Seq. No.
                  310951
                  uC-zmroteosintel18b09b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3242783
BLAST score
                  231
E value
                  3.0e-19
Match length
                  133
% identity
NCBI Description
                  (AF055354) respiratory burst oxidase protein B [Arabidopsis
                  thaliana]
Seq. No.
                  310952
Seq. ID
                  uC-zmroteosintel18d01b1
Method
                  BLASTN
NCBI GI
                  g2345153
BLAST score
                  101
E value
                  8.0e-50
Match length
                  173
% identity
                  90
NCBI Description Zea mays ribsomal protein S4 (rps4) mRNA, complete cds
Seq. No.
                  310953
Seq. ID
                  uC-zmroteosintel18d08b1
Method
                  BLASTX
NCBI GI
                  g168489
BLAST score
                  197
E value
                  2.0e-26
Match length
                  75
% identity
                  95
```

44328

(M16901) glutathione S-transferase I [Zea mays]

(M16902) glutathione S-transferase I [Zea mays] >qi 168491

>gi 225458 prf 1303351A transferase, glutathione S [Zea



```
310954
Seq. No.
Seq. ID
                  uC-zmroteosintel18e10b1
Method
                  BLASTX
NCBI GI
                   q2911073
BLAST score
                   356
                   4.0e-40
E value
Match length
                  168
% identity
                   56
                  (AL021960) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  310955
Seq. ID
                  uC-zmroteosintel18g07b1
Method
                  BLASTX
NCBI GI
                  g1421730
BLAST score
                   345
E value
                  2.0e-32
Match length
                  141
                  57
% identity
NCBI Description (U43082) RF2 [Zea mays]
Seq. No.
                  310956
Seq. ID
                  uC-zmroteosintel18g08b1
Method
                  BLASTX
NCBI GI
                  g2293566
BLAST score
                  592
E value
                  2.0e-61
Match length
                  121
% identity
                  96
NCBI Description (AF012896) ADP-ribosylation factor 1 [Oryza sativa]
Seq. No.
                  310957
                  uC-zmroteosintel18h01b1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1421730
BLAST score
                  428
                  4.0e-44
E value
Match length
                  133
% identity
                  72
NCBI Description
                  (U43082) RF2 [Zea mays]
Seq. No.
                  310958
Seq. ID
                  uC-zmroteosintel18h02b1
Method
                  BLASTX
NCBI GI
                  g1421730
BLAST score
                  270
E value
                  7.0e-24
Match length
                  108
% identity
                  54
NCBI Description (U43082) RF2 [Zea mays]
Seq. No.
                  310959
Seq. ID
                  uC-zmroteosintel18h11b1
Method
                  BLASTX
```

NCBI GI g3928543
BLAST score 183
E value 2.0e-20
Match length 119

```
% identity
                  (AB016819) UDP-glucose glucosyltransferase [Arabidopsis
NCBI Description
                  thalianal
                  310960
Seq. No.
Seq. ID
                  uC-zmroteosintell9a04b1
```

Method BLASTX NCBI GI g1619836 BLAST score 306 E value 4.0e-28 Match length 90 % identity 69

NCBI Description (U67921) REP [Bacillus thuringiensis israelensis]

Seq. No. 310961 Seq. ID

uC-zmroteosintel19a10b1

Method BLASTX NCBI GI g4416302 BLAST score 459 E value 6.0e-46 Match length 97 % identity 92

NCBI Description (AF105716) copia-type pol polyprotein [Zea mays]

310962 Seq. No.

Seq. ID uC-zmroteosinte119b07b1

Method BLASTX g913228 NCBI GI BLAST score 270 E value 8.0e-24 Match length 112 53 % identity

NCBI Description transcription factor X1DP-2 [Xenopus laevis, embryos,

Peptide, 376 aa]

Seq. No. 310963

Seq. ID uC-zmroteosinte119b09b1

Method BLASTN NCBI GI q1616660 BLAST score 47 1.0e-17 E value Match length 59 97 % identity

Zea mays adenylosuccinate synthetase mRNA, complete cds NCBI Description

>gi 1601661 gb I21307 I21307 Sequence 3 from patent US 5519125 >gi_3011201_gb_175060_175060 Sequence 3 from patent

Seq. No. 310964

Seq. ID uC-zmroteosinte119c06b2

Method BLASTX NCBI GI g1899025 BLAST score 378 E value 2.0e-36 Match length 150 % identity 53

NCBI Description (U28215) hexokinase 2 [Arabidopsis thaliana] >gi_3687232





(AC005169) hexokinase [Arabidopsis thaliana]

```
Seq. No.
                  310965
Seq. ID
                  uC-zmroteosintel19c10b1
Method
                  BLASTN
NCBI GI
                  g2944039
BLAST score
                  48
E value
                  7.0e-18
                                                                          7
Match length
                  72
                  94
% identity
NCBI Description Zea mays indeterminate spikelet 1 (ids1) mRNA, complete cds
                  310966
Seq. No.
Seq. ID
                  uC-zmroteosinte119d04b1
                  BLASTX
Method
NCBI GI
                  g1616661
BLAST score
                  260
E value
                  1.0e-22
Match length
                  53
                  94
% identity
                  (U49388) adenylosuccinate synthetase [Zea mays]
NCBI Description
                  310967
Seq. No.
Seq. ID
                  uC-zmroteosinte119d06b1
Method
                  BLASTX
NCBI GI
                  g1350986
BLAST score
                  234
E value
                  6.0e-20
Match length
                  84
% identity
                  62
NCBI Description
                  40S RIBOSOMAL PROTEIN S3A (CYC07 PROTEIN)
                  >gi_483431_dbj_BAA05059_ (D26060) cyc07 [Oryza sativa]
Seq. No.
                  310968
Seq. ID
                  uC-zmroteosinte119e09b2
Method
                  BLASTX
NCBI GI
                  g549638
BLAST score
                  149
E value
                  2.0e-09
Match length
                  136
% identity
                  32
                  HYPOTHETICAL 39.6 KD PROTEIN IN MTD1-NUP133 INTERGENIC
NCBI Description
                  REGION >gi_539279_pir__S38159 hypothetical protein YKR081c
                  - yeast (Saccharomyces cerevisiae) >gi_415901_emb_CAA81632_
                  (Z27116) ORF YKR401 [Saccharomyces cerevisiae]
                  >gi_486561_emb_CAA82160_ (Z28306) ORF YKR081c
                  [Saccharomyces cerevisiae]
Seq. No.
                  310969
Seq. ID
                  uC-zmroteosintel19f02b2
Method
                  BLASTX
NCBI GI
                  g3378652
BLAST score
                  255
E value
                  7.0e-22
Match length
                  63
% identity
```

44331

NCBI Description (AJ005039) CaM-1 [Nicotiana plumbaginifolia]





```
>gi_3378654_emb_CAA06307_ (AJ005040) CaM-2 [Nicotiana
plumbaginifolia]
```

310970 Seq. No. uC-zmroteosintel19f04b1 Seq. ID Method BLASTN NCBI GI g829147 46 BLAST score 6.0e-17 E value 90 Match length % identity 88

NCBI Description Z.mays gene for cyclophilin

Seq. No. 310971 Seq. ID

uC-zmroteosintel19f05b1

Method BLASTX NCBI GI g4566505 BLAST score 211 E value 8.0e-18 Match length 57 % identity 72

NCBI Description (AF102868) beta-D-glucan exohydrolase isoenzyme ExoI

[Hordeum vulgare]

Seq. No. 310972

Seq. ID uC-zmroteosintel19f09b1

Method BLASTN g2668737 NCBI GI BLAST score 64 8.0e-28 E value Match length 92 92 % identity

NCBI Description Zea mays translation initiation factor 5A (TIF5A) mRNA,

complete cds

Seq. No. 310973

Seq. ID uC-zmroteosintel19f11b1

Method BLASTX NCBI GI q1351014 BLAST score 212 E value 4.0e-17 Match length 52 % identity 83

NCBI Description 40S RIBOSOMAL PROTEIN S8 >gi 968902 dbj BAA07207 (D38010)

ribosomal protein S8 [Oryza sativa]

Seq. No. 310974

Seq. ID uC-zmroteosintel19q06b2

Method BLASTX NCBI GI q120669 BLAST score 158 2.0e-15 E value Match length 71 70 % identity

GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC NCBI Description

>gi_66014_pir__DEJMG glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora

>gi_19566_emb_CAA42905_ (X60347) glyceraldehyde
3-phosphate dehydrogenase [Magnolia liliiflora]

Seq. No. 310975

Seq. ID uC-zmroteosinte120a10b2

Method BLASTX
NCBI GI g4416302
BLAST score 342
E value 4.0e-42
Match length 125
% identity 76

NCBI Description (AF105716) copia-type pol polyprotein [Zea mays]

Seq. No. 310976

Seq. ID uC-zmroteosinte120d08b1

Method BLASTX
NCBI GI g629844
BLAST score 172
E value 1.0e-19
Match length 104
% identity 60

NCBI Description heat shock protein hsp70-5 - maize (fragment)

>gi 498775 emb CAA55184 (X78415) heat shock protein 70 kDa

[Zea mays]

Seq. No. 310977

Seq. ID uC-zmroteosinte120h06b2

Method BLASTX
NCBI GI g4262167
BLAST score 192
E value 4.0e-18
Match length 152
% identity 41

NCBI Description (AC005275) putative LRR receptor-linked protein kinase

[Arabidopsis thaliana]

Seq. No. 310978

Seq. ID uer700576742.h1

Method BLASTX
NCBI GI g3776557
BLAST score 220
E value 3.0e-18
Match length 79
% identity 52

NCBI Description (AC005388) Contains similarity to gi 2924495 hypothetical

protein Rv1920 from Mycobacterium tuberculosis genome

gb AL022020. [Arabidopsis thaliana]

Seq. No. 310979

Seq. ID uer700576770.h1

Method BLASTN
NCBI GI g22378
BLAST score 54
E value 1.0e-21
Match length 97
% identity 50

NCBI Description Z.mays gene for nucleic acid binding protein

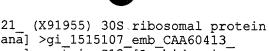
```
310980
Seq. No.
Seq. ID
                   uer700576772.h1
                   BLASTN
Method
NCBI GI
                   g4514725
BLAST score
                   36
E value
                   6.0e-11
Match length
                   68
% identity
                   88
NCBI Description
                  Oryza brachyantha ObENOD40 gene, complete cds
                   310981
Seq. No.
Seq. ID
                   uer700576834.h1
Method
                   BLASTX
NCBI GI
                   g1653702
BLAST score
                   182
E value
                   8.0e-14
Match length
                   84
% identity
                   45
NCBI Description
                   (D90915) dihydrolipoamide acetyltransferase component (E2)
                   of pyruvate dehydrogenase complex [Synechocystis sp.]
Seq. No.
                   310982
Seq. ID
                   uer700576960.h1
Method
                  BLASTX
NCBI GI
                   g729479
BLAST score
                   182
E value
                   2.0e-20
Match length
                   74
% identity
                  73
NCBI Description
                  FERREDOXIN--NADP REDUCTASE PRECURSOR (FNR) >gi 551131
                   (U14956) ferredoxin NADP+ reductase precursor [Vicia faba]
Seq. No.
                   310983
Seq. ID
                  uer700577025.h1
Method
                  BLASTX
NCBI GI
                   q1857256
BLAST score
                   242
E value
                   9.0e-21
Match length
                  85
% identity
                  54
NCBI Description
                  (U75360) MURAZC [Zea mays]
Seq. No.
                  310984
                  uer700577063.h1
                  BLASTX
                  g1173194
                  147
                  7.0e-10
```

Seq. ID Method NCBI GI BLAST score E value Match length 32

% identity 81

30S RIBOSOMAL PROTEIN S13, CHLOROPLAST PRECURSOR (CS13) NCBI Description >gi 2119093 pir__S59594 ribosomal protein S13 precursor, chloroplast - Arabidopsis thaliana >gi_16767_emb_CAA79013 (Z17611) chloroplast 30S ribosomal protein ST3 [Arabidopsis thaliana] >gi_662869_emb_CAA88028_ (Z47986) chloroplast

ribosomal protein S13 [Arabidopsis thaliana]



>gi_1107483_emb_CAA63021_ (X91955) 30S ribosomal protein
S13 [Arabidopsis thaliana] >gi_1515107_emb_CAA60413_ (X86734) plastid ribosomal protein S13 [Arabidopsis] thalianal

Seq. No. 310985

Seq. ID uer700577080.h1

Method BLASTX NCBI GI g3702327 BLAST score 176 E value 3.0e-13 Match length 49 % identity

NCBI Description (AC005397) unknown protein [Arabidopsis thaliana]

Seq. No. 310986

Seq. ID uer700577102.h1

Method BLASTX NCBI GI q421929 BLAST score 153 E value 1.0e-10 Match length 57 % identity 10

NCBI Description ubiquitin - tomato >gi 312160 emb CAA51679 (X73156)

ubiquitin [Lycopersicon esculentum]

Seq. No. 310987

Seq. ID uer700577125.h1

Method BLASTX NCBI GI q4033421 BLAST score 140 E value 3.0e-15 Match length 64 % identity 56

NCBI Description SOLUBLE INORGANIC PYROPHOSPHATASE (PYROPHOSPHATE

PHOSPHO-HYDROLASE) (PPASE) >gi_2570501 (AF022733) inorganic

pyrophosphatase [Oryza sativa]

Seq. No. 310988

Seq. ID uer700577141.h1

Method BLASTX NCBI GI g2911072 BLAST score 287 E value 4.0e-26 Match length 72 % identity 69

(AL021960) putative protein [Arabidopsis thaliana] NCBI Description

Seq. No.

310989

Seq. ID uer700577253.h1

Method BLASTX NCBI GI q3928891 BLAST score 191 E value 8.0e-15 Match length 90 % identity 46

NCBI Description (AF093617) chlorophyll a/b binding protein [Acetabularia

NCBI GI



acetabulum]

```
Seq. No.
                   310990
Seq. ID
                   uer700577269.h1
Method
                   BLASTX
NCBI GI
                   g4263509
BLAST score
                   181
E value
                   1.0e-13
Match length
                   42
% identity
                   81
NCBI Description (AC004044) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   310991
Seq. ID
                   uer700577328.h1
Method
                   BLASTX
NCBI GI
                   g3941480
BLAST score
                   395
E value
                   9.0e-39
Match length
                   79
% identity
                   85
                  (AF062894) putative transcription factor [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   310992
Seq. ID
                   uer700577338.h1
Method
                   BLASTX
NCBI GI
                   q1651771
BLAST score
                   192
                   2.0e-16
E value
Match length
                   86
% identity
                   46
NCBI Description
                  (D90900) glycogen operon protein GlgX [Synechocystis sp.]
Seq. No.
                   310993
Seq. ID
                   uer700577367.h1
Method
                   BLASTX
NCBI GI
                   q4490325
BLAST score
                   243
E value
                   6.0e-21
Match length
                   66
% identity
                   68
                  (AL035656) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   310994
Seq. ID
                   uer700577465.hl
Method
                  BLASTN
NCBI GI
                   g1688044
BLAST score
                   56
E value
                   7.0e-23
Match length
                   56
% identity
                  100
NCBI Description Corn mRNA for cysteine proteinase, clone CCP2, complete cds
Seq. No.
                  310995
Seq. ID
                  uer700577467.h1
Method
                  BLASTX
```

g2654210

```
BLAST score
E value
                   5.0e-23
Match length
                   72
% identity
                   79
NCBI Description
                   (AF035457) heat shock 70 protein [Spinacia oleracea]
Seq. No.
                   310996
Seq. ID
                   uer700577575.hl
Method
                   BLASTX
NCBI GI
                   q2864618
BLAST score
                   144
E value
                   2.0e-09
Match length
                   62
% identity
                   47
NCBI Description
                   (AL021811) putative protein [Arabidopsis thaliana]
Seq. No.
                   310997
Seq. ID
                   uer700577630.h1
Method
                   BLASTX
NCBI GI
                   q4538959
BLAST score
                   249
E value
                   1.0e-21
Match length
                   58
% identity
                   83
NCBI Description
                   (AL049488) putative protein [Arabidopsis thaliana]
Seq. No.
                   310998
Seq. ID
                   uer700577755.h1
Method
                   BLASTX
                   g3763933
NCBI GI
BLAST score
                   304
E value
                   4.0e-28
Match length
                   86
% identity
                   84
NCBI Description
                   (AC004450) unknown protein [Arabidopsis thaliana]
Seq. No.
                   310999
Seq. ID
                   uer700577780.h1
Method
                   BLASTX
NCBI GI
                   q4468986
BLAST score
                   261
E value
                   5.0e-23
Match length
                   88
% identity
                   55
NCBI Description
                  (AL035605) putative protein [Arabidopsis thaliana]
Seq. No.
                   311000
Seq. ID
                   uer700577788.h1
Method
                   BLASTX
NCBI GI
                   g3980412
BLAST score
                   232
E value
                   1.0e-19
Match length
                   67
% identity
                   63
```

No. 311001

NCBI Description

Seq. No.

(AC004561) pumilio-like protein [Arabidopsis thaliana]



```
uer700577801.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2827992
BLAST score
                  149
                  7.0e-10
E value
Match length
                  28
% identity
                  82
                  (AF034743) UDP-glucuronosyltransferase [Pisum sativum]
NCBI Description
Seq. No.
                  311002
Seq. ID
                  uer700577804.h1
Method
                  BLASTN
NCBI GI
                  g1935910
BLAST score
                  37
                  2.0e-11
E value
Match length
                  81
                  86
% identity
NCBI Description
                 Zea mays lethal leaf-spot 1 (lls1) gene, partial cds
                  311003
Seq. No.
                  uer700577894.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4006860
BLAST score
                  317
E value
                  2.0e-34
Match length
                  89
% identity
                  82
NCBI Description
                  (Z99707) thiol-disulfide interchange like protein
                  [Arabidopsis thaliana]
Seq. No.
                  311004
                  uer700577948.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q113220
BLAST score
                  250
E value
                  1.0e-21
Match length
                  49
% identity
                  92
NCBI Description ACTIN 1 >gi_71640_pir_ ATZM1 actin - maize
Seq. No.
                  311005
Seq. ID
                  uer700578028.h1
Method
                  BLASTX
NCBI GI
                  q120670
BLAST score
                  191
E value
                  5.0e-15
Match length
                  39
% identity
                  100
NCBI Description
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
                  >gi_100879_pir__S06879 glyceraldehyde-3-phosphate
                  dehydrogenase (EC 1.2.1.12) C - maize
                  >gi_295853_emb_CAA33620_ (X15596) GAPDH [Zea mays]
```

Seq. No. 311006

Seq. ID uer700578043.h1

Method BLASTX NCBI GI g2129655

BLAST score

197

```
BLAST score
                  6.0e-10
E value
Match length
                  46
% identity
                  63
NCBI Description
                  OBP32pep protein - Arabidopsis thaliana (fragment)
                  >gi_1022799 (U37698) OBP32pep [Arabidopsis thaliana]
Seq. No.
                  311007
Seq. ID
                  uer700578206.h1
Method
                  BLASTX
NCBI GI
                  g2181190
BLAST score
                  258
E value
                  1.0e-22
Match length
                  78
                  65
% identity
NCBI Description
                  (Y12531) serine/threonine kinase [Brassica oleracea]
Seq. No.
                  311008
Seq. ID
                  uer700578331.h1
Method
                  BLASTX
NCBI GI
                  q112994
BLAST score
                  306
E value
                  2.0e-28
Match length
                  64
% identity
                  95
NCBI Description
                  GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN
                  >gi_82685_pir__S04536 embryonic abundant protein,
                  glycine-rich - maize >gi 22313 emb CAA31077 (X12564)
                  ABA-inducible gene protein [Zea mays]
                  >gi 226091 prf 1410284A abscisic acid inducible gene [Zea
                  mays]
Seq. No.
                  311009
Seq. ID
                  uer700578514.h1
Method
                  BLASTX
NCBI GI
                  q4589660
BLAST score
                  166
E value
                  4.0e-12
Match length
                  56
% identity
                  59
                 (AB023225) KIAA1008 protein [Homo sapiens]
NCBI Description
Seq. No.
                  311010
Seq. ID
                  uer700578546.hl
Method
                  BLASTX
NCBI GI
                  g1917019
BLAST score
                  196
                  1.0e-15
E value
Match length
                  45
% identity
                  82
NCBI Description (U92045) ribosomal protein S6 RPS6-1 [Zea mays]
                  311011
Seq. No.
Seq. ID
                  uer700578595.h1
                  BLASTX
Method
NCBI GI
                  g2960364
```



```
E value
                   1.0e-15
Match length
                   63
% identity
                   63
NCBI Description
                   (AJ224986) cinnamoyl CoA reductase [Populus balsamifera
                   subsp. trichocarpa]
Seq. No.
                   311012
Seq. ID
                   uer700578627.hl
Method
                   BLASTX
NCBI GI
                   q3255941
BLAST score
                   195
E value
                   3.0e-15
Match length
                   57
% identity
                   68
NCBI Description
                   (AJ007332) PP1A protein [Catharanthus roseus]
Seq. No.
                   311013
Seq. ID
                   uer700578643.h1
Method
                   BLASTN
NCBI GI
                   q643596
BLAST score
                   186
E value
                   1.0e-100
Match length
                   251
% identity
                   97
NCBI Description Corn mRNA for cysteine proteinase, clone CCP, complete cds
Seq. No.
                   311014
Seq. ID
                   uer700578694.h1
Method
                   BLASTX
NCBI GI
                   q3522943
BLAST score
                   199
E value
                   4.0e-26
Match length
                   87
% identity
                   42
NCBI Description
                   (AC004411) putative p-glycoprotein [Arabidopsis thaliana]
Seq. No.
                   311015
Seq. ID
                   uer700578788.h1
Method
                   BLASTX
NCBI GI
                   g4006854
BLAST score
                   195
E value
                   3.0e-15
Match length
                   93
% identity
                   51
NCBI Description
                  (Z99707) putative protein [Arabidopsis thaliana]
Seq. No.
                   311016
Seq. ID
                   uer700578908.h1
Method
                  BLASTN
NCBI GI
                   q168619
```

NCBI GI g168619
BLAST score 98
E value 3.0e-48
Match length 114
% identity 96

NCBI Description Maize superoxide dismutase-2 (Sod-2) mRNA, complete cds. >gi_168621_gb_M15175_MZESOD2A Maize superoxide dismutase 2

(SOD2) mRNA, complete cds

```
Seq. No.
                   311017
Seq. ID
                   uer700578917.hl
Method
                   BLASTN
NCBI GI
                   q4336605
BLAST score
                   102
E value
                   8.0e-51
Match length
                   102
% identity
                   100
                   Zea mays sigma factor (sig1) mRNA, nuclear gene encoding
NCBI Description
                   chloroplast protein, complete cds
Seq. No.
                   311018
Seq. ID
                   uer700578922.h1
Method
                   BLASTX
NCBI GI
                   q2668744
BLAST score
                   384
E value
                   2.0e-37
Match length
                   73
% identity
                   95
NCBI Description
                   (AF034946) ubiquitin conjugating enzyme [Zea mays]
Seq. No.
                   311019
Seq. ID
                   uer700578946.h1
Method
                   BLASTX
NCBI GI
                   q4574137
BLAST score
                   140
E value
                   4.0e-09
Match length
                   31
% identity
                   87
NCBI Description
                  (AF073696) cysteine synthase [Oryza sativa]
Seq. No.
                   311020
Seq. ID
                   uer700578955.h1
Method
                   BLASTX
NCBI GI
                   q2244807
BLAST score
                   175
E value
                   3.0e-13
Match length
                   72
% identity
                   42
NCBI Description
                  (Z97336) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   311021
Seq. ID
                   uer700578982.h1
Method
                  BLASTX
NCBI GI
                   g3738339
BLAST score
                   282
E value
                  1.0e-25
Match length
                   74
                   72
% identity
NCBI Description
                  (AC005170) putative kinase [Arabidopsis thaliana]
Seq. No.
                   311022
Seq. ID
                  uer700579079.h1
Method
                  BLASTN
NCBI GI
                  g1276937
```

44341

r die

BLAST score



```
E value 1.0e-73
Match length 152
% identity 99
NCBI Description Zea mays USDA Ames 15820 ITS1, 5.8S ribosomal RNA, ITS2
Seq. No. 311023
Seq. ID uer700579084.h1
Method BLASTX
NCBI GI g4455294
```

NCBI GI g4455294
BLAST score 166
E value 1.0e-15
Match length 60
% identity 62

NCBI Description (AL035528) putative protein [Arabidopsis thaliana]

 Seq. No.
 311024

 Seq. ID
 uer700579095.h1

 Method
 BLASTX

 NCBI GI
 g3929647

 DLAGT
 160

NCBI GI g3929647
BLAST score 160
E value 8.0e-20
Match length 68
% identity 74

NCBI Description (AJ004881) Immutans protein [Arabidopsis thaliana]

Seq. No. 311025

Seq. ID uer700579124.h1

Method BLASTX
NCBI GI g231547
BLAST score 159
E value 4.0e-11
Match length 71
% identity 44

NCBI Description ALPHA-AMYLASE PRECURSOR (1,4-ALPHA-D-GLUCAN

GLUCANOHYDROLASE) >gi_98954_pir__S14063 alpha-amylase (EC 3.2.1.1) - Streptomyces griseus >gi_3805971_emb_CAA40798_

(X57568) alpha-amylase [Streptomyces griseus]

Seq. No.

Seq. ID uer700579166.h1

Method BLASTN
NCBI GI g168527
BLAST score 99
E value 5.0e-49
Match length 103
% identity 99

NCBI Description Maize NADP-dependent malic enzyme (Me1) mRNA, complete cds

Seq. No.

311027

311026

Seq. ID uer700579322.h1

Method BLASTN
NCBI GI 9474405
BLAST score 34
E value 1.0e-09
Match length 34
% identity 100

NCBI Description Z.mays mRNA for gamma-tubulin

Seq. No.

Seq. ID

311033

uer700579633.h1



```
Seq. No.
                  311028
Seq. ID
                  uer700579391.hl
Method
                  BLASTN
NCBI GI
                  q4351
BLAST score
                  71
E value
                  4.0e-32
Match length
                  75
% identity
                  99
NCBI Description Yeast cytosol gene for 5S ribosomal RNA
Seq. No.
                  311029
Seq. ID
                  uer700579536.h1
Method
                  BLASTX
NCBI GI
                  q584825
BLAST score
                  178
E value
                  3.0e-13
Match length
                  47
                  74
% identity
NCBI Description
                  B2 PROTEIN >gi_322726 pir S32124 B2 protein - carrot
                  >gi_297889_emb_CAA51078_ (X72385) B2 protein [Daucus
                  carota]
Seq. No.
                  311030
Seq. ID
                  uer700579544.h1
Method
                  BLASTX
NCBI GI
                  q1223579
BLAST score
                  152
E value
                  3.0e-10
Match length
                  89
% identity
                  40
NCBI Description (X96481) cDNA101 [Arabidopsis thaliana]
Seq. No.
                  311031
Seq. ID
                  uer700579576.h1
Method
                  BLASTX
NCBI GI
                  g1170242
BLAST score
                  332
E value
                  2.0e-31
Match length
                  86
% identity
                  79
NCBI Description
                  FERROCHELATASE PRECURSOR (PROTOHEME FERRO-LYASE) (HEME
                  SYNTHETASE) >gi_474966_dbj_BAA05101 (D26105)
                  ferrochelatase [Hordeum vulgare]
Seq. No.
                  311032
Seq. ID
                  uer700579601.h1
Method
                  BLASTX
NCBI GI
                  g4099833
BLAST score
                  263
E value
                  4.0e-23
Match length
                  66
% identity
NCBI Description (U90265) bifunctional nuclease [Zinnia elegans]
```



```
Method
NCBI GI
                   q22330
BLAST score
                   46
E value
                   7.0e-17
Match length
                   54
                   96
% identity
NCBI Description Z.mays Zmhoxla mRNA for homeobox protein
Seq. No.
                   311034
Seq. ID
                   uer700579679.h1
Method
                   BLASTX
NCBI GI
                   g3776557
BLAST score
                   147
                   1.0e-09
E value
Match length
                   49
% identity
                   57
NCBI Description
                   (AC005388) Contains similarity to gi 2924495 hypothetical
                   protein Rv1920 from Mycobacterium tuberculosis genome
                   gb AL022020. [Arabidopsis thaliana]
Seq. No.
                   311035
Seq. ID
                   uer700579738.h1
Method
                   BLASTX
NCBI GI
                   g3980413
BLAST score
                   174
                                          ر
س عار
                   4.0e-13
E value
Match length
                   50
% identity
                   64
NCBI Description
                  (AC004561) pumilio-like protein [Arabidopsis thaliana]
Seq. No.
                   311036
Seq. ID
                   uer700579767.h1
Method
                   BLASTX
NCBI GI
                   q3659909
BLAST score
                   298
E value
                   2.0e-27
Match length
                   86
% identity
                   66
NCBI Description
                  (AF020715) histidyl-tRNA synthetase [Arabidopsis thaliana]
Seq. No.
                   311037
Seq. ID
                   uer700579794.h1
Method
                   BLASTX
NCBI GI
                   g4467134
BLAST score
                   292
E value
                   9.0e-27
Match length
                   82
% identity
                   63
NCBI Description
                   (AL035540) protein kinase like protein [Arabidopsis
                   thaliana]
```

Seq. No. 311038

Seq. ID uer700579847.h1

Method BLASTX NCBI GI g2984709 BLAST score 192 E value 3.0e-15

```
Match length
% identity
                  80
NCBI Description
                  (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]
Seq. No.
                  311039
                  uer700580087.h1
Seq. ID
Method
                  BLASTX
                  g1001135
NCBI GI
BLAST score
                  230
                  2.0e-19
E value
Match length
                  78
% identity
                  59
NCBI Description
                  (D64001) acetolactate synthase [Synechocystis sp.]
Seq. No.
                  311040
Seq. ID
                  uer700580129.h1
Method
                  BLASTX
NCBI GI
                  g3549626
BLAST score
                  236
E value
                  5.0e-26
Match length
                  90
% identity
                  66
NCBI Description
                  (AJ009696) wall-associated kinase 1 [Arabidopsis thaliana]
Seq. No.
                  311041
Seq. ID
                  uer700580137.h1
Method
                  BLASTX
                  g4006872
NCBI GI
BLAST score
                  271
E value
                  4.0e-24
Match length
                  93
% identity
                  54
NCBI Description
                  (Z99707) methionyl aminopeptidase-like protein [Arabidopsis
                  thaliana]
Seq. No.
                  311042
Seq. ID
                  uer700580164.h1
Method
                  BLASTX
```

Method BLASTX
NCBI GI g3242403
BLAST score 283
E value 1.0e-25
Match length 55
% identity 89

NCBI Description (D83178) endonuclease [Hordeum vulgare]

Seq. No. 311043

Seq. ID uer700580187.h1

Method BLASTN
NCBI GI g22204
BLAST score 84
E value 1.0e-39
Match length 128
% identity 91

NCBI Description Maize Bz-McC gene for UDPqlucose flavonoid

glycosyl-transferase

Seq. No. 311044



```
Seq. ID
                  uer700580246.h1
Method
                  BLASTN
NCBI GI
                  q3819189
BLAST score
                  50
E value
                  1.0e-19
Match length
                  129
% identity
                  85
NCBI Description Hordeum vulgare partial mRNA; clone cMWG0654
Seq. No.
                  311045
Seq. ID
                  uer700580279.h1
Method
                  BLASTN
NCBI GI
                  q442525
BLAST score
                  199
                  1.0e-108
E value
Match length
                  235
% identity
                  96
NCBI Description ZmERabp4=auxin-binding protein [Zea mays=corn, seedling,
                  mRNA, 917 nt]
Seq. No.
                  311046
Seq. ID
                  uer700580350.h1
Method
                  BLASTX
                  g2499987
NCBI GI
BLAST score
                  156
                5.0e-11
E value
Match length
                  54
% identity
                  59
NCBI Description PEPTIDYL-TRNA HYDROLASE (PTH) >gi 1870014 emb CAB06865
                  (Z92539) pth [Mycobacterium tuberculosis]
Seq. No.
                  311047
                  uer700580525.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4154281
BLAST score
                  290
                  1.0e-27
E value
Match length
                  80
                  79
% identity
NCBI Description (AF082347) C13 endopeptidase NP1 precursor [Zea mays]
Seq. No.
                  311048
Seq. ID
                  uer700580570.h1
Method
                  BLASTX
NCBI GI
                  g3107905
BLAST score
                  160
E value
                  2.0e-11
Match length
                  51
% identity
NCBI Description (D85101) leaf protein [Ipomoea nil]
Seq. No.
                  311049
Seq. ID
                  uer700580617.h1
Method
                  BLASTX
```

Method BLASTX
NCBI GI g1079321
BLAST score 263
E value 3.0e-23



Match length 88 % identity 56

NCBI Description XPMC2 protein - African clawed frog >gi 595380 (U10185)

XPMC2 protein [Xenopus laevis]

Seq. No. 311050

Seq. ID uer700580634.h1

Method BLASTX
NCBI GI g3913633
BLAST score 198
E value 1.0e-15
Match length 51
% identity 76

NCBI Description HYPOTHETICAL PROTEIN F8A5.25 >gi 2462742 (AC002292) Unknown

protein [Arabidopsis thaliana]

Seq. No. 311051

Seq. ID uer700580652.h1

Method BLASTX
NCBI GI g4432864
BLAST score 400
E value 3.0e-39
Match length 90
% identity 78

NCBI Description (AC006300) hypothetical protein [Arabidopsis thaliana]

Seq. No. 311052

Seq. ID uer700580661.h1

Method BLASTX
NCBI GI g2262172
BLAST score 250
E value 9.0e-22
Match length 82
% identity 61

NCBI Description (AC002329) predicted protein of unknown function

[Arabidopsis thaliana]

Seq. No. 311053

Seq. ID uer700580760.h1

Method BLASTX
NCBI GI g3242702
BLAST score 249
E value 8.0e-22
Match length 77
% identity 58

NCBI Description (AC003040) hypothetical protein [Arabidopsis thaliana]

Seq. No. 311054

Seq. ID uer700580842.h1

Method BLASTN
NCBI GI g2114206
BLAST score 33
E value 4.0e-09

Match length 37 % identity 97

NCBI Description Oryza sativa DNA for glutaredoxin, complete cds



```
Seq. No.
Seq. ID
                   uer700580934.h1
Method
                   BLASTX
NCBI GI
                   q133830
BLAST score
                   147
                   7.0e-10
E value
Match length
                   30
% identity
                   93
                   40S RIBOSOMAL PROTEIN S17 >gi_71200_pir__R4RT17 ribosomal
NCBI Description
                   protein S17 - rat >gi 206745 (K02933) ribosomal protein S17
                   [Rattus norvegicus]
Seq. No.
                   311056
Seq. ID
                   uer700580946.h1
Method
                   BLASTX
                   g140739
NCBI GI
BLAST score
                   148
E value
                   1.0e-09
Match length
                   98
                   34
% identity
NCBI Description
                   HYPOTHETICAL 31.0 KD PROTEIN IN RNPB-SOHA INTERGENIC REGION
                   (ORF 2) >gi 78519 pir JQ0613 3-hydroxyisobutyrate
                   dehydrogenase (EC 1.1.1.31) homolog - Escherichia coli
                   >gi_216632_dbj_BAA14238_ (D90212) ORF2 [Escherichia coli]
>gi_606065 (U18997) ORF_f299 [Escherichia coli] >gi_1789513
                    (AE000394) putative dehydrogenase [Escherichia coli]
Seq. No.
                   311057
Seq. ID
                   uer700581111.h1
Method
                   BLASTX
NCBI GI
                   g4467135
BLAST score
                   251
E value
                   8.0e-22
Match length
                   63
% identity
                   67
NCBI Description
                   (AL035540) putative protein [Arabidopsis thaliana]
Seq. No.
                   311058
Seq. ID
                   uer700581127.h1
Method
                   BLASTN
NCBI GI
                   q3695004
                   133
BLAST score
E value
                   4.0e-09
Match length
                   33
% identity
                   100
NCBI Description
                   Zea mays pyruvate dehydrogenase kinase isoform 2 mRNA,
                   nuclear gene encoding mitochondrial protein, complete cds
```

Seq. No. 311059

Seq. ID uer700581214.h1

Method BLASTX NCBI GI g401237 BLAST score 283 E value 1.0e-25 Match length 90 76 % identity

NCBI Description UBIQUITIN-ACTIVATING ENZYME E1 2 >gi 170684 (M90663)

Method

NCBI GI

BLASTX

g35782





ubiquitin activating enyme [Triticum aestivum]

```
Seq. No.
                   311060
Seq. ID
                   uer700581365.h1
Method
                   BLASTX
                   g3132472
NCBI GI
BLAST score
                   163
E value
                   1.0e-11
Match length
                   38
                   79
% identity
NCBI Description
                  (AC003096) unknown protein [Arabidopsis thaliana]
Seq. No.
                   311061
Seq. ID
                   uer700581439.h1
Method
                   BLASTX
NCBI GI
                   g4538965
BLAST score
                   147
E value
                   8.0e-10
Match length
                   54
% identity
                   46
NCBI Description
                  (AL049488) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   311062
Seq. ID
                   uer700581471.h1
Method
                   BLASTX
                   g2129880
NCBI GI
BLAST score
                   208
E value
                   5.0e-24
Match length
                   85
% identity
                   68
                  cytochrome P450 - garden pea >gi_1360118_emb_CAA89260_
NCBI Description
                   (Z49263) cytochrome P450 [Pisum sativum]
Seq. No.
                   311063
Seq. ID
                   uer700581512.h1
Method
                   BLASTX
                   g3451067
NCBI GI
BLAST score
                   154
E value
                   2.0e-10
Match length
                   47
% identity
                   64
NCBI Description
                  (AL031326) putative protein [Arabidopsis thaliana]
Seq. No.
                   311064
Seq. ID
                  uer700581525.h1
Method
                  BLASTX
NCBI GI
                  g2832697
BLAST score
                  142
E value
                  7.0e-15
Match length
                   68
% identity
NCBI Description
                  (AL021713) putative protein [Arabidopsis thaliana]
Seq. No.
                  311065
Seq. ID
                  uer700581565.h1
```

```
BLAST score
                   185
E value
                   2.0e-14
Match length
                   39
% identity
                   95
NCBI Description
                   (X62055) protein-tyrosine phosphatase 1C [Homo sapiens]
                   >gi 228043 prf 1715334A protein Tyr phosphatase [Homo
                   sapiens]
Seq. No.
                   311066
Seq. ID
                   uer700581676.h1
Method
                   BLASTX
NCBI GI
                   q2104679
BLAST score
                   306
E value
                   2.0e-28
Match length
                   87
% identity
                   67
NCBI Description
                   (X97906) transcription factor [Vicia faba]
Seq. No.
                   311067
Seq. ID
                   uer700581732.h1
Method
                   BLASTX
NCBI GI
                   q417154
BLAST score
                   374
E value
                   3.0e-36
Match length
                   94
                   82
% identity
NCBI Description
                   HEAT SHOCK PROTEIN 82 >gi_100685_pir__S25541 heat shock
                   protein 82 - rice (strain Taichung Native One)
                   >gi_20256_emb_CAA77978_ (Z11920) heat shock protein 82
                   (HSP82) [Oryza sativa]
Seq. No.
                   311068
Seq. ID
                   uer700581778.h1
Method
                   BLASTX
NCBI GI
                   g125576
BLAST score
                   227
                   5.0e-19
E value
Match length
                   49
% identity
                   88
                   PHOSPHORIBULOKINASE PRECURSOR (PHOSPHOPENTOKINASE) (PRKASE)
NCBI Description
                   (PRK) >gi_99744_pir__S16583 phosphoribulokinase (EC 2.7.1.19) precursor - Arabidopsis thaliana
                   >gi 16441 emb CAA41155 (X58149) Ribulose-5-phosphate
                   kinase [Arabidopsis thaliana]
Seq. No.
                   311069
Seq. ID
                   uer700581804.h1
Method
                   BLASTN
NCBI GI
                   q507844
BLAST score
                   46
                   4.0e-17
E value
Match length
                   62
% identity
                   94
```

Seq. No. 311070

NCBI Description

Seq. ID uer700581892.h1

Zea mays A188 retrotransposon gag gene, complete cds



```
Method
                   BLASTX
NCBI GI
                   g1657619
BLAST score
                   278
E value
                   5.0e-25
Match length
                   91
% identity
                   58
NCBI Description
                  (U72504) G5p [Arabidopsis thaliana] >gi 3068710 (AF049236)
                   putative transmembrane protein G5p [Arabidopsis thaliana]
Seq. No.
                   311071
Seq. ID
                   uer700582092.h1
Method
                   BLASTN
NCBI GI
                   g1419369
BLAST score
                   85
E value
                   3.0e-40
Match length
                   222
% identity
                   92
NCBI Description Z.mays ZmABP3 mRNA for actin depolymerizing factor
Seq. No.
                   311072
Seq. ID
                  uer700582095.h1
Method
                  BLASTX
NCBI GI
                  g4006877
BLAST score
                   223
E value
                   1.0e-18
Match length
                   51
% identity
                   75
NCBI Description (Z99707) RNA-binding like protein [Arabidopsis thaliana]
Seq. No.
                  311073
Seq. ID
                  uer700582118.h1
Method
                  BLASTX
NCBI GI
                  g4539459
BLAST score
                  140
E value
                  8.0e-09
Match length
                  33
                  .73
% identity
                  (AL049500) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  311074
Seq. ID
                  uer700582179.h1
Method
                  BLASTX
NCBI GI
                  g3080420
BLAST score
                  162
E value
                  2.0e-11
Match length
                  58
% identity
                  60
NCBI Description
                  (AL022604) putative sugar transporter protein [Arabidopsis
                  thaliana]
Seq. No.
                  311075
Seq. ID
                  uer700582222.h1
```

Method BLASTX

NCBI GI g3004565 BLAST score 383 E value 3.0e-37 Match length 92



% identity 76
NCBI Description (AC003673) putative protein kinase [Arabidopsis thaliana]

Seq. No. 311076

Seq. ID uer700582350.h1

Method BLASTX
NCBI GI g2864613
BLAST score 213
E value 2.0e-17
Match length 85
% identity 54

NCBI Description (AL021811) S-receptor kinase -like protein [Arabidopsis

thaliana] >gi_4049333_emb_CAA22558_ (AL034567) S-receptor

kinase-like protein [Arabidopsis thaliana]

Seq. No. 311077

Seq. ID uer700582445.h1

Method BLASTX
NCBI GI g464863
BLAST score 250
E value 1.0e-30
Match length 84
% identity 78

NCBI Description 26S PROTEASE REGULATORY SUBUNIT 8 (TAT-BINDING PROTEIN

HOMOLOG 10) >gi_422297_pir__JN0610 probable transcription factor DdTBP10 - slime mold (Dictyostelium discoideum) (fragment) >gi_290057 (L16579) HIV1 TAT-binding protein

[Dictyostelium discoideum]

Seq. No. 311078

Seq. ID uer700582482.h1

Method BLASTX
NCBI GI g4586117
BLAST score 208
E value 2.0e-23
Match length 88
% identity 61

NCBI Description (AL049638) putative protein [Arabidopsis thaliana]

Seq. No. 311079

Seq. ID uer700582674.h1

Method BLASTX
NCBI GI g2660677
BLAST score 293
E value 9.0e-27
Match length 78
% identity 64

NCBI Description (AC002342) unknown protein [Arabidopsis thaliana]

Seq. No. 311080

Seq. ID uer700582712.h1

Method BLASTX
NCBI GI g2911265
BLAST score 437
E value 1.0e-43
Match length 91
% identity 89



```
NCBI Description
                  (AC002550) Unknown gene product [Homo sapiens]
                   311081
Seq. No.
                   uer700582776.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2344887
BLAST score
                   380
                   5.0e-37
E value
Match length
                   83
% identity
                   84
                  (AC002388) unknown protein [Arabidopsis thaliana]
NCBI Description
                   311082
Seq. No.
                   uer700582805.h1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3242402
BLAST score
                   45
E value
                   3.0e-16
Match length
                   69
% identity
                   91
NCBI Description Hordeum vulgare mRNA for endonuclease, complete cds
Seq. No.
                   311083
                   uer700582866.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4519270
BLAST score
                   143
E value
                   3.0e-09
Match length
                   33
                   70
% identity
NCBI Description
                  (AB011414) Kruppel-type zinc finger protein [Homo sapiens]
Seq. No.
                   311084
                   uer700582934.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4105794
BLAST score
                   144
E value
                   1.0e-15
Match length
                   71
% identity
                   66
NCBI Description
                  (AF049928) PGP224 [Petunia x hybrida]
Seq. No.
                   311085
                   uer700583015.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4062534
BLAST score
                   188
```

E value 2.0e-14 Match length 87 % identity 46

NCBI Description (D90734) Hypothetical protein [Escherichia coli]

Seq. No.

311086

uer700583066.h1 Seq. ID

Method BLASTX NCBI GI g576773 BLAST score 312

```
3.0e-30
E value
Match length
                  82
% identity
                  20
NCBI Description
                  (U16956) polyubiquitin [Filobasidiella neoformans]
                  311087
Seq. No.
                  uer700583152.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4539660
BLAST score
                  267
                  1.0e-23
E value
Match length
                  93
% identity
                  51
NCBI Description
                  (AF061282) polyprotein [Sorghum bicolor]
                  311088
Seq. No.
Seq. ID
                  uer700583166.h1
Method
                  BLASTX
NCBI GI
                  g4416302
BLAST score
                  368
                  2.0e-35
E value
Match length
                  94
                  78
% identity
NCBI Description
                  (AF105716) copia-type pol polyprotein [Zea mays]
Seq. No.
                  311089
                  uer700583192.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2624403
BLAST score
                  480
E value
                  1.0e-48
Match length
                  94
% identity
                  98
NCBI Description
                  (Y14276) plastid RNA polymerase sigma factor [Sorghum
                  bicolor]
Seq. No.
                  311090
Seq. ID
                  uer700583215.hl
Method
                  BLASTX
NCBI GI
                  q3367522
BLAST score
                  180
                  2.0e-13
E value
Match length
                  62
% identity
                  45
NCBI Description
                  (AC004392) EST gb T04691 comes from this gene. [Arabidopsis
                  thaliana]
Seq. No.
                  311091
Seq. ID
                  uer700583337.hl
```

Method BLASTN NCBI GI g22348 BLAST score 86 E value 3.0e-41 Match length 106 % identity 96

NCBI Description Z.mays mRNA for iojap protein

```
Seq. No.
                   311092
Seq. ID
                   uer700583387.h1
Method
                   BLASTX
NCBI GI
                   q3319342
BLAST score
                   218
E value
                   6.0e-18
Match length
                   61
                   70
% identity
NCBI Description
                   (AF077407) similar to mitochondrial carrier proteins (Pfam:
                   mit_carr.hmm, score: 79.74 and 42.50) [Arabidopsis
                   thaliana]
Seq. No.
                   311093
                   uer700583428.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4115379
BLAST score
                   152
E-value
                   3.0e-10
Match length
                   41
% identity
                   68
NCBI Description
                   (AC005967) putative carbonyl reductase [Arabidopsis
                   thaliana]
Seq. No.
                   311094
Seq. ID
                   uer700583452.h1
Method
                   BLASTX
NCBI GI
                   g169363
BLAST score
                   143
E value
                   1.0e-10
Match length
                   54
                   59
% identity
NCBI Description
                   (M75856) PVPR3 [Phaseolus vulgaris]
Seq. No.
                   311095
Seq. ID
                   uer700583515.h1
Method
                   BLASTX
NCBI GI
                   q2739044
BLAST score
                   154
E value
                   2.0e-10
Match length
                   84
% identity
                   44
NCBI Description
                   (AF024651) polyphosphoinositide binding protein Sshlp
                   [Glycine max]
Seq. No.
                   311096
Seq. ID
                  uer700583614.h1
Method
                  BLASTX
```

NCBI GI g3757521 BLAST score 150 E value 6.0e-10 Match length 34 % identity 85

NCBI Description (AC005167) unknown protein [Arabidopsis thaliana]

Seq. No.

311097

Seq. ID uer700583731.h1

Method BLASTX



```
NCBI GI
                   a3461884
BLAST score
                   156
                   2.0e-18
E value
Match length
                   69
% identity
                   68
NCBI Description
                   (AB006082) phosphoribosyl-ATP pyrophosphohydrolase
                   [Arabidopsis thaliana] >gi_3461886_dbj_BAA32529_ (AB006083)
                   phosphoribosyl-ATP pyrophosphohydrolase [Arabidopsis
                   thaliana]
Seq. No.
                   311098
Seq. ID
                  uer700583911.h1
Method
                   BLASTX
NCBI GI
                   q2346966
BLAST score
                   168
E value
                   4.0e-12
Match length
                   63
% identity
                   54
                   (AB004871) CPC [Arabidopsis thaliana]
NCBI Description
                   >gi 4559383 gb AAD23043.1 AC006526 8 (AC006526) putative
                   DNA binding protein CPC [Arabidopsis thaliana]
Seq. No.
                   311099
Seq. ID
                   uer700583978.h1
Method
                   BLASTX
NCBI GI
                   q3915737
BLAST score
                   201
E value
                   5.0e-16
Match length
                   83
                   57
% identity
NCBI Description
                  IMPORTIN ALPHA SUBUNIT (KARYOPHERIN ALPHA SUBUNIT) (KAP
                  ALPHA) >gi_3228370 (AF017252) importin alpha [Lycopersicon
                   esculentum]
Seq. No.
                   311100
Seq. ID
                   uer700584138.hl
Method
                  BLASTN
NCBI GI
                   g21800
BLAST score
                   120
E value
                   5.0e-61
Match length
                  180
                   92
% identity
                  T.aestivum L mRNA for histone H2B
NCBI Description
Seq. No.
                  311101
                  uer700584260.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4008131
BLAST score
                  274
E value
                  1.0e-24
Match length
                  72
```

% identity 82

(AF107894) chaperonin 10 [Homo sapiens] NCBI Description

311102 Seq. No.

Seq. ID uer700584286.h1

BLASTX Method

NCBI GI

```
NCBI GI
                  q1854445
BLAST score
                  141
E value
                  3.0e-09
Match length
                  39
                  59
% identity
                  (D83971) CPRD14 protein [Vigna unguiculata]
NCBI Description
Seq. No.
                  311103
                  uwc700149637.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g433041
BLAST score
                  93
E value
                  6.0e-45
Match length
                  211
                  88
% identity
NCBI Description
                  Zea mays W-22 clone PREM-1B retroelement PREM-1, partial
                  sequence
Seq. No.
                  311104
Seq. ID
                  uwc700149718.h1
Method
                  BLASTX
NCBI GI
                  g3024122
BLAST score
                  158
E value
                  8.0e-21
Match length
                  74
% identity
                  76
NCBI Description
                  S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE
                  ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2) >gi 1778821
                  (U82833) S-adenosyl-L-methionine synthetase [Oryza sativa]
Seq. No.
                  311105
                  uwc700149720.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g464843
BLAST score
                  172
E value
                  9.0e-13
Match length
                  31
                  97
% identity
                  [Segment 1 of 2] TUBULIN ALPHA-4 CHAIN
NCBI Description
                  >gi_22152_emb_CAA44864_ (X63179) alpha-tubulin #4 [Zea
                  mays]
Seq. No.
                  311106
Seq. ID
                  uwc700149753.h1
Method
                  BLASTX
NCBI GI
                  q730536
BLAST score
                  182
E value
                  5.0e-14
Match length
                  36
                  94
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L23 >gi_310933 (L18915) 60S ribosomal
                  protein subunit L17 [Nicotiana tabacum]
Seq. No.
                  311107
Seq. ID
                  uwc700149756.h1
Method
                  BLASTX
```

44357

g3157927

Match length



```
BLAST score
E value
                  3.0e-15
Match length
                   48
                  73
% identity
NCBI Description
                   (AC002131) Contains similarity to GDP-dissociation
                   inhibitor gb_L07918 from Mus musculus. [Arabidopsis
                  thaliana]
Seq. No.
                  311108
Seq. ID
                  uwc700149786.h1
Method
                  BLASTX
NCBI GI
                  g1353193
BLAST score
                  181
E value
                  7.0e-14
Match length
                  52
% identity
                  65
NCBI Description
                  O-METHYLTRANSFERASE ZRP4 (OMT) >gi 542186 pir JQ2268
                  O-methyltransferase (EC 2.1.1.-) - maize >gi 404070
                   (L14063) O-methyltransferase [Zea mays]
Seq. No.
                  311109
Seq. ID
                  uwc700149818.hl
Method
                  BLASTX
NCBI GI
                  g4218535
BLAST score
                  165
E value
                  5.0e-12
Match length
                  40
                  72
% identity
NCBI Description
                  (AJ010829) GRAB1 protein [Triticum sp.]
Seq. No.
                  311110
Seq. ID
                  uwc700149822.h1
Method
                  BLASTX
NCBI GI
                  g4115377
BLAST score
                  365
E value
                  3.0e-35
Match length
                  83
% identity
                  81
NCBI Description (AC005967) unknown protein [Arabidopsis thaliana]
Seq. No.
                  311111
Seq. ID
                  uwc700149968.h1
Method
                  BLASTN
NCBI GI
                  g459267
BLAST score
                  116
E value
                  1.0e-58
Match length
                  136
% identity
NCBI Description Z.mays gene for HMG protein
Seq. No.
                  311112
Seq. ID
                  uwc700149975.h1
Method
                  BLASTX
NCBI GI
                  g4505499
BLAST score
                  156
E value
                  8.0e-11
```

```
% identity
```

O-GlcNAc transferase (uridine NCBI Description

diphospho-N-acetylglucosamine:polypeptide

beta-N-acetylglucosaminyl transferase) >gi 2266994 (U77413)

- 4th. . .

O-linked GlcNAc transferase [Homo sapiens]

Seq. No. 311113

uwc700150016.h1 Seq. ID

Method BLASTN NCBI GI g473602 BLAST score 123 7.0e-63 E value Match length 207 % identity 90

NCBI Description Zea mays W-22 histone H2A mRNA, complete cds

Seq. No.

uwc700150064.h1 Seq. ID

311114

Method BLASTX NCBI GI q3021409 BLAST score 186 2.0e-14 E value Match length 76 57 % identity

(Y12781) transducin (beta) like 1 protein [Homo sapiens] NCBI Description

Seq. No. 311115

uwc700150178.h1 Seq. ID

Method BLASTX NCBI GI q3775989 BLAST score 315 2.0e-29 E value Match length 84 73

% identity

(AJ010458) RNA helicase [Arabidopsis thaliana] NCBI Description

311116 Seq. No.

Seq. ID uwc700150206.h1

Method BLASTN g4140643 NCBI GI BLAST score 36 E value 6.0e-11 Match length 138 88 % identity

Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster, NCBI Description

complete sequence

Seq. No.

311117

Seq. ID

uwc700150235.hl

Method BLASTX NCBI GI q2190549 BLAST score 177 E value 2.0e-13 Match length 49 65 % identity

NCBI Description (AC001229) No definition line found [Arabidopsis thaliana]

```
311118
Seq. No.
                   uwc700150237.h1
Seq. ID
                   BLASTX
Method
                   g3540195
NCBI GI
                   138
BLAST score
                   1.0e-08
E value
Match length
                   40
                   62
% identity
NCBI Description (AC004260) Unknown protein [Arabidopsis thaliana]
                   311119
Seq. No.
                   uwc700150246.h1
Seq. ID
                   BLASTX
Method
                   q2500501
NCBI GI
BLAST score
                   153
E value
                   1.0e-10
Match length
                   41
                   76
% identity
                   40S RIBOSOMAL PROTEIN S27 (MANGANESE EFFICIENCY RELATED
NCBI Description
                   PROTEIN 1) >gi 1076733 pir S53124 zinc finger protein -
                   barley >qi 732\overline{8}11 emb \overline{CAA597}32 (X85544) putative zinc
                   finger protein [Hordeum vulgare]
                   311120
Seq. No.
                   uwc700150263.h1
Seq. ID
Method
                   BLASTX
                   g4455192
NCBI GI
BLAST score
                   172
                   9.0e-13
E value
                   78
Match length
% identity
                   49
                  (AL035440) putative protein [Arabidopsis thaliana]
NCBI Description
                   311121
Seq. No.
                   uwc700150317.h1
Seq. ID
                   BLASTX
Method
                   g3935150
NCBI GI
BLAST score
                   203
                   2.0e-16
E value
Match length
                   52
% identity
                   69
NCBI Description (AC005106) T25N20.14 [Arabidopsis thaliana]
                   311122
Seq. No.
                   uwc700150326.h1
Seq. ID
                   BLASTX
                   g4539404
```

Method NCBI GI BLAST score 165 5.0e-12 E value Match length 32

% identity 88

NCBI Description (ALO49524) putative protein [Arabidopsis thaliana]

311123 Seq. No.

uwc700150332.h1 Seq. ID

Method BLASTN NCBI GI q168619



```
BLAST score
                  6.0e-60
E value
                  173
Match length
                  94
% identity
                  Maize superoxide dismutase-2 (Sod-2) mRNA, complete cds.
NCBI Description
                  >gi 168621_gb_M15175_MZESOD2A Maize superoxide dismutase 2
                   (SOD2) mRNA, complete cds
                  311124
Seq. No.
Seq. ID
                  uwc700150349.h1
Method
                  BLASTX
NCBI GI
                  g4336747
                  221
BLAST score
                   2.0e-18
E value
                  77
Match length
                   57
% identity
                  (AF104924) unconventional myosin heavy chain [Zea mays]
NCBI Description
Seq. No.
                   311125
                   uwc700150360.h1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2267006
                   260
BLAST score
                   4.0e-23
E value
                   54
Match length
% identity
                   (AF006825) endosperm lumenal binding protein [Oryza sativa]
NCBI Description
                   311126
Seq. No.
Seq. ID
                   uwc700150376.h1
Method
                   BLASTX
                   q4581047
NCBI GI
BLAST score
                   230
E value
                   1.0e-19
Match length
                   54
                   76
% identity
                   (AF134807) putative dihydroflavonol reductase [Oryza
NCBI Description
                   sativa]
                   311127
Seq. No.
                   uwc700150426.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2804280
BLAST score
                   220
                   2.0e-18
E value
Match length
                   47
                   79
% identity
                   (AB003687) 6-4 photolyase [Arabidopsis thaliana]
NCBI Description
                   >gi 3929918 dbj BAA34711_ (AB017331) 6-4 photolyase
                   [Arabidopsis thaliana]
```

Seq. No. 311128

Seq. ID uwc700150450.h1

Method BLASTX NCBI GI g1184774 BLAST score 292 E value 9.0e-27



Match length 56 % identity 100

NCBI Description (U45856) cytosolic glyceroldehyde-3-phosphate dehydrogenase

GAPC3 [Zea mays]

Seq. No. 311129

Seq. ID uwc700150494.h1

Method BLASTX
NCBI GI g140207
BLAST score 185
E value 3.0e-14
Match length 49
% identity 63

NCBI Description PROBABLE 40S RIBOSOMAL PROTEIN S9 >gi_102109_pir__S12674

ribosomal protein S9.e - Trypanosoma brucei

>qi 10399 emb CAA36818 (X52586) ald orfU protein (AA 1 -

190) [Trypanosoma brucei]

Seq. No. 311130

Seg. ID uwc700150508.h1

Method BLASTX
NCBI GI g3080740
BLAST score 300
E value 1.0e-27
Match length 74
% identity 74

NCBI Description (U77366) pasticcino 1-D [Arabidopsis thaliana]

Seq. No. 311131

Seq. ID uwc700150520.h1

Method BLASTX
NCBI GI 94262148
BLAST score 250
E value 7.0e-22
Match length 71
% identity 65

NCBI Description (AC005275) predicted protein of unknown function

[Arabidopsis thaliana]

Seq. No. 311132

Seq. ID uwc700150534.h1

Method BLASTN
NCBI GI g1864000
BLAST score 126
E value 8.0e-65
Match length 142
% identity 97

NCBI Description Maize DNA for Fd III, complete cds

Seq. No. 311133

Seq. ID uwc700150553.h1

Method BLASTX
NCBI GI g3935173
BLAST score 268
E value 5.0e-24
Match length 75

% identity 63

```
NCBI Description (AC004557) F17L21.16 [Arabidopsis thaliana]
                  311134
Seq. No.
                  uwc700150674.h1
Seq. ID
                  BLASTX
```

g4588906 NCBI GI 218 BLAST score 4.0e-18 E value 49 Match length % identity 86

Method

(AF118149) ribosomal protein S7 [Secale cereale] NCBI Description

311135 Seq. No. uwc700150731.h1 Seq. ID Method BLASTX g1418331 NCBI GI

242 BLAST score 6.0e-21 E value Match length 78 64 % identity

(X95909) receptor like protein kinase [Arabidopsis NCBI Description

thaliana]

311136 Seq. No.

uwc700150777.h1 Seq. ID

Method BLASTX g2129948 NCBI GI BLAST score 301 5.0e-28 E value 73 Match length 81 % identity

inorganic pyrophosphatase (EC 3.6.1.1) (clone TVP31) -NCBI Description

common tobacco

311137 Seq. No.

uwc700150804.h1 Seq. ID

Method BLASTX NCBI GI g1321661 250 BLAST score 1.0e-21 E value Match length 53 92 % identity

NCBI Description (D45423) ascorbate peroxidase [Oryza sativa]

311138 Seq. No.

uwc700150837.h1 Seq. ID

Method BLASTX g2791278 NCBI GI BLAST score 140 E value 6.0e-09 Match length 79 % identity 41

(Z69257) beta-xylosidase [Hypocrea jecorina] NCBI Description

311139 Seq. No.

uwc700150848.h1 Seq. ID

Method BLASTX

BLAST score

E value

36 4.0e-11

```
g1136122
NCBI GI
BLAST score
                  468
                  2.0e-47
E value
                  85
Match length
                  100
% identity
NCBI Description (X91807) alfa-tubulin [Oryza sativa]
                  311140
Seq. No.
                  uwc700150873.h1
Seq. ID
Method
                  BLASTX
                  g4262234
NCBI GI
                  249
BLAST score
                  7.0e-22
E value
Match length
                  56
% identity
                  73
NCBI Description (AC006200) unknown protein [Arabidopsis thaliana]
                  311141
Seq. No.
                  uwc700150885.h1
Seq. ID
Method
                  BLASTX
                  g3420057
NCBI GI
BLAST score
                  237
                  2.0e-20
E value
                  74
Match length
                  51
% identity
NCBI Description (AC004680) putative ABC transporter [Arabidopsis thaliana]
                  311142
Seq. No.
                  uwc700150890.h1
Seq. ID
                  BLASTX
Method
                  g3176690
NCBI GI
                  190
BLAST score
                  5.0e-15
E value
                  63
Match length
                  65
% identity
                  (AC003671) Similar to ubiquitin ligase gb_D63905 from S.
NCBI Description
                  cerevisiae. EST gb R65295 comes from this gene.
                . [Arabidopsis thaliana]
                  311143
Seq. No.
Seq. ID
                  uwc700150891.h1
Method
                  BLASTX
                  g1705678
NCBI GI
                   310
BLAST score
E value
                   6.0e-29
                   59
Match length
                   97
% identity
                  CELL DIVISION CYCLE PROTEIN 48 HOMOLOG (VALOSIN CONTAINING
NCBI Description
                   PROTEIN HOMOLOG) (VCP) >gi 862480 (U20213)
                   valosin-containing protein [Glycine max]
Seq. No.
                   311144
                   uwc700150896.h1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3821780
```



```
Match length
                   36
                  100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                  311145
Seq. No.
                  uwc700150972.h1
Seq. ID
Method
                  BLASTX
                  g3738316
NCBI GI
BLAST score
                  189
                   7.0e-15
E value
                   59
Match length
                   58
% identity
```

(AC005170) unknown protein [Arabidopsis thaliana] NCBI Description

311146 Seq. No. uwc700150977.h1 Seq. ID Method BLASTN NCBI GI g1772598 46

BLAST score 5.0e-17 E value Match length 82 89 % identity

NCBI Description T.aestivum mRNA for germin-like protein 2, partial

311147 Seq. No. uwc700151029.h1 Seq. ID Method BLASTX NCBI GI g4559380 BLAST score 142

E value 2.0e-09 Match length 38 58 % identity

(AC006526) putative auxin-responsive GH3 protein NCBI Description

[Arabidopsis thaliana]

Seq. No. 311148

Seq. ID uwc700151052.h1

Method BLASTX q1402918 NCBI GI BLAST score 337 5.0e-32 E value Match length 82 80 % identity

(X98320) peroxidase [Arabidopsis thaliana] NCBI Description

>gi_1429215_emb_CAA67310_ (X98774) peroxidase ATP6a

[Arabidopsis thaliana]

Seq. No. 311149

Seq. ID uwc700151120.hl

Method BLASTX NCBI GI g3377507 BLAST score 147 7.0e-10 E value Match length 33 % identity 82

(AF056026) auxin transport protein EIR1 '[Arabidopsis NCBI Description thaliana] >gi_3661620 (AF093241) putative auxin efflux



carrier AGR [Arabidopsis thaliana] >gi_3746886 (AF087459) polar-auxin-transport efflux component AGRAVITROPIC 1 [Arabidopsis thaliana] >gi_4206709 (AF086906) root gravitropism control protein [Arabidopsis thaliana]

311150 Seq. No. uwc700151141.hl Seq. ID Method BLASTX g1170034 NCBI GI 294 BLAST score 5.0e-27 E value Match length 61 93 % identity GLUTAMATE--CYSTEINE LIGASE PRECURSOR NCBI Description (GAMMA-GLUTAMYLCYSTEINE SYNTHETASE) (GAMMA-ECS) (GCS) >gi_2129598_pir__S60128 glutamate--cysteine ligase (EC 6.3.2.2) precursor, chloroplast - Arabidopsis thaliana >qi 488615 emb CAA82626 (Z29490) gamma-glutamylcysteine synthetase [Arabidopsis thaliana] Seq. No. 311151 uwc700151189.h1 Seq. ID BLASTX Method NCBI GI g3063445 BLAST score 193 E value 2.0e-15 73 Match length % identity 52 (AC003981) F22013.7 [Arabidopsis thaliana] NCBI Description Seq. No. 311152 uwc700151223.h1 Seq. ID Method BLASTX NCBI GI g4467100 BLAST score 169 2.0e-12 E value Match length 53 64 % identity (AL035538) MADS-box protein AGL17-like protein [Arabidopsis NCBI Description thaliana] 311153 Seq. No. uwc700151243.h1 Seq. ID Method BLASTX NCBI GI g66009 BLAST score 297 E value 3.0e-27 Match length 56 % identity 100 glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) C, NCBI Description

Seq. No. 311154

Seq. ID uwc700151265.h1

Method BLASTN NCBI GI g3821780

(AA 1-337) [Zea mays]

cytosolic - maize >gi_22238_emb_CAA30151_ (X07156) GADPH



```
BLAST score
                  36
                  4.0e-11
E value
Match length
                  36
% identity
                  100
NCBI Description Xenopus laevis cDNA clone 27A6-1
                  311155
Seq. No.
                  uwc700151325.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2464905
BLAST score
                  223
E value
                  9.0e-19
Match length
                   61
                  75
% identity
                  (Z99708) minor allergen [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   311156
                  uwc700151333.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q1431872
BLAST score
                   174
E value
                   4.0e-13
Match length
                   52
                   63
% identity
                   (U48831) WRKY1 [Petroselinum crispum]
NCBI Description
Seq. No.
                   311157
Seq. ID
                   uwc700151344.h1
Method
                   BLASTN
                   g4185305
NCBI GI
BLAST score
                   164
E value
                   2.0e-87
                   208
Match length
                   95
% identity
                   Zea mays cosmid IV.1E1 22-kDa alpha zein protein 21
NCBI Description
                   (sz22-21) gene, complete cds; retrotransposon Opie-2 gag
                   protein, polyprotein, and copia protein genes, complete
                   cds; and unknown genes
Seq. No.
                   311158
                   uwc700151358.h1
Seq. ID
Method
                   BLASTX
                   g1350680
NCBI GI
                   177
BLAST score
                   2.0e-13
E value
                   83
Match length
```

46 % identity

60S RIBOSOMAL PROTEIN L1 NCBI Description

311159 Seq. No.

uwc700151376.h1 Seq. ID

Method BLASTX q2906011 NCBI GI 207 BLAST score 9.0e-17 E value Match length 75 51 % identity



NCBI Description (AF036894) sphingosine-1-phosphate lyase; pyridoxal-phosphate protein; SPL [Mus musculus]

Seq. No. 311160

Seq. ID uwc700151401.h1

Method BLASTN
NCBI GI g1935046
BLAST score 228
E value 1.0e-125
Match length 232
% identity 100

NCBI Description Zea mays helix-loop-helix type transcription factor R

(R-d:Catspaw allele) gene, exon 1, inverted repeat, partial

cds

Seq. No. 311161

Seq. ID uwc700151403.h1

Method BLASTX
NCBI GI g4567283
BLAST score 313
E value 3.0e-29
Match length 77
% identity 75

NCBI Description (AC006841) unknown protein [Arabidopsis thaliana]

Seq. No. 311162

Seq. ID uwc700151409.h1

Method BLASTX
NCBI GI g2129825
BLAST score 295
E value 3.0e-27
Match length 64
% identity 84

NCBI Description dynamin-like protein phragmoplastin 12 - soybean

>gi_1217994 (U25547) SDL [Glycine max]

Seq. No. 311163

Seq. ID uwc700151423.h1

Method BLASTX
NCBI GI g4539314
BLAST score 159
E value 5.0e-17
Match length 70
% identity 70

NCBI Description (AL035679) kinesin like protein [Arabidopsis thaliana]

Seq. No. 311164

Seq. ID uwc700151429.h1

Method BLASTX
NCBI GI 94218991
BLAST score 260
E value 4.0e-23
Match length 74
% identity 64

NCBI Description (AF098632) subtilisin-like protease [Arabidopsis thaliana]

Seq. No. 311165

```
uwc700151435.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3122071
BLAST score
                  397
E value
                  3.0e - 39
Match length
                  73
                  100
% identity
                  ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)
NCBI Description
                  >gi_2130148_pir__S66339 translation elongation factor eEF-1
                  alpha chain - maize >gi 1321656_dbj_BAA08249_ (D45408)
                   alpha subunit of tlanslation elongation factor 1 [Zea mays]
                   311166
Seq. No.
Seq. ID
                  uwc700151470.hl
Method
                  BLASTX
NCBI GI
                   q4468153
BLAST score
                   278
E value
                   4.0e-25
                   79
Match length
                   62
% identity
NCBI Description (AJ132000) sucrose synthase [Craterostigma plantagineum]
Seq. No.
                   311167
                   uwc700151520.h1
Seq. ID
                   BLASTX
Method
                   g3811007
NCBI GI
BLAST score
                   231
                   2.0e-19
E value
                   90
Match length
% identity
                   (AB019327) NADP specific isocitrate dehydrogenase [Daucus
NCBI Description
Seq. No.
                   311168
Seq. ID
                   uwc700151543.h1
Method
                   BLASTN
NCBI GI
                   g485376
BLAST score
                   46
                   6.0e-17
E value
Match length
                   50
% identity
                   98
                   Zea mays alpha-3-tubulin gene, complete cds
NCBI Description
                   311169
Seq. No.
                   uwc700151577.h1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g1408221
```

BLAST score 38 4.0e-12 E value

50 Match length % identity

Sorghum bicolor pathogenesis-related protein (PR-10) mRNA, NCBI Description

complete cds

311170 Seq. No.

uwc700151586.hl Seq. ID

Method BLASTX

```
X_{i}^{\infty}
                    q629858
 NCBI GI
                    278
 BLAST score
                    3.0e-25
 E value
                    78
 Match length
 % identity
                    72
 NCBI Description protein kinase C inhibitor - maize
                    311171
 Seq. No.
                    uwc700151629.h1
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g2244750
 BLAST score
                    191
                    6.0e-15
 E value
 Match length
                    76
 % identity
                    (Z97335) adenosylhomocysteinase [Arabidopsis thaliana]
 NCBI Description
                    >gi_3088579 (AF059581) S-adenosyl-L-homocysteine hydrolase
                    [Arabidopsis thaliana]
 Seq. No.
                    311172
 Seq. ID
                    uwc700151630.hl
 Method
                    BLASTN
                    g3821780
 NCBI GI
 BLAST score
                    36
                    5.0e-11
 E value
                    48
 Match length
  % identity
 NCBI Description Xenopus laevis cDNA clone 27A6-1
 Seq. No.
                    311173
 Seq. ID
                    uwc700151656.hl
 Method
                    BLASTX
 NCBI GI
                    q1208776
 BLAST score
                    217
                    5.0e-18
  E value
 Match length
                    79
  % identity
                    47
                    (U48367) alcohol dehydrogenase [Pinus banksiana]
  NCBI Description
                    >gi_1208788 (U48373) alcohol dehydrogenase [Pinus
                    banksiana]
                    311174
  Seq. No.
                    uwc700151692.h1
  Seq. ID
                    BLASTX
  Method
                    q3641837
  NCBI GI
                    248
  BLAST score
                    1.0e-21
  E value
  Match length
                    73
                    70
  % identity
                     (AL023094) Nonclathrin coat protein gamma - like protein
  NCBI Description
                     [Arabidopsis thaliana]
                    311175
```

uwc700151703.hl Seq. ID

Method BLASTX NCBI GI g3913427 250 BLAST score

```
8.0e-22
E value
Match length
                  74
                  97
% identity
                  S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC)
NCBI Description
                  (SAMDC) >gi 1532073 emb CAA69075 (Y07767)
                  S-adenosylmethionine decarboxylase [Zea mays]
Seq. No.
                  uwc700151721.h1
Seq. ID
                  BLASTN
Method
NCBI GI
                  q3288882
                  45
BLAST score
                  2.0e-16
E value
                  77
Match length
                  90
% identity
                  Oryza sativa mRNA for SAR DNA binding protein, partial cds
NCBI Description
                  311177
Seq. No.
                  uwc700151851.h1
Seq. ID
                  BLASTX
Method
                  q1632831
NCBI GI
BLAST score
                  152
                   2.0e-10
E value
Match length
                   32
% identity
                  (Z49698) orf [Ricinus communis]
NCBI Description
Seq. No.
                   311178
                   uwc700151857.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3355477
BLAST score
                   164
                   9.0e-12
E value
                   79
Match length
% identity
                   49
                  (AC004218) putative P-glycoprotein, pgp1 [Arabidopsis
NCBI Description
                   thaliana]
                   311179
Seq. No.
                   uwc700151858.h1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4336606
BLAST score
                   317
                   9.0e-36
E value
                   80
Match length
                   99
% identity
                  (AF099110) sigma factor; Sig1 [Zea mays]
NCBI Description
                   311180
Seq. No.
                   uwc700151887.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q82695
BLAST score
                   266
```

NCBI Description glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) 3 - 44371

9.0e-24

56 98

E value Match length

% identity



maize (fragment) >gi_293887 (L13431)
glyceraldehyde-3-phosphate dehydrogenase [Zea mays]

Seq. No. 311181 Seq. ID uwc700151963.h1

Method BLASTX
NCBI GI g4455220
BLAST score 264
E value 2.0e-23
Match length 75

% identity 63 NCBI Description (AL035440) putative aconitase [Arabidopsis thaliana]

Seq. No. 311182

Seq. ID uwc700151981.hl

Method BLASTX
NCBI GI g4468798
BLAST score 313
E value 2.0e-29
Match length 74
% identity 74

NCBI Description (AJ010440) GST7 protein [Zea mays]

Seq. No. 311183

Seq. ID uwc700151993.h1

Method BLASTX
NCBI GI 94455188
BLAST score 152
E value 2.0e-10

Match length 69 % identity 43

NCBI Description (AL035521) putative protein [Arabidopsis thaliana]

Seq. No. 311184

Seq. ID uwc700152057.h1

Method BLASTN
NCBI GI g3821780
BLAST score 36

E value 6.0e-11
Match length 45
% identity 65

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 311185

Seq. ID uwc700152066.h1

Method BLASTX
NCBI GI g1402918
BLAST score 261
E value 3.0e-23
Match length 69
% identity 71

NCBI Description (X98320) peroxidase [Arabidopsis thaliana]

>gi_1429215_emb_CAA67310_ (X98774) peroxidase ATP6a

[Arabidopsis thaliana]

Seq. No. 311186

Seq. ID uwc700152129.h1

Method BLASTX
NCBI GI g115511
BLAST score 302
E value 5.0e-28
Match length 59
% identity 100

NCBI Description

CALMODULIN >gi_231682_sp P29612 CALM ORYSA CALMODULIN >gi 71682 pir MCBH calmodulin - barley >gi 100666 pir S24952 calmodulin 1 (clone lambda DASH) rice >gi_20188_emb_CAA78287_ (Z12827) calmodulin [Oryza sativa] >gi_167008 (M27303) calmodulin [Hordeum vulgare] >gi_170072 (L01431) calmodulin [Glycine max] >gi_310315 (L18913) calmodulin [Oryza sativa] >gi_506850 (L20691) calmodulin [Vigna radiata] >gi_1478370_bbs_176852 (S81594) auxin-regulated calmodulin, arCaM [Vigna radiata=mung bean, Wilczek, seedling, Peptide, 149 aa] [Vigna radiata] >gi 1742989_emb_CAA70982 (Y09853) CaM protein [Cicer arietinum] $\overline{}$ gi $\overline{}$ 7754991 ($\overline{}$ 48242) calmodulin TaCaM1-1 [Triticum aestīvum] >gi 1754993 (U48688) calmodulin TaCaM1-2 [Triticum aestivum] >gi_1754995 (U48689) calmodulin TaCaM1-3 [Triticum aestivum] >gi_1755003 (U48693) calmodulin TaCaM3-1 [Triticum aestivum] >gi 1755005 (U49103) calmodulin TaCaM3-2 [Triticum aestivum] >gi 1755007 (U49104) calmodulin TaCaM3-3 [Triticum aestivum] >gi 1755009 (U49105) calmodulin TaCaM4-1 [Triticum aestīvum] >gi 3617842 (AF042840) calmodulin [Oryza sativa] >gi 226769 prf__1604476A

calmodulin [Hordeum vulgare var. distichum]
>gi 1583768 prf 2121384B calmodulin [Glycine max]

Seq. No. 311187 Seq. ID uwc700152131.h1

Method BLASTX
NCBI GI g113621
BLAST score 338
E value 2.0e-32
Match length 67

% identity 99

NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME

>gi_68196_pir__ADZM fructose-bisphosphate aldolase (EC

4.1.2.13), cytosolic - maize >gi_168420 (M16220) aldolase

[Zea mays] >gi_295850_emb_CAA31366_ (X12872) fructose

bisphosphate aldolase [Zea mays] >gi_225624_prf__1307278A

cytoplasmic aldolase [Zea mays]

Seq. No. 311188

Seq. ID uwc700152134.h1

Method BLASTN
NCBI GI g1870202
BLAST score 120
E value 4.0e-61
Match length 159
% identity 94

NCBI Description Z.mays cyp71c3 gene

Seq. No. 311189

Seq. ID uwc700152142.h1

```
BLASTX
Method
                  q4049341
NCBI GI
BLAST score
                  165
                  6.0e-12
E value
                  54
Match length
                  57
% identity
NCBI Description (AL034567) putative protein [Arabidopsis thaliana]
                  311190
Seq. No.
                  uwc700152157.h1
Seq. ID
                  BLASTX
Method
                  g3757523
NCBI GI
                  221
BLAST score
                  1.0e-18
E value
Match length
                  57
                  70
% identity
NCBI Description (AC005167) putative transportin [Arabidopsis thaliana]
                  311191
Seq. No.
                  uwc700152161.h1
Seq. ID
Method
                  BLASTN
                  g662367
NCBI GI
                  190
BLAST score
                  1.0e-103
E value
Match length
                  215
% identity
                  98
                  Zea mays farnesyl pyrophosphate synthetase (fps) mRNA,
NCBI Description
                  complete cds
                  311192
Seq. No.
                  uwc700152180.h1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4539665
BLAST score
                   215
E value
                   1.0e-17
Match length
                  76
                   54
% identity
NCBI Description (AF061282) polyprotein [Sorghum bicolor]
                   311193
Seq. No.
                   uwc700152271.h1
Seq. ID
Method
                   BLASTN
NCBI GI
                   q440170
                   193
BLAST score
E value
                   1.0e-104
                   233
Match length
% identity
                   96
NCBI Description Z.mays (C6000237) trpA gene
Seq. No.
                   311194
Seq. ID
                   uwc700152291.h1
```

Method BLASTX NCBI GI q1171579 BLAST score 190 E value 7.0e-15 Match length 49 % identity 67



39

thaliana]

% identity

NCBI Description

```
NCBI Description (X95342) cytochrome P450 [Nicotiana tabacum]
                  311195
Seq. No.
                  uwc700152302.h1
Seq. ID
                  BLASTN
Method
                  g22322
NCBI GI
BLAST score
                  63
                  3.0e-27
E value
Match length
                  63
                  100
% identity
NCBI Description Z.mays mRNA for H2B histone (clone cH2B214)
                  311196
Seq. No.
                  uwc700152353.h1
Seq. ID
Method
                  BLASTX
                  q100921
NCBI GI
                  299
BLAST score
                  1.0e-27
E value
                  59
Match length
                   97
% identity
NCBI Description regulatory protein B-Peru - maize >gi_22195_emb_CAA40544_
                   (X57276) regulatory protein [Zea mays]
                   311197
Seq. No.
                  uwc700152385.h1
Seq. ID
Method
                  BLASTX
                   g2642165
NCBI GI
                   230
BLAST score
                   1.0e-19
E value
                   64
Match length
                   62
% identity
                   (AC003000) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   311198
Seq. No.
                   uwc700152386.h1
Seq. ID
Method
                   BLASTN
                   g4185305
NCBI GI
                   35
BLAST score
                   2.0e-10
E value
Match length
                   43
                   95
% identity
                   Zea mays cosmid IV.1E1 22-kDa alpha zein protein 21
NCBI Description
                   (sz22-21) gene, complete cds; retrotransposon Opie-2 gag
                   protein, polyprotein, and copia protein genes, complete
                   cds; and unknown genes
                   311199
Seq. No.
                   uwc700152416
Seq. ID
Method
                   BLASTX
                   g2832629
NCBI GI
BLAST score
                  - 148
E value
                   7.0e-10
                   70
Match length
```

(ALO21711) 4-coumarate-CoA ligase - like [Arabidopsis

NCBI GI

BLAST score

g66009 264

```
311200
Seq. No.
                  uwc700152422
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1346957
BLAST score
                  186
                  2.0e-14
E value
                  35 .
Match length
                  100
% identity
NCBI Description RAS-RELATED PROTEIN RAB-2-B >gi_722328 (U22433) GTP binding
                  protein [Zea mays]
                  311201
Seq. No.
                  uwc700152445
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2894534
BLAST score
                   206
                   1.0e-22
E value
Match length
                   56
                   91
% identity
NCBI Description (AJ224327) aquaporin [Oryza sativa]
Seq. No.
                   311202
                   uwc700152496.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4646232
BLAST score
                   166
E value
                   5.0e-12
Match length
                   73
% identity
                   (AC007266) putative ligand-gated ion channel protein
NCBI Description
                   [Arabidopsis thaliana]
                   311203
Seq. No.
                   uwc700152504.hl
Seq. ID
                   BLASTX
Method
                   g3093294
NCBI GI
                   291
BLAST score
                   1.0e-26
E value
                   76
Match length
                   71
% identity
                   (Y12782) putative villin [Arabidopsis thaliana]
NCBI Description
                   311204
Seq. No.
                   uwc700152522.h1
Seq. ID
                   BLASTX
Method
                   g4503527
NCBI GI
                   138
BLAST score
                   7.0e-09
E value
                   59
Match length
                   46
 % identity
                   UNKNOWN >gi_1778051 (U62583) Prt1 homolog [Homo sapiens]
NCBI Description
                   311205
 Seq. No.
                   uwc700152546.h1
 Seq. ID
                   BLASTX
Method
```

```
E value

1.0e-23

Match length
% identity

NCBI Description

NCBI Description

(AA 1-337) [Zea mays]

Seq. No.

Seq. ID

1.0e-23

52

100

glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) C, cytosolic - maize >gi_22238_emb_CAA30151_ (X07156) GADPH
(AA 1-337) [Zea mays]
```

Method BLASTX
NCBI GI g2499535
BLAST score 351
E value 1.0e-33
Match length 76
% identity 91

NCBI Description 2-OXOGLUTARATE/MALATE TRANSLOCATOR PRECURSOR >gi_595681 (U13238) 2-oxoglutarate/malate translocator [Spinacia

oleracea]

 Seq. No.
 311207

 Seq. ID
 uwc700152584.h1

 Method
 BLASTX

 NCBI GI
 g3395431

 BLAST score
 245

 E value
 3.0e-21

E value 3.06
Match length 70
% identity 63

NCBI Description (AC004683) unknown protein [Arabidopsis thaliana]

Seq. No. 311208 Seq. ID uwc700152613.h1

Method BLASTX
NCBI GI g479356
BLAST score 244
E value 4.0e-21
Match length 75

NCBI Description protein kinase PK1 (EC 2.7.1.-), receptor-like - maize

Seq. No. 311209

% identity

Seq. ID uwc700152620.h1

65

Method BLASTX
NCBI GI g4539423
BLAST score 314
E value 2.0e-29
Match length 77
% identity 78

NCBI Description (AL049171) pyrophosphate-dependent phosphofructo-1-kinase

[Arabidopsis thaliana]

Seq. No. 311210

Seq. ID uwc700152639.h1

Method BLASTN
NCBI GI g22322
BLAST score 75
E value 3.0e-34
Match length 99



% identity 94

NCBI Description Z.mays mRNA for H2B histone (clone cH2B214)

Seq. No. 311211

Seq. ID uwc700152647.h1

Method BLASTX
NCBI GI g3367536
BLAST score 143
E value 2.0e-09
Match length 33
% identity 82

NCBI Description (AC004392) Contains similarity to symbiosis-related like

protein F1N20.80 gi_2961343 from A. thaliana BAC gb AL022140. EST gb_T04695 comes from this gene.

[Arabidopsis thaliana]

Seq. No. 311212

Seq. ID uwc700152691.hl

Method BLASTX
NCBI GI g4263712
BLAST score 166
E value 4.0e-12
Match length 37
% identity 81

NCBI Description (AC006223) putative ribosomal protein S12 [Arabidopsis

thaliana]

Seq. No. 311213

Seq. ID uwc700152720.h1

Method BLASTX
NCBI GI g2924781
BLAST score 198
E value 6.0e-16
Match length 63
% identity 62

NCBI Description (AC002334) putative cellulose synthase [Arabidopsis

thaliana]

Seq. No. 311214

Seq. ID uwc700152721.h1

Method BLASTX
NCBI GI g3850588
BLAST score 201
E value 3.0e-16
Match length 70
% identity 54

NCBI Description (AC005278) Contains similarity to gb_AB011110 KIAA0538

protein from Homo sapiens brain and to phospholipid-binding domain C2 PF_00168. ESTs gb_AA585988 and gb_T04384 come

from this gene. [Arabidopsis thaliana]

Seq. No. 311215

Seq. ID uwc700152744.h1

Method BLASTX
NCBI GI g2935342
BLAST score 242
E value 4.0e-21



Match length 65 75 % identity

(AF044216) steroid 22-alpha-hydroxylase; DWF4; CYP90B1 NCBI Description

[Arabidopsis thaliana]

Seq. No. 311216

uwc700152789.h1 Seq. ID

Method BLASTX NCBI GI g2996096 BLAST score 272 2.0e-24 E value 55 Match length % identity 96

NCBI Description (AF030517) translation elongation factor-1 alpha; EF-1

alpha [Oryza sativa]

Seq. No. 311217

uwc700152819.h1 🐣 Seq. ID

BLASTX Method NCBI GI g1708777 BLAST score 166 4.0e-12 E value Match length 61 56 % identity

(Z83202) potassium channel [Arabidopsis thaliana] NCBI Description

>gi_3063705_emb_CAA18596.1_ (AL022537) potassium channel protein [Arabidopsis thaliana] >gi_4090537 (U73325) K+ inward rectifying channel protein [Arabidopsis thaliana]

>qi 4098949 (U81239) K+ inward rectifying channel

[Arabidopsis thaliana]

Seq. No. 311218

uwc700152866.h1 Seq. ID

Method BLASTX NCBI GI g2252631 BLAST score 143 E value 2.0e-09 Match length 41 % identity 66

NCBI Description (U95973) hypothetical protein [Arabidopsis thaliana]

311219 Seq. No.

Seq. ID uwc700152875.h1

Method BLASTX NCBI GI g2108252 BLAST score 234 E value 4.0e-20 Match length 73 % identity

(Y10228) P-glycoprotein-2 [Arabidopsis thaliana] NCBI Description

>gi_2108254_emb_CAA71276_ (Y10227) P-glycoprotein-2
[Arabidopsis thaliana] >gi_4538925_emb_CAB39661.1
(AL049483) P-glycoprotein-2 (pgp2) [Arabidopsis thaliana]

Seq. No. 311220

uwc700152925.h1 Seq. ID

Method BLASTX

Match length

% identity

65

62

```
q1498053
NCBI GI
                  162
BLAST score
                  1.0e-11
E value
Match length
                  45
                  69
% identity
NCBI Description (U64436) ribosomal protein S8 [Zea mays]
                  311221
Seq. No.
                  uwc700152959.h1
Seq. ID
                  BLASTX
Method
                  g4102600
NCBI GI
                  370
BLAST score
                  6.0e-36
E value
Match length
                  79
% identity
                  89
NCBI Description (AF013467) ARF6 [Arabidopsis thaliana]
                  311222
Seq. No.
                  uwc700153010.hl
Seq. ID
                  BLASTX
Method
                  g131772
NCBI GI
BLAST score
                  168
                  2.0e-12
E value
Match length
                  36
                  94
% identity
NCBI Description 40S RIBOSOMAL PROTEIN S14 (CLONE MCH1)
                  >gi 82723_pir__A30097 ribosomal protein S14 (clone MCH1) -
                  maize
                  311223
Seq. No.
                  uwc700153036.h1
Seq. ID
                  BLASTN
Method
                  q1129085
NCBI GI
                   51
BLAST score
                   5.0e-20
E value
Match length
                   83
                   90
% identity
NCBI Description Wheat mRNA for protein H2A, complete cds, clone wcH2A-9
                   311224
Seq. No.
                   uwc700153041.h1
Seq. ID
                   BLASTX
Method
                   q1352461
NCBI GI
                   245
BLAST score
                   2.0e-21
E value
Match length
                   49
                   98
% identity
NCBI Description IN2-2 PROTEIN
                   311225
Seq. No.
Seq. ID
                   uwc700153072.h1
                   BLASTX
Method
                   q4512685
NCBI GI
                   210
BLAST score
                   2.0e-17
E value
```



(AC006931) hypothetical protein [Arabidopsis thaliana] >gi_4559325_gb_AAD22987.1_AC007087_6 (AC007087) NCBI Description hypothetical protein [Arabidopsis thaliana]

311226 Seq. No.

uwc700153077.h1 Seq. ID

BLASTX Method NCBI GI g2660676 351 BLAST score 7.0e-34 E value 73 Match length 79 % identity

(AC002342) Dreg-2 like protein [Arabidopsis thaliana] NCBI Description

Seq. No. 311227

uwc700153082.h1 Seq. ID

BLASTN

Method g1100216 NCBI GI 99 BLAST score 7.0e-49 E value Match length 103 99 % identity

Zea mays sucrose synthase (SUS1) gene, exons 1-2 NCBI Description

311228 Seq. No.

uwc700153156.h1 Seq. ID

Method BLASTX g2924781 NCBI GI 178 BLAST score 2.0e-13 E value 51 Match length 59 % identity

(ACO02334) putative cellulose synthase [Arabidopsis NCBI Description

thaliana]

311229 Seq. No.

uwc700153185.h1 Seq. ID

Method BLASTX a1173187 NCBI GI BLAST score 193 3.0e-15 E value Match length 39 97 % identity

40S RIBOSOMAL PROTEIN S23 (S12) >gi 1362041 pir_ S56673 NCBI Description

ribosomal protein S23.e, cytosolic (clone RJ3) - garden strawberry >gi_643074 (U19940) putative 40S ribosomal

protein s12 [Fragaria x ananassa]

Seq. No. 311230

uwc700153264.h1 Seq. ID

Method BLASTX q3367568 NCBI GI BLAST score 189 1.0e-14 E value Match length 47 % identity 70

(AL031135) protein kinase - like protein [Arabidopsis NCBI Description



thaliana]

311231 Seq. No. Seq. ID uwc700153510.hl Method BLASTX g3914006 NCBI GI 339 BLAST score 2.0e-32 E value Match length 66 98 % identity NCBI Description MITOCHONDRIAL LON PROTEASE HOMOLOG 2 PRECURSOR >gi_1816588 (U85495) LON2 [Zea mays] 311232 Seq. No. uwc700153516.hl Seq. ID Method BLASTX NCBI GI g2286153 BLAST score 206 1.0e-16 E value 43 Match length % identity NCBI Description (AF007581) cytoplasmic malate dehydrogenase [Zea mays] 311233 Seq. No. uwc700153520.h1 Seq. ID Method BLASTX NCBI GI g1762142 BLAST score 143 E value 2.0e-09 Match length 45 % identity 56 NCBI Description (U48434) putative cytochrome P450 [Solanum chacoense] 311234 Seq. No. uwc700153526.h1 Seq. ID BLASTX Method g2660670 NCBI GI 260 BLAST score 5.0e-23 E value 73 Match length 68 % identity (AC002342) putative Cu2+-transporting ATPase [Arabidopsis NCBI Description thaliana] 311235 Seq. No. uwc700153557.h1 Seq. ID BLASTX Method g4038594 NCBI GI 175 BLAST score 5.0e-13 E value Match length 49 % identity 53 (AJ222798) tDET1 protein [Lycopersicon esculentum] NCBI Description

Seq. No. 311236

[Lycopersicon esculentum]

>gi 4454332_emb_CAA11914_ (AJ224356) tDET1 protein



```
Seq. ID
                   uwc700153566.h1
 Method
                   BLASTX
 NCBI GI
                   g3367537
 BLAST score
                   298
E value
                   2.0e-27
Match length
                   83
 % identity
                   63
                   (AC004392) Contains similarity to ANK repeat region of
NCBI Description
                   Fowlpox virus BamHI-orf7 protein homolog C18F10.7 gi 485107
                   from Caenorhabditis elegans cosmid gb_U00049. This gene is
                   continued from unannotated gene on BAC F19K23 gb_AC000375.
                   [Arabid
Seq. No.
                   311237
Seq. ID
                   uwc700153583.h1
Method
                   BLASTN
NCBI GI
                   g2062705
BLAST score
                   34
                   8.0e-10
E value
Match length
                   34
% identity
                   100
NCBI Description Human butyrophilin (BTF5) mRNA, complete cds
Seq. No.
                   311238
Seq. ID
                   uwc700153632.h1
Method-
                   BLASTX
NCBI GI
                   q3080398
BLAST score
                   144
E value
                   2.0e-09
Match length
                   55
% identity
                   47
NCBI Description
                  (AL022603) putative protein [Arabidopsis thaliana]
Seq. No.
                   311239
Seq. ID
                   uwc700153638.h1
Method
                   BLASTX
NCBI GI
                   g1498053
BLAST score
                   239
E value
                   1.0e-20
Match length
                   58
% identity
                   81
NCBI Description
                  (U64436) ribosomal protein S8 [Zea mays]
Seq. No.
                   311240
Seq. ID
                  uwc700153639.h1
Method
                  BLASTX
NCBI GI
                  g3776581
BLAST score
                  249
E value
                  7.0e-22
```

Match length 70 % identity 61

NCBI Description (AC005388) Similar to Beta integral membrane protein

homolog gb_U43629 from A. thaliana. [Arabidopsis thaliana]

Seq. No. 311241

Seq. ID uwc700153714.h1

Method BLASTX

```
NCBI GI
                  g2191135
BLAST score
                  152
E value
                  2.0e-10
Match length
                  47
                  51
% identity
                  (AF007269) A IG002N01.14 gene product [Arabidopsis
NCBI Description
                  thaliana]
                  311242
Seq. No.
                  uwc700153742.h1
Seq. ID
Method
                  BLASTX
                  g1498053
NCBI GI
BLAST score
                  302
E value
                  5.0e-28
Match length
                  75
% identity
                  81
NCBI Description (U64436) ribosomal protein S8 [Zea mays]
                  311243
Seq. No.
                  uwc700153780.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3928543
BLAST score
                  206
E value
                  7.0e-17
Match length
                  69
% identity
                  52
NCBI Description
                  (AB016819) UDP-glucose glucosyltransferase [Arabidopsis
                  thaliana]
Seq. No.
                  311244
                  uwc700153786.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3821780
BLAST score
                  36
E value
                  5.0e-11
Match length
                  36
                  100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                  311245
Seq. No.
Seq. ID
                  uwc700153841.h1
Method
                  BLASTN
NCBI GI
                  g1063665
BLAST score
                  102
E value
                  1.0e-50
Match length
                  113
% identity
                  98
NCBI Description Zea mays unknown protein mRNA, complete cds
                  311246
Seq. No.
Seq. ID
                  uwc700153936.h1
```

Method BLASTX
NCBI GI g2190544
BLAST score 277
E value 5.0e-25
Match length 76
% identity 71



(AC001229) Similar to Saccharomyces hypothetical protein NCBI Description P9642.2 (gb U40828). [Arabidopsis thaliana] 311247 Seq. No. uwc700153967.h1 Seq. ID BLASTX Method q4581139 NCBI GI BLAST score 217 4.0e-18 E value 59 Match length 59 % identity (AC006919) putative ABC transporter [Arabidopsis thaliana] NCBI Description Seq. No. 311248 uwc700153989.h1 Seq. ID BLASTX Method g1632831 NCBI GI BLAST score 166 5.0e-12 E value Match length 35 % identity 89 (Z49698) orf [Ricinus communis] NCBI Description 311249 Seq. No. Seq. ID uwc700153991.hl Method BLASTN g3511235 NCBI GI BLAST score 36 5.0e-11 E value Match length 36 100 % identity Zea mays starch branching enzyme IIb (ae) gene, complete NCBI Description cds Seq. No. 311250 uwc700154089.h1 Seq. ID Method BLASTX g1871196 NCBI GI BLAST score 277 E value 5.0e-25 Match length 61 90 % identity (U90439) GMP kinase isolog [Arabidopsis thaliana] NCBI Description >gi 2335091 (AC002339) putative GMP kinase [Arabidopsis thaliana]

Seq. No. 311251

uwc700154150.h1 Seq. ID

Method BLASTX q4063760 NCBI GI BLAST score 147 E value 6.0e-10 Match length 59 47 % identity

(AC005561) putative POL3 protein [Arabidopsis thaliana] NCBI Description

Seq. No. 311252

Seq. ID

311257

uwc700154333.hl

```
uwc700154223.h1
Seq. ID
                  BLASTN
Method
                  g3821780
NCBI GI
                  36
BLAST score
                  4.0e-11
E value
Match length
                  36
                  100
% identity
                  Xenopus laevis cDNA clone 27A6-1
NCBI Description
                  311253
Seq. No.
                  uwc700154225.h1
Seq. ID
                  BLASTX
Method
                  g3287946
NCBI GI
BLAST score
                   232
                   7.0e-20
E value
                   69
Match length
                   68
% identity
                  PUTATIVE HELICASE C6F12.16 IN CHROMOSOME I
NCBI Description
                   >gi_2330862_emb_CAB11099_ (Z98533) putative rna helicase
                   [Schizosaccharomyces pombe]
                   311254
Seq. No.
                   uwc700154260.h1
Seq. ID
                   BLASTX
Method
                   g3776564
NCBI GI
                   151
BLAST score
                   2.0e-10
E value
Match length
                   42
% identity
                   64
                   (AC005388) Similar to hypothetical protein T1D16.16
NCBI Description
                   gi_3075397 from A. thaliana BAC gb_AC004484. [Arabidopsis
                   thaliana]
                   311255
Seq. No.
                   uwc700154264.h1
Seq. ID
                   BLASTX
Method
                   g3047117
NCBI GI
BLAST score
                   229
                   2.0e-19
E value
Match length
                   46
                   96
% identity
                   (AF058919) similar to ATP-dependent RNA helicases
NCBI Description
                   [Arabidopsis thaliana]
                   311256
Seq. No.
                   uwc700154328.h1
Seq. ID
                   BLASTX
Method
                   q4210330
NCBI GI
BLAST score
                   369
                   7.0e-36
E value
Match length
                   77
                   90
% identity
                   (AJ223802) 2-oxoglutarate dehydrogenase, E1 subunit
NCBI Description
                   [Arabidopsis thaliana]
```

```
BLASTX
Method
NCBI GI
                  q1514643
                  161
BLAST score
                  1.0e-11
E value
                  50
Match length
                   66
% identity
                  (Z70524) PDR5-like ABC transporter [Spirodela polyrrhiza]
NCBI Description
                   311258
Seq. No.
                  uwc700154401.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2655098
BLAST score
                   196
                   1.0e-15
E value
                   69
Match length
                   58
% identity
NCBI Description (AF023472) peptide transporter [Hordeum vulgare]
                   311259
Seq. No.
                   uwc700154406.h1
Seq. ID
                   BLASTX
Method
                   g2522195
NCBI GI
                   246
BLAST score
                   8.0e-27
E value
Match length
                   72
                   82
% identity
                   (AF022915) ornithine/acetylornithine aminotransferase
NCBI Description
                   [Triticum aestivum]
                   311260
Seq. No.
                   uwc700154438.h1
Seq. ID
                   BLASTX
Method
                   g3746071
NCBI GI
BLAST score
                   232
                   7.0e-20
E value
Match length
                   61
                   72
% identity
                   (AC005311) putative GTP-binding protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   311261
                   uwc700154550.h1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g3821780
BLAST score
                   36
                   5.0e-11
E value
                   36
Match length
                   100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                   311262
                   uwc700154563.hl
Seq. ID
                   BLASTX
Method
```

44387

g1870700

217 4.0e-18

43

NCBI GI BLAST score

E value Match length



```
% identity
  NCBI Description (U84116) cleavage stage histone H3 [Psammechinus miliaris]
                     311263
  Seq. No.
                     uwc700154568.h1
  Seq. ID
                     BLASTX
  Method
  NCBI GI
                     g2262100
                     298
  BLAST score
                     2.0e-27
  E value
                     72
  Match length
                     78
  % identity
  NCBI Description (AC002343) unknown protein [Arabidopsis thaliana]
  Seq. No.
                     311264
                     uwc700154595.h1
  Seq. ID
                     BLASTN
  Method
                     g559535
  NCBI GI
                     203
  BLAST score
                     1.0e-110
  E value
                     231
  Match length
                     97
  % identity
  NCBI Description Z.mays mRNA for metallothionein
                     311265
  Seq. No.
                     uwc700154672.h1
  Seq. ID
                     BLASTN
  Method
                     g3821780
  NCBI GI
                      36
  BLAST score
                      5.0e-11
  E value
  Match length
                      36
                     100
  % identity
  NCBI Description Xenopus laevis cDNA clone 27A6-1
                      311266
  Seq. No.
                      uwc700154676.h1
  Seq. ID
  Method
                      BLASTX
  NCBI GI
                      q4588008
                      163
  BLAST score
                      1.0e-11
  E value
  Match length
                      66
  % identity
                      45
                     (AF085279) hypothetical protein [Arabidopsis thaliana]
  NCBI Description
                      311267
  Seq. No.
                      uwc700154839.h1
  Seq. ID
  Method
                      BLASTX
                      g3024018
  NCBI GI
                      314
  BLAST score
  E value
                      2.0e-29
                      59
  Match length
% identity
                      100
                      INITIATION FACTOR 5A (EIF-5A) (EIF-4D)
  NCBI Description
                      >gi_1546919_emb_CAA69225_ (Y07920) translation initiation factor 5A [Zea mays] >gi_2668738 (AF034943) translation
```

initiation factor 5A [Zea mays]



```
uwc700154859.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3122357
                  171
BLAST score
                  2.0e-12
E value
Match length
                   49
                   67
% identity
                  PUTATIVE LIPOATE-PROTEIN LIGASE B (LIPOATE BIOSYNTHESIS
NCBI Description
                  PROTEIN B) >gi_2494127 (AC002376) Contains similarity to
                  Mycobacterium LIPB gene (gb_Q104041). [Arabidopsis
                  thaliana]
                  311269
Seq. No.
Seq. ID
                  uwc700154866.h1
Method
                  BLASTX
NCBI GI
                  g2811226
BLAST score
                  153
                  2.0e-10
E value
Match length
                   41
% identity
                  73
                   (AF042669) fimbrin 2 [Arabidopsis thaliana] >gi_2811232
NCBI Description
                   (AF042671) fimbrin 2 [Arabidopsis thaliana]
                   311270
Seq. No.
                  uwc700154895.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g4587550
BLAST score
                   169
                   3.0e-12
E value
Match length
                   76
% identity
                   43
                   (AC006577) EST gb R64848 comes from this gene. [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   311271
Seq. ID
                   uwc700154952.h1
Method
                  BLASTX
                   g4454466
NCBI GI
BLAST score
                   189
                   1.0e-14
E value
Match length
                   47
                   70
% identity
                  (AC006234) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   311272
                   uwc700154956.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4006827
BLAST score
                   152
E value
                   3.0e-10
Match length
                   58
                   50
% identity
NCBI Description
                  (AC005970) subtilisin-like protease [Arabidopsis thaliana]
```

Seq. ID uwc700154958.h1

Method BLASTX

```
q2827143
NCBI GI
BLAST score
                   269
                   5.0e-24
E value
                   67
Match length
% identity
                   73
NCBI Description
                   (AF027174) cellulose synthase catalytic subunit
                   [Arabidopsis thaliana]
Seq. No.
                   311274
Seq. ID
                   uwc700154978.h1
Method
                   BLASTX
NCBI GI
                   g3962377
BLAST score
                   290
E value
                   2.0e-26
Match length
                   55
% identity
                   98
NCBI Description
                   (AJ002551) heat shock protein 70 [Arabidopsis thaliana]
Seq. No.
                   311275
Seq. ID
                   uwc700155006.h1
Method
                   BLASTX
NCBI GI
                   q1408460
BLAST score
                   198
E value
                   9.0e-16
Match length
                   42
                   88
% identity
NCBI Description
                   (U40161) type 2A protein serine/threonine phosphatase 55
                   kDa B regulatory subunit [Arabidopsis thaliana]
Seq. No.
                   311276
Seq. ID
                   uwc700155029.h1
Method
                   BLASTX
NCBI GI
                   g113621
BLAST score
                   283
E value
                   8.0e-26
Match length
                   56
% identity
                   100
NCBI Description
                   FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME
                   >gi 68196 pir ADZM fructose-bisphosphate aldolase (EC
                   4.1.2.13), cytosolic - maize >gi_168420 (M16220) aldolase [Zea mays] >gi_295850 emb_CAA31366 (X12872) fructose
                   bisphosphate aldolase [Zea mays] >gi 225624 prf 1307278A
                   cytoplasmic aldolase [Zea mays]
Seq. No.
                   311277
Seq. ID
                   uwc700155036.h1
```

Method BLASTX NCBI GI g3738297 BLAST score 145 E value 1.0e-09 Match length 49 27 % identity

NCBI Description (AC005309) unknown protein [Arabidopsis thaliana]

Seq. No.

Seq. ID uwc700155038.h1

311278

Method BLASTN

```
NCBI GI
                   g1296954
BLAST score
                   39
                   6.0e-13
E value
                   84
Match length
% identity
                  96
NCBI Description O.sativa mRNA for novel protein, osr40c1
                   311279
Seq. No.
                  uwc700155054.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1718235
BLAST score
                   75
E value
                   3.0e-34
Match length
                   231
% identity
                   83
NCBI Description
                  Hordeum vulgare (1,4)-beta-xylan endohydrolase isoenzyme
                  X-I mRNA, complete cds
Seq. No.
                   311280
                   uwc700155104.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1345588
BLAST score
                   235
E value
                   2.0e-23
Match length
                   65
% identity
                   98
NCBI Description
                  14-3-3-LIKE PROTEIN GF14-12 >gi 998432 bbs 164524
                   GF14-12=GRF2 product/14-3-3 protein homolog [Zea mays,
                  XL80, Peptide, 261 aa]
                   311281
Seq. No.
Seq. ID
                   uwc700155165.h1
Method
                   BLASTN
NCBI GI
                   q293888
BLAST score
                   92
E value
                   1.0e-44
Match length
                   163
% identity
                   96
NCBI Description
                  Zea mays, qlyceraldehyde-3-phosphate dehydrogenase mRNA, 3'
                   end (clone GAPC2)
                   311282
Seq. No.
                   uwc700155173.h1
Seq. ID
Method
                  BLASTX
                   g3150414
NCBI GI
BLAST score
                   167
E value
                   3.0e-12
Match length
                   42
                   74
% identity
NCBI Description
                  (AC004165) AtRanBP1b protein [Arabidopsis thaliana]
```

Seq. ID uwc700155224.h1

Method BLASTX NCBI GI g3183989 BLAST score 189 E value 9.0e-15



```
Match length
                   52
% identity
                  (AJ005172) P69E protein [Lycopersicon esculentum]
NCBI Description
                   311284
Seq. No.
Seq. ID.
                   uwc700155247.h1
Method
                  BLASTX
NCBI GI
                   q4582924
                   323
BLAST score
                   2.0e-30
E value
Match length
                   72
% identity
                   83
                  (AF047842) phosphoglycerate mutase [Solanum tuberosum]
NCBI Description
                   311285
Seq. No.
Seq. ID
                   uwc700155313.h1
                   BLASTX
Method
                   g632500
NCBI GI
                   140
BLAST score
                   6.0e-09
E value
Match length
                   31
                   77
% identity
                   (U17394) polyadenylation factor 64 kDa subunit [Xenopus
NCBI Description
                   laevis]
Seq. No.
                   311286
                   uwc700155357.h1
Seq. ID
                   BLASTN
Method
                   g517257
NCBI GI
BLAST score
                   56
E value
                   5.0e-23
Match length
                   91
                   91
% identity
NCBI Description Z.mays MNB1a mRNA for DNA-binding protein
Seq. No.
                   311287
Seq. ID
                   uwc700155406.h1
Method
                   BLASTX
NCBI GI
                   g1845197
BLAST score
                   215
                   9.0e-18
E value
Match length
                   48
% identity
                   85
NCBI Description
                  (Y08298) HMGc2 [Zea mays]
Seq. No.
                   311288
Seq. ID
                   uwc700155465.hl
Method
                   BLASTX
                   g3451079
NCBI GI
BLAST score
                   138
```

7.0e-09 E value 49 Match length 55 % identity

(AL031326) putative protein [Arabidopsis thaliana] NCBI Description

311289 Seq. No.

uwc700155540.h1 Seq. ID

Match length

```
BLASTX
Method
NCBI GI
                  q4371296
BLAST score
                  176
E value
                  2.0e-13
Match length
                  68
% identity
                  50
                   (AC006260) putative receptor protein kinase [Arabidopsis
NCBI Description
                  thaliana]
                  311290
Seq. No.
Seq. ID
                  uwc700155609.h1
Method
                  BLASTX
                  q4165488
NCBI GI
BLAST score
                  315
                  2.0e-29
E value
                  79
Match length
% identity
                  78
                  (AJ132399) alpha-tubulin 3 [Hordeum vulgare]
NCBI Description
Seq. No.
                  311291
Seq. ID
                  uwc700155647.h1
Method
                  BLASTN
NCBI GI
                  g3821780
BLAST score
                  36
E value
                  5.0e-11
Match length
                  36
% identity
                  100
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                  311292
Seq. ID
                  uwc700155682.h1
Method
                  BLASTX
NCBI GI
                  g3256035
BLAST score
                  311
E value
                  5.0e-29
                  63
Match length
                  100
% identity
NCBI Description
                  (Y14274) putative serine/threonine protein kinase [Sorghum
                  bicolor]
                  311293
Seq. No.
Seq. ID
                  uwc700155703.h1
Method
                  BLASTX
NCBI GI
                  g1669599
BLAST score
                  152
                  2.0e-10
E value
                  78
Match length
% identity
                  42
NCBI Description (D88746) AR791 [Arabidopsis thaliana]
Seq. No.
                  311294
Seq. ID
                  uwc700155750.h1
Method
                  BLASTX
                  g1346197
NCBI GI
BLAST score
                  321
E value
                  4.0e-30
```

```
% identity
NCBI Description GLUTATHIONE REDUCTASE, CYTOSOLIC (GR) (GRASE)
                   311295
Seq. No.
Seq. ID
                   uwc700155760.h1
Method
                  BLASTX
                   g4510396
NCBI GI
BLAST score
                   255
E value
                   2.0e-22
Match length
                  82
% identity
                   56
NCBI Description (AC006587) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   311296
Seq. ID
                  uwc700155766.h1
Method
                  BLASTN
NCBI GI
                   g1648930
BLAST score
                   201
E value
                   1.0e-109
Match length
                   222
% identity
                   97
NCBI Description Z.mays mRNA for Hox1b protein
Seq. No.
                   311297
Seq. ID
                  uwc700155775.h1
Method
                  BLASTX
                                                                    - 2
NCBI GI
                  q3096922
BLAST score
                   238
E value
                   2.0e-20
Match length
                   66
% identity
                  73
NCBI Description (AL023094) putative protein [Arabidopsis thaliana]
Seq. No.
                  311298
Seq. ID
                  uwc700155806.h1
Method
                  BLASTX
NCBI GI
                  g4510406
BLAST score
                  147
E value
                  7.0e-10
Match length
                  58
% identity
                  53
NCBI Description (AC006587) putative protein kinase [Arabidopsis thaliana]
Seq. No.
                  311299
Seq. ID
                  uwc700155821.h1
Method
                  BLASTN
NCBI GI
                  g2062691
BLAST score
                  33
E value
                  3.0e-09
Match length
                  33
```

cds

NCBI Description

% identity

Seq. No. 311300
Seq. ID uwc700155886.h1

100

Method BLASTX

44394

Human sodium phosphate transporter (NPT4) mRNA, complete

```
q3386605
NCBI GI
BLAST score
                  210
                  3.0e-17
E value
                  78
Match length
% identity
                  60
NCBI Description (AC004665) hypothetical protein [Arabidopsis thaliana]
                  311301
Seq. No.
                  uwc700155912.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4006827
BLAST score
                  141
E value
                  3.0e-09
Match length
                  36
% identity
                  78
NCBI Description (AC005970) subtilisin-like protease [Arabidopsis thaliana]
Seq. No.
                  311302
Seq. ID
                  uwc700155991.h1
Method
                  BLASTX
NCBI GI
                  q4371279
BLAST score
                  206
E value
                  1.0e-16
Match length
                  74
% identity
NCBI Description (AC006260) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  311303
Seq. ID
                  uwc700156007.h1
Method
                  BLASTN
NCBI GI
                  g998429
BLAST score
                  97
E value
                  1.0e-47
Match length
                  151
% identity
                  98
                  GRF1=general regulatory factor [Zea mays, XL80, Genomic,
NCBI Description
                  5348 nt]
Seq. No.
                  311304
Seq. ID
                  uwc700156087.h1
Method
                  BLASTX
NCBI GI
                  g4234852
BLAST score
                  195
E value
                  2.0e-15
                  73
Match length
% identity
                  70
NCBI Description (AF082133) gag-pol polyprotein [Zea mays]
                  311305
```

Seq. ID uwc700156113.h2

Method BLASTN NCBI GI g758352 BLAST score 103 2.0e-51 E value Match length 103 100 % identity

NCBI Description Z.mays mRNA for cysteine synthase

```
Seq. No.
                   311306
Seq. ID
                   uwc700156119.h2
Method
                   BLASTX
NCBI GI
                   g4584521
BLAST score
                   225
E value
                   7.0e-19
Match length
                   78
% identity
                   50
NCBI Description
                   (AL049607) putative protein [Arabidopsis thaliana]
Seq. No.
                   311307
Seq. ID
                   uwc700156151.h1
Method
                   BLASTX
NCBI GI
                   q461929
BLAST score
                   198
E value
                   6.0e-16
Match length
                   46
% identity
                   87
NCBI Description
                   PROBABLE TONOPLAST INTRINSIC PROTEIN DIP
                   >gi_1076688_pir__S51781 integral membrane protein - garden
                   snapdragon >gi_414088_emb CAA49854 (X70417) integral
                   membrane protein [Antirrhinum majus]
Seq. No.
                   311308
Seq. ID
                   uwc700156160.h1
Method
                   BLASTX
NCBI GI
                   q2465925
BLAST score
                   194
E value
                   3.0e-15
Match length
                   61
% identity
                   61
NCBI Description
                   (AF024649) receptor-like serine/threonine kinase
                   [Arabidopsis thaliana]
Seq. No.
                   311309
Seq. ID
                   uwc700156185.h1
Method
                  BLASTX
NCBI GI
                   g4455182
BLAST score
                   223
E value
                  1.0e-18
Match length
                  59
% identity
                  58
NCBI Description
                  (AL035521) putative protein [Arabidopsis thaliana]
Seq. No.
                  311310
Seq. ID
                  uwc700156312.h1
Method
                  BLASTX
NCBI GI
                  g1181331
BLAST score
                  444
E value
                  1.0e-44
Match length
                  76
% identity
                  99
NCBI Description
                  (X77569) calnexin [Zea mays]
Seq. No.
                  311311
Seq. ID
                  uwc700156315.h1
```

```
Method
                   BLASTX
NCBI GI
                   q1351945
BLAST score
                   174
E value
                   5.0e-13
Match length
                   49
                   63
% identity
NCBI Description
                  FLORAL HOMEOTIC PROTEIN APETALA2 >gi 533709 (U12546)
                  APETALA2 protein [Arabidopsis thaliana]
                   >gi_2464888_emb_CAB16765.1 (Z99707) APETALA2 protein
                   [Arabidopsis thaliana]
Seq. No.
                   311312
Seq. ID
                  uwc700156336.hl
Method
                  BLASTN
NCBI GI
                   q440170
BLAST score
                   212
E value
                   1.0e-116
Match length
                   220
% identity
                   99
NCBI Description
                  Z.mays (C6000237) trpA gene
                   311313
Seq. No.
Seq. ID
                  uwc700156361.h1
Method
                  BLASTX
NCBI GI
                   g3122673
BLAST score
                   192
E value
                   3.0e-15
Match length
                   37
                   92
% identity
NCBI Description
                  60S RIBOSOMAL PROTEIN L15 >gi 2245027 emb CAB10447
                   (Z97341) ribosomal protein [Arabidopsis thaliana]
Seq. No.
                   311314
Seq. ID
                   uwc700156367.h1
Method
                   BLASTX
NCBI GI
                   g1491931
BLAST score
                   347
E value
                   3.0e-33
Match length
                   78
% identity
                   77
NCBI Description
                  (U52078) kinesin-like protein [Nicotiana tabacum]
Seq. No.
                   311315
Seq. ID
                   uwh700207103.h1
Method
                  BLASTX
NCBI GI
                   q2498077
BLAST score
                   237
E value
                   3.0e-20
Match length
                   43
% identity
                   100
NCBI Description
                  NUCLEOSIDE DIPHOSPHATE KINASE I (NDK I) (NDP KINASE I)
```

(PP18) >gi 1777930 (U55019) nucleoside diphosphate kinase

[Saccharum officinarum]

Seq. No.

311316 Seq. ID uwh700207116.h1

Method BLASTX

```
g266944
NCBI GI
                  209
BLAST score
                  7.0e-17
E value
Match length
                  75
                  57
% identity
                  60S RIBOSOMAL PROTEIN L2 (L8) (RIBOSOMAL PROTEIN TL2)
NCBI Description
                  >gi_71078_pir__R5TOL8 ribosomal protein L8, cytosolic -
                  tomato >gi 19343 emb CAA45863 (X64562) ribosomal protein
                  L2 [Lycopersicon esculentum]
                  311317
Seq. No.
                  uwh700207130.h1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2065531
BLAST score
                  429
                  1.0e-42
E value
Match length
                  89
                  85
% identity
                  (U78526) endo-1,4-beta-glucanase [Lycopersicon esculentum]
NCBI Description
Seq. No.
                  311318
                uwh700207144.h1
Seq. ID
                  BLASTX
Method
                  g3023535
NCBI GI
BLAST score
                  197
                  2.0e-15
E value
Match length
                  54
                  69
% identity
                  MOLYBDOPTERIN BIOSYNTHESIS CNX2 PROTEIN (MOLYBDENUM
NCBI Description
                  COFACTOR BIOSYNTHESIS ENZYME CNX2) >gi_662871_emb_CAA88107_
                  (Z48047) Cnx2 [Arabidopsis thaliana]
                  311319
Seq. No.
                  uwh700207177.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g444044
BLAST score
                  127
E value
                  2.0e-65
Match length
                  177
                  93
% identity
                  Z.mays mRNA for group 3 Lea protein MGL3
NCBI Description
                  >gi_452559_gb_U05226_ZMU05226 Zea mays group 3 Lea protein
                  MGL3 mRNA, complete cds. >gi_454872_dbj_D26552_MZEG3LP
                  Maize mRNA for group 3 Lea protein MGL3, complete cds
```

Seq. ID uwh700207179.h1

Method BLASTX
NCBI GI g2589162
BLAST score 465
E value 7.0e-47
Match length 98
% identity 98

NCBI Description (D88451) aldehyde oxidase [Zea mays]

Seq. No. 311321

Seq. ID uwh700207182.h1

```
Method
NCBI GI
                  q3281846
BLAST score
                  146
E value
                  8.0e-10
                  35
Match length
                  74
% identity
NCBI Description
                  (AJ006404) late elongated hypocotyl [Arabidopsis thaliana]
Seq. No.
                  311322
                  uwh700207257.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g444046
BLAST score
                  68
E value
                  2.0e-30
Match length
                  100
                  92
% identity
NCBI Description Z.mays OBF1 mRNA for ocs-element binding factor
Seq. No.
                  311323
                  uwh700207272.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4539298
BLAST score
                  165
                  5.0e-12
E value
Match length
                  40
% identity
                  78
                  (AL049480) putative calmodulin-binding protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  311324
                  uwn700281629.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g22123
BLAST score
                  35
                  2.0e-10
E value
Match length
                  103
% identity
                  42
NCBI Description Maize alcohol dehydrogenase 1 gene (Adh1-1S)
Seq. No.
                  311325
                  uwn700281764.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2286121
BLAST score
                  168
E value
                  2.0e-12
Match length
                  51
                  63
% identity
NCBI Description
                  (U88068) sec14 like protein [Oryza sativa]
```

Seq. ID uwn700281787.h1

Method BLASTX
NCBI GI g3249105
BLAST score 144
E value 4.0e-09
Match length 63
% identity 44



```
(AC003114) Contains similarity to protein phosphatase 2C
NCBI Description
                  (ABI1) gb_X78886 from A. thaliana. [Arabidopsis thaliana]
                  311327
Seq. No.
                  vfk700404710.hl
Seq. ID
                  BLASTN
Method
                  g3983662
NCBI GI
BLAST score
                  35
                  8.0e-11
E value
                  51
Match length
% identity
NCBI Description Oryza sativa mRNA for importin-betal, complete cds
Seq. No.
                  311328
                  vfk700404717.hl
Seq. ID
                  BLASTX
Method
                  g3421413
NCBI GI
BLAST score
                  200
                  5.0e-16
E value
                  46
Match length
                  80
% identity
                   (AF081922) protein phosphatase 2A 55 kDa B regulatory
NCBI Description
                  subunit [Oryza sativa] >gi_3421415 (AF081923) protein
                  phosphatase 2A 55 kDa B regulatory subunit [Oryza sativa]
Seq. No.
                  311329
                  vfk700404737.hl
Seq. ID
                  BLASTX
Method
                  g430947
NCBI GI
                   234
BLAST score
                   4.0e-20
E value
                   51
Match length
                   88
% identity
                   (U01103) PSI type III chlorophyll a/b-binding protein
NCBI Description
                   [Arabidopsis thaliana]
                   311330
Seq. No.
                   vfk700404757.h1
Seq. ID
                   BLASTN
Method
                   g22272
NCBI GI
                   89
BLAST score
                   5.0e-43
E value
                   100
Match length
                   98
% identity
NCBI Description Maize mRNA for enolase (2-phospho-D-glycerate hydrolase)
                   311331
Seq. No.
                   vfk700404768.hl
Seq. ID
Method
                   BLASTN
```

NCBI GI g949979
BLAST score 46
E value 7.0e-17
Match length 69
% identity 91

NCBI Description Z.mays Glossy2 locus DNA

Seq. No. 311332

```
Seq. ID
                   vfk700404810.h1
Method
                   BLASTX
NCBI GI
                   g1172836
BLAST score
                   304
E value
                   6.0e-31
Match length
                   70
% identity
                   97
                  GTP-BINDING NUCLEAR PROTEIN RAN-B1 >gi_496272 (L16787)
NCBI Description
                   small ras-related protein [Nicotiana tabacum]
Seq. No.
                   311333
Seq. ID
                   vfk700404832.h1
Method
                  BLASTN
NCBI GI
                   q625147
BLAST score
                   157
E value
                   3.0e-83
Match length
                   225
                                                     Ġ,
% identity
                   93
NCBI Description
                  Zea mays protein disulfide isomerase (pdi) mRNA, complete
Seq. No.
                  311334
Seq. ID
                  vfk700404896.h1
Method
                  BLASTX
NCBI GI
                  g2642158
BLAST score
                  177
E value
                  4.0e-13
Match length
                  83
% identity
                  48
NCBI Description
                  (AC003000) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  311335
Seq. ID
                  vmj700053764.r1
Method
                  BLASTX
NCBI GI
                  g1170619
BLAST score
                  205
                                               ķ.,
E value
                  1.0e-16
Match length
                  96
% identity
                  48
NCBI Description
                  KINESIN-LIKE PROTEIN A >gi_479594_pir___S34830
                  kinesin-related protein katA - Arabidopsis thaliana
```

>gi_303502_dbj_BAA01972_ (D11371) kinesin-like motor

protein heavy chain [Arabidopsis thaliana]

>gi_2911084_emb_CAA17546.1_ (AL021960) kinesin-related

protein katA [Arabidopsis thaliana]

Seq. No. 311336

Seq. ID vmj700053769.r1

Method BLASTX NCBI GI g4371296 BLAST score 192 E value 6.0e-15 Match length 68 % identity 51

NCBI Description (AC006260) putative receptor protein kinase [Arabidopsis

thaliana]

```
135-
                  311337
Seq. No.
Seq. ID
                  vmj700053801.rl
                  BLASTX
Method
NCBI GI
                  g2160166
BLAST score
                  218
                  6.0e-18
E value
                  97
Match length
                  46
% identity
                  (ACO00132) No definition line found [Arabidopsis thaliana]
NCBI Description
                  311338
Seq. No.
                  vqh700053156.rl
Seq. ID
                  BLASTX
Method
                  q2119719
NCBI GI
                  271
BLAST score
                  3.0e-24
E value
                  59
Match length
% identity
                  86
                  heat-shock cognate protein 70-3 - tomato >gi 762844
NCBI Description
                   (L41253) Hsc70 [Lycopersicon esculentum]
Seq. No.
                  311339
                  vqh700053189.rl
Seq. ID
Method
                  BLASTX
                  q231675
NCBI GI
                  144
BLAST score
                  2.0e-09
E value
Match length
                  41
                  63
% identity
                  CINNAMYL-ALCOHOL DEHYDROGENASE (CAD) >gi 282955 pir S23525
NCBI Description
                  cinnamyl-alcohol dehydrogenase (EC 1.1.1.195) - common
                  tobacco >gi_19839_emb_CAA44216_ (X62343) cinnamyl-alcohol
                  dehydrogenase [Nicotiana tabacum]
                  311340
Seq. No.
                  vqh700053232.r1
Seq. ID
                  BLASTX
Method
                  g2829895
NCBI GI
BLAST score
                  314
                  3.0e-29
E value
                  88
Match length
                   62
% identity
                  (AC002311) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  311341
Seq. No.
                  vqh700053248.r1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4454051
BLAST score
                  207
```

6.0e-17 E value Match length 52 73 % identity

(AL035394) putative polygalacturonase [Arabidopsis NCBI Description

thaliana]

Seq. No. 311342

Seq. ID vux700156477.h1

BLAST score

E value

139

2.0e-72

```
Method
                   BLASTN
                   g1707867
NCBI GI
BLAST score
                   90
E value
                   2.0e-43
Match length
                   90
% identity
                   100
NCBI Description Z.mays mRNA for 40S ribosomal subunit protein S21
                   311343
Seq. No.
Seq. ID
                   vux700156542.h1
Method
                   BLASTX
NCBI GI
                   q4138647
BLAST score
                   192
E value
                   3.0e-15
Match length
                   73
% identity
                   52
NCBI Description (AJ011939) peroxidase [Trifolium repens]
Seq. No.
                   311344
Sea. ID
                   vux700156628.h1
Method
                   BLASTX
NCBI GI
                   q2914706
BLAST score
                   220
E value
                   6.0e-22
Match length
                   80
                   60
% identity
NCBI Description (AC003974) putative homeobox protein [Arabidopsis thaliana]
Seq. No.
                   311345
Seq. ID
                   vux700156658.h1
Method
                   BLASTX
NCBI GI
                   g4262162
BLAST score
                   155
                   8.0e-11
E value
Match length
                   50
                   56
% identity
                   (AC005275) putative glycosylation enzyme [Arabidopsis
NCBI Description
                   thaliana]
                   311346
Seq. No.
                   vux700156660.h1
Seq. ID
Method
                   BLASTX
                   g2129946
NCBI GI
BLAST score
                   332
                   2.0e-31
E value
                   78
Match length
% identity
                   86
                   ADP-ribosylation factor homolog GTP-binding protein NTGB1 -
NCBI Description
                   common tobacco (fragment) >gi_1184987 (U46927) NTGB1
                   [Nicotiana tabacum]
Seq. No.
                   311347
Seq. ID
                   vux700156730.h1
Method
                   BLASTN
                   g168487
NCBI GI
```

```
Match length
                  94
% identity
NCBI Description Maize glutathione S-transferase gene (GST-I), exons 2 and 3
                  311348
Seq. No.
                  vux700156744.h1
Seq. ID
```

Method BLASTX NCBI GI g1769887 247 BLAST score 2.0e-21 E value Match length 76

% identity 61

(X95736) amino acid permease 6 [Arabidopsis thaliana] NCBI Description

311349 Seq. No. vux700156775.h1 Seq. ID

Method BLASTX g3319876 NCBI GI 188 BLAST score 2.0e-14 E value 39 Match length 85 % identity

(AJ007791) Msh3 protein [Arabidopsis thaliana] NCBI Description

311350 Seq. No.

vux700156779.hl Seq. ID

BLASTN Method g22176 NCBI GI BLAST score 33 E value 4.0e-09 53 Match length 91 % identity

NCBI Description Z.mays P gene

311351 Seq. No.

vux700156853.h1 Seq. ID

Method BLASTX NCBI GI g2500376 BLAST score 304 E value 4.0e-28 64 Match length 91 % identity

60S RIBOSOMAL PROTEIN L34 >gi 4262177 gb_AAD14494 NCBI Description

(AC005508) 23552 [Arabidopsis thaliana]

311352 Seq. No.

vux700156859.h1 Seq. ID

Method BLASTX g2224846 NCBI GI BLAST score 215 8.0e-18 E value 43 Match length 93 % identity

(Y13905) anionic peroxidase [Zea mays] NCBI Description

311353 Seq. No.

vux700156878.h1 Seq. ID

BLAST score

E value

365

8.0e-37

```
BLASTX
Method
NCBI GI
                  g2935573
BLAST score
                  242
E value
                   4.0e-21
Match length
                  83
% identity
                  67
NCBI Description (AF050180) KNOX class homeodomain protein [Oryza sativa]
Seq. No.
                  311354
Seq. ID
                  vux700156907.h1
Method
                  BLASTX
NCBI GI
                  g2183249
BLAST score
                   320
E value
                   5.0e-30
Match length
                  85
% identity
                  74
NCBI Description
                   (AF002211) glutathione-S-transferase [Triticum aestivum]
                  >gi 4185800 (AF109714) glutathione S-transferase [Triticum
                  aestivum]
                   311355
Seq. No.
Seq. ID
                  vux700156926.h1
Method
                  BLASTN
NCBI GI
                  g2443856
BLAST score
                  38
E value
                   2.0e-12
Match length
                  70
% identity
                   89
NCBI Description
                  Zea mays vacuolar sorting receptor homolog mRNA, partial
Seq. No.
                  311356
Seq. ID
                  vux700156994.h1
Method
                  BLASTX
NCBI GI
                  q3859116
                   408
BLAST score
E value
                  2.0e-40
Match length
                  86
% identity
                  91
NCBI Description (AF031609) unknown [Oryza sativa]
Seq. No.
                  311357
Seq. ID
                  vux700157015.h1
Method
                  BLASTX
NCBI GI
                  g4371280
                  143
BLAST score
E value
                  3.0e-09
Match length
                  38
                  76
% identity
NCBI Description (AC006260) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  311358
Seq. ID
                  vux700157051.h1
Method
                  BLASTX
NCBI GI
                  g1709000
```

```
Match length
% identity
                  86
                  S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
NCBI Description
                  ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                  >gi_960357_dbj_BAA09895_ (D63835) S-adenosylmethionine
                  synthetase [Hordeum vulgare]
                  311359
Seq. No.
                  vux700157117.h1
Seq. ID
Method
                  BLASTX
                  g485517
NCBI GI
BLAST score
                  388
E value
                  6.0e-38
Match length
                  85
% identity
                  84
NCBI Description ADP, ATP carrier protein - rice
Seq. No.
                  311360
                  vux700157156.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g550438
BLAST score
                  222
E value
                  1.0e-18
Match length
                  42
% identity
                  95
NCBI Description
                  (X81829) cytochrome P450 [Zea mays]
                  >gi 1870201 emb CAA72208 (Y11404) cytochrome p450 [Zea
Seq. No.
                  311361
Seq. ID
                  vux700157161.h1
Method
                  BLASTN
NCBI GI
                  q168436
BLAST score
                  60
E value
                  3.0e-25
Match length
                  96
% identity
                  91
NCBI Description Zea mays catalase (Cat3) gene, complete cds
Seq. No.
                  311362
                  vux700157186.hl
Seq. ID
Method
                  BLASTN
```

NCBI GI g3925232

BLAST score 40 E value 1.0e-13 Match length 52 % identity 94

NCBI Description Zea mays putative peroxidase P7X mRNA, partial cds

Seq. No. 311363 vux700157206.h1 Seq. ID Method BLASTX NCBI GI g4455275

335 BLAST score E value 1.0e-31 88 Match length % identity 73

Seq. ID

Method

```
NCBI Description (AL035527) putative protein [Arabidopsis thaliana]
Seq. No.
                  311364
Seq. ID
                  vux700157246.h1
Method
                  BLASTX
NCBI GI
                  q950299
BLAST score
                  241
E value
                   6.0e-21
Match length
                  56
                  82
% identity
NCBI Description
                  (L46792) xyloglucan endotransglycosylase precursor
                   [Actinidia deliciosa]
                   311365
Seq. No.
                  vux700157267.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1076294
BLAST score
                  312
                  5.0e-29
E value
Match length
                  87
% identity
                  66
NCBI Description ATAF2 protein - Arabidopsis thaliana
Seq. No.
                  311366
Seq. ID
                  vux700157321.h1
Method
                  BLASTX
                  q3367522
NCBI GI
BLAST score
                  286
E value
                   5.0e-26
Match length
                   67
                  76
% identity
NCBI Description
                   (AC004392) EST gb_T04691 comes from this gene. [Arabidopsis
                  thaliana]
Seq. No.
                  311367
Seq. ID
                  vux700157413.h1
Method
                  BLASTX
NCBI GI
                  q3582328
BLAST score
                  219
                   4.0e-18
E value
Match length
                  84
% identity
                  51
NCBI Description (AC005496) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   311368
                  vux700157573.h1
Seq. ID
Method
                  BLASTX
                  g1772601
NCBI GI
BLAST score
                  169
E value
                  2.0e-12
Match length
                  38
                  74
% identity
NCBI Description (Y09917) pSBGer3 [Triticum aestivum]
                  311369
Seq. No.
```

44407

vux700157578.h1

BLASTX



```
q4371284
NCBI GI
BLAST score
                  335
                  1.0e-31
E value
                  88
Match length
                  74
% identity
                  (AC006260) putative plasma membrane intrinsic protein 2B
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  311370
                  vux700157611.h1
Seq. ID
                  BLASTX
Method
                  g1172833
NCBI GI
BLAST score
                  471
                  1.0e-47
E value
Match length
                  87
                  98
% identity
                  GTP-BINDING NUCLEAR PROTEIN RAN-1 >gi_495729 (L16789) small
NCBI Description
                  ras-related protein [Arabidopsis thalīana]
                  >qi 2058278 emb CAA66047 (X97379) atran1 [Arabidopsis
                  thaliana]
                  311371
Seq. No.
                  vux700157622.h1
Seq. ID
                  BLASTN
Method
                  g22170
NCBI GI
                  130
BLAST score
                   5.0e-67
E value
                  270
Match length
                  87
% identity
NCBI Description Maize nuclear ARS2 DNA autonomously replicating in yeast
                   311372
Seq. No.
                   vux700157631.h1
Seq. ID
                  BLASTX
Method
NCBI GI
                   g3169059
                   305
BLAST score
                   4.0e-28
E value
Match length
                   93
                   66
% identity
                   (AL023704) weak similarity to B.subtilis spore outgrowth
NCBI Description
                   factor B [Schizosaccharomyces pombe]
                   311373
Seq. No.
                   vux700157637.h1
Seq. ID
Method
                   BLASTX
                   g927428
NCBI GI
BLAST score
                   273
                   4.0e-32
E value
Match length
                   87
                   76
% identity
                  (X86733) fis1 [Linum usitatissimum]
NCBI Description
Seq. No.
                   311374
                   vux700157702.h1
Seq. ID
```

44408

BLASTX

185

g2497219

Method NCBI GI

BLAST score



```
E value
                  4.0e-14
Match length
                  81
% identity
NCBI Description
                  HYPOTHETICAL 15.4 KD PROTEIN IN HAS1-JNM1 INTERGENIC REGION
                  >gi 626266 pir S47453 probable membrane protein YMR292w -
                  yeast (Saccharomyces cerevisiae) >gi_530349_emb_CAA56801_
                   (X80836) len:138, CAI:0.12, potential spliced gene,
                  hydropho bic composition [Saccharomyces cerevisiae]
Seq. No.
                  311375
Seq. ID
                  vux700157703.h1
Method
                  BLASTN
NCBI GI
                  q1657762
BLAST score
                  182
E value
                  4.0e-98
Match length
                  238
% identity
                  94
NCBI Description
                  Zea mays retrotransposon Huck-2 5' LTR and primer binding
                  site DNA sequence
Seq. No.
                  311376
Seq. ID
                  vux700157718.h1
Method
                  BLASTN
NCBI GI
                  q1154858
BLAST score
                  99
E value
                  1.0e-48
                  210
Match length
                  87
% identity
NCBI Description H.vulgare mRNA for L24 ribosomal protein
Seq. No.
                  311377
Seq. ID
                  vux700157760.h1
Method
                  BLASTX
NCBI GI
                  g1296955
BLAST score
                  315
E value
                  2.0e-29
Match length
                  59
% identity
                  47
NCBI Description
                  (X95402) duplicated domain structure protein [Oryza sativa]
Seq. No.
                  311378
Seq. ID
                  vux700157794.h1
Method
                  BLASTX
NCBI GI
                  g1495259
BLAST score
                  240
E value
                  1.0e-20
Match length
                  79
% identity
                  56
NCBI Description (X97826) orf04 [Arabidopsis thaliana]
Seq. No.
                  311379
                  vux700157860.h1
Seq. ID
```

Method BLASTX NCBI GI g2655098 2̃73 BLAST score 2.0e-24 E value Match length 84

NCBI Description

```
% identity
NCBI Description
                    (AF023472) peptide transporter [Hordeum vulgare]
                    311380
Seq. No.
Seq. ID
                    vux700157864.h1
Method
                    BLASTN
NCBI GI
                    g1213276
BLAST score
                    55
E value
                    3.0e-22
Match length
                    67
% identity
                    96
NCBI Description Z.mays ZEMa gene
Seq. No.
                    311381
Seq. ID
                    vux700157870.h1
Method
                    BLASTN
NCBI GI
                    g1931636
BLAST score
                    38
E value
                    4.0e-12
Match length
                    50
                    94
% identity
NCBI Description Arabidopsis thaliana BAC T19D16 genomic sequence
Seq. No.
                    311382
Seq. ID
                    vux700157919.h1
Method
                    BLASTX
NCBI GI
                    q4539660
BLAST score
                    387
E value
                    8.0e-38
Match length
                    86
% identity
                    80
NCBI Description
                    (AF061282) polyprotein [Sorghum bicolor]
Seq. No.
                    311383
Seq. ID
                    vux700158052.h1
Method
                    BLASTX
NCBI GI
                    g4102839
BLAST score
                    265
E value
                    2.0e-23
Match length
                    88
% identity
                    52
NCBI Description (AF016713) LeOPT1 [Lycopersicon esculentum]
Seq. No.
                    311384
Seq. ID
                    vux700158141.h1
Method
                    BLASTX
NCBI GI
                    g122087
BLAST score
                    368
E value
                    1.0e-35
Match length
                    76
% identity
                    99
                    HISTONE H3 >gi_81849_pir__S04520 histone H3 (clone pH3c-1) - alfalfa >gi_82609_pir__A26014 histone H3 - wheat >gi_19607_emb_CAA31964_ (X13673) histone H3 (AA 1-136)
```

44410

[Medicago sativa] >gi_19609_emb_CAA31965 (X13674) histone H3 (AA 1-136) [Medicago sativa] >gi_21797_emb_CAA25451_ (X00937) H3 histone [Triticum aestivum] >gi 488565 (U09459)



311385

histone H3.1 [Medicago sativa] >gi_2565419 (AF026803) histone H3 [Onobrychis viciifolia]

Seq. ID vux700158183.h1
Method BLASTX
NCBI GI g70774
BLAST score 300
E value 1.0e-27
Match length 61
% identity 98

Seq. No.

NCBI Description histone H4 (TH091) - wheat >gi_170747 (M12277) histone H4

[Triticum aestivum]

Seq. No. 311386

Seq. ID vux700158204.h1

Method BLASTX
NCBI GI g1491776
BLAST score 177
E value 2.0e-13
Match length 44
% identity 73

NCBI Description (M37636) cationic peroxidase [Arachis hypogaea]

Seq. No. 311387

Seq. ID vux700158280.h1

Method BLASTX
NCBI GI g3135543
BLAST score 261
E value 3.0e-23
Match length 74
% identity 70

NCBI Description (AF062393) aquaporin [Oryza sativa]

Seq. No. 311388

Seq. ID vux700158357.h1

Method BLASTX
NCBI GI g122022
BLAST score 205
E value 1.0e-16
Match length 59
% identity 82

NCBI Description HISTONE H2B >gi_283025_pir__S22323 histone H2B - wheat

>gi 21801 emb CAA42530 (X59873) histone H2B [Triticum

٠.`

aestivum]

Seq. No. 311389

Seq. ID vux700158374.h1

Method BLASTX
NCBI GI 94581143
BLAST score 150
E value 5.0e-10
Match length 83
% identity 36

NCBI Description (AC006919) hypothetical protein [Arabidopsis thaliana]

Seq. No. 311390



```
Seq. ID
                   vux700158493.h1
Method
                  BLASTN
NCBI GI
                   q4416300
BLAST score
                   103
E value
                   5.0e-51
Match length
                   199
% identity
                   88
NCBI Description
                  Zea mays chromosome 4 22 kDa zein-associated intercluster
                  region, complete sequence
Seq. No.
                   311391
Seq. ID
                   vux700158535.h1
Method
                  BLASTN
NCBI GI
                   q22233
BLAST score
                   80
E value
                   1.0e-37
Match length
                   105
% identity
                   92
NCBI Description
                  Maize mRNA for catalase
                   311392
Seq. No.
Seq. ID
                   vux700158543.h1
Method
                  BLASTX
NCBI GI
                   g445612
BLAST score
                   165
E value
                   4.0e-12
Match length
                   49
                   80
% identity
NCBI Description
                  ribosomal protein S19 [Solanum tuberosum]
Seq. No.
                   311393
Seq. ID
                   vux700158544.h1
Method
                  BLASTX
NCBI GI
                   g4586449
BLAST score
                   233
E value
                   7.0e-20
Match length
                   61
                  70
% identity
NCBI Description
                   (AB025187) cytochrome c oxidase subunit 6b-1 [Oryza sativa]
Seq. No.
                   311394
Seq. ID
                   vux700158555.h1
                  BLASTX
Method
NCBI GI
                   g4584346
BLAST score
                   204
E value
                  1.0e-16
Match length
                   45
                  73
% identity
NCBI Description
                  (AC007127) unknown protein [Arabidopsis thaliana]
Seq. No.
                  311395
Seq. ID
                  vux700158623.h1
                  BLASTX
Method
```

NCBI GI g1709923 BLAST score 324 E value 2.0e-30 Match length 86

```
% identity
                 PHOSPHORIBOSYLGLYCINAMIDE FORMYLTRANSFERASE PRECURSOR
NCBI Description
                  (GART) (GAR TRANSFORMYLASE) (5'-PHOSPHORIBOSYLGLYCINAMIDE
                  TRANSFORMYLASE) >gi_984818 (U30875) glycinamide
                  ribonucleotide transformylase (GART) [Vigna unguiculata]
                  311396
Seq. No.
```

Seq. ID vux700158693.h1 Method BLASTX g2194127 NCBI GI 229 BLAST score 2.0e-19 E value 81 Match length

57 % identity

(AC002062) Strong similarity to Arabidopsis receptor-like NCBI Description protein kinase (gb_ATLECGENE) and F20P5.16. [Arabidopsis

thaliana]

311397 Seq. No.

vux700158879.h1 Seq. ID

BLASTX Method g3192881 NCBI GI BLAST score 203 3.0e-16 E value 46 Match length 78 % identity

(AF068834) starch synthase [Ipomoea batatas] NCBI Description

311398 Seq. No.

vux700158971.h1 Seq. ID

BLASTX Method g3688205 NCBI GI 200 BLAST score 4.0e-16 E value Match length 49 78 % identity

(AJ010321) endopeptidase clp [Caulobacter crescentus] NCBI Description

311399 Seq. No.

vux700159049.h1 Seq. ID

BLASTN Method q2431766 NCBI GI 102 BLAST score 2.0e-50 E value Match length 102 100 % identity

Zea mays acidic ribosomal protein P3a (rpp3a) mRNA, NCBI Description

complete cds

311400 Seq. No.

vux700159089.h1 Seq. ID

Method BLASTX g1418331 NCBI GI BLAST score 334 E value 1.0e-31 82 Match length % identity 73



```
(X95909) receptor like protein kinase [Arabidopsis
NCBI Description
                  thaliana]
                  311401
Seq. No.
Seq. ID
                  vux700159184.h1
Method
                  BLASTX
NCBI GI
                  g1169533
BLAST score
                  139
E value
                  8.0e-09
Match length
                  49
                  63
% identity
                  ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
NCBI Description
                  (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE)
                  >gi 515827 emb CAA56645 (X80474) enolase [Neocallimastix
                  frontalis]
                  311402
Seq. No.
                                                         ¢
                  vux700159208.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3769673
BLAST score
                  248
E value
                  2.0e-21
Match length
                  86
% identity
                  47
NCBI Description (AF095285) Tic20 [Pisum sativum]
                  311403
Seq. No.
                  vux700159242.h1
Seq. ID
Method
                  BLASTX
                  g3287826
NCBI GI
BLAST score
                  194
E value
                  3.0e-15
Match length
                  80
                  47
% identity
NCBI Description
                  (+)-DELTA-CADINENE SYNTHASE ISOZYME C2 (D-CADINENE
                  SYNTHASE) >gi_2879841_emb_CAA76223.1_ (Y16432)
                  (+)-delta-cadinene synthase [Gossypium arboreum]
Seq. No.
                  311404
Seq. ID
                  vux700159305.h1
Method
                  BLASTX
NCBI GI
                  g1076283
BLAST score
                  383
E value
                  2.0e-37
Match length
                  82
                  83
% identity
                  adenylylsulfate kinase (EC 2.7.1.25) precursor -
NCBI Description
                  Arabidopsis thaliana >gi_414737_emb_CAA53426_ (X75782) APS
```

kinase [Arabidopsis thaliana] >gi_450235 (U05238) APS kinase [Arabidopsis thaliana] >gi_1575322 (U59759) APS kinase [Arabidopsis thaliana] >gi_3252812 (AC004705) APS

kinase [Arabidopsis thaliana]

311405 Seq. No.

Seq. ID vux700159355.h1

Method BLASTN NCBI GI g451192

% identity

56



```
BLAST score
E value
                   6.0e-19
Match length
                   145
% identity
                   83
NCBI Description Triticum aestivum (wali7) mRNA, 3' end, partial cds
                   311406
Seq. No.
Seq. ID
                   vux700159363.h1
Method
                   BLASTX
NCBI GI
                   q1353047
BLAST score
                   176
E value
                   2.0e-13
Match length
                   81
% identity
                   48
NCBI Description
                   HYPOTHETICAL 67.0 KD PROTEIN IN PRE3-SAG1 INTERGENIC REGION
                   >gi_1077861 pir S55189 hypothetical protein YJR002w -
                   yeast (Saccharomyces cerevisiae) >gi_854574_emb_CAA60923_
                   (X87611) ORF YJR83.5 [Saccharomyces cerevisiae]
                   >gi 1015622 emb CAA89524 (Z49502) ORF YJR002w
                   [Saccharomyces cerevisiae]
Seq. No.
                   311407
Seq. ID
                   vux700159368.h1
Method
                   BLASTX
                   g2583135
NCBI GI
BLAST score
                   223
E value
                   1.0e-18
Match length
                   49
                   90
% identity
                   (AC002387) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   >gi_3822216 (AF074948) FIL [Arabidopsis thaliana]
                   >gi 4322477 gb AAD16053 (AF087015) abnormal floral organs
                   protein [Arabidopsis thaliana]
Seq. No.
                   311408
Seq. ID
                   vux700159417.h1
Method
                   BLASTX
NCBI GI
                   q4056469
BLAST score
                   285
E value
                   3.0e-31
Match length
                   71
% identity
                   97
NCBI Description
                   (AC005990) Strong similarity to gb_M95166 ADP-ribosylation
                   factor from Arabidopsis thaliana. ESTs gb Z25826, gb R90191, gb N65697, gb AA713150, gb T46332, gb AA040967,
                   gb_AA712956, gb_T46403, gb_T46050, gb_AI100391 and
                   gb Z25043 come from t
Seq. No.
                   311409
Seq. ID
                   vux700159421.h1
Method
                   BLASTX
NCBI GI
                   g2118132
BLAST score
                   253
E value
                   3.0e-22
Match length
                   79
```

NCBI Description cysteine proteinase (EC 3.4.22.-) - Douglas fir >gi 1208549

BLAST score

E value Match length 286 5.0e-26

86



(U41902) Pseudotzain [Pseudotsuga menziesii]

Seq. No. 311410 vux700159494.h1 Seq. ID Method BLASTX NCBI GI g1709000 BLAST score 375 E value 1.0e-36 Match length 74 93 % identity NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1) >gi_960357_dbj_BAA09895_ (D63835) S-adenosylmethionine synthetase [Hordeum vulgare] 311411 Seq. No. vux700159496.h1 Seq. ID Method BLASTX g3928090 NCBI GI BLAST score 164 E value 6.0e-12 Match length 70 49 % identity NCBI Description (AC005770) putative MTN3 protein [Arabidopsis thaliana] Seq. No. 311412 vux700159507.h1 Seq. ID Method BLASTX NCBI GI q4406773 BLAST score 189 1.0e-14 E value Match length 93 % identity 42 NCBI Description (AC006836) putative cell division control protein 48 [Arabidopsis thaliana] Seq. No. 311413 Seq. ID vux700159524.h1 Method BLASTX NCBI GI q1352081 BLAST score 199 E value 2.0e-22 Match length 68 93 % identity NCBI Description BETA-GLUCOSIDASE, CHLOROPLAST PRECURSOR (GENTIOBIASE) (CELLOBIASE) (BETA-D-GLUCOSIDE GLUCOHYDROLASE) >gi 799377 (U25157) beta-D-glucosidase [Zea mays] >gi_1399390 (U44773) beta-D-glucosidase [Zea mays] >gi_4096602 (U33816) beta-D-glucosidase [Zea mays] Seq. No. 311414 Seq. ID vux700159601.h2 Method BLASTX NCBI GI g4115914

\$. .



% identity NCBI Description (AF118222) contains similarity to Iron/Ascorbate family of oxidoreductases (Pfam: PF00671, Score=297.8, E=1.3e-85, N=1) [Arabidopsis thaliana] >gi_4539410_emb_CAB40043.1_ (AL049524) putative Fe(II)/ascorbate oxidase [Arabidopsis thaliana]

Seq. No. 311415

Seq. ID vux700159730.h1

Method BLASTX NCBI GI g2459441 BLAST score 261 5.0e-23 E value Match length 88 % identity 55

(AC002332) putative SWI/SNF complex subunit BAF170 NCBI Description

[Arabidopsis thaliana]

Seq. No. 311416

vux700159881.h1 Seq. ID

BLASTX Method g2653446 NCBI GI BLAST score 371 E value 5.0e-36 Match length 81 % identity 85

NCBI Description (AB009077) proton pyrophosphatase [Vigna radiata]

311417 Seq. No.

Seq. ID vux700159896.h1

Method BLASTX g3075392 NCBI GI BLAST score 302 E value 7.0e-28 Match length 83 % identity 63

(AC004484) putative steroid dehydrogenase [Arabidopsis NCBI Description

thaliana]

Seq. No. 311418

Seq. ID vux700159929.h1

Method BLASTX NCBI GI g1170737 BLAST score 211 E value 3.0e-17 Match length 54 69 % identity

D-LACTATE DEHYDROGENASE >gi_1073978_pir__164134 D-lactate NCBI Description

dehydrogenase (dld) homolog - Haemophilus influenzae (strain Rd KW20) >gi_1574498 (U32838) D-lactate dehydrogenase (dld) [Haemophilus influenzae Rd]

Seq. No. 311419

vux700159935.h1 Seq. ID

Method BLASTX g987693 NCBI GI BLAST score 155

```
8.0e-23
E value
Match length
                  83
% identity
                  71
                  (D16685) lactate dehydrogenase [Oryza sativa]
NCBI Description
                  311420
Seq. No.
                  vux700160042.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3688156
BLAST score
                  327
E value
                  7.0e-31
Match length
                  66
% identity
                  85
NCBI Description
                  (AJ005587) gamma-glutamylcysteine synthetase [Brassica
                  juncea]
                  311421
Seq. No.
                  vux700160045.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2257755
BLAST score
                  37
                  1.0e-11
E value
Match length
                  45
% identity
                  96
NCBI Description
                  Zea mays nucleolar histone deacetylase HD2-p39 mRNA,
                  complete cds
Seq. No.
                  311422
Seq. ID
                  vux700160149.h1
Method
                  BLASTX
NCBI GI
                  g4454019
BLAST score
                  261
                   4.0e-23
E value
Match length
                  78
                   59
% identity
NCBI Description
                   (AL035396) SRG1-like protein [Arabidopsis thaliana]
Seq. No.
                   311423
Seq. ID
                   vux700160175.h1
Method
                  BLASTX
NCBI GI
                   q3023275
BLAST score
                   231
E value
                   1.0e-19
Match length
                   79
```

% identity 63

NCBI Description ALPHA-GLUCOSIDASE PRECURSOR (MALTASE)

>gi_2130027_pir__S65057 alpha-glucosidase (EC 3.2.1.20) - barley >gi_944901 (U22450) alpha-glucosidase [Hordeum

vulgare]

Seq. No. 311424

Seq. ID vux700160209.h1

Method BLASTX g2760328 NCBI GI BLAST score 146 E value 1.0e-09 Match length 86

```
% identity
NCBI Description
                  (AC002130) F1N21.13 [Arabidopsis thaliana]
                   311425
Seq. No.
Seq. ID
                   vux700160215.h1
Method
                   BLASTX
NCBI GI
                   q2129855
BLAST score
                   354
E value
                   6.0e-34
Match length
                   89
% identity
                   70
NCBI Description
                  mitogen-activated protein kinase MMK2 (EC 2.7.1.-) -
                   alfalfa
                   311426
Seq. No.
Seq. ID
                   vux700160226.h1
Method
                   BLASTX
NCBI GI
                   q2129636
BLAST score
                   161
                   2.0e-11
E value
Match length
                   86
% identity
                   41
NCBI Description
                   lipase - Arabidopsis thaliana >gi_1145627 (U38916) lipase
                   [Arabidopsis thaliana]
Seq. No.
                   311427-
Seq. ID
                   vux700160234.h1
Method
                   BLASTX
NCBI GI
                   q1353193
BLAST score
                   173
E value
                   9.0e-13
Match length
                   49
                   69
% identity
NCBI Description
                   O-METHYLTRANSFERASE ZRP4 (OMT) >gi_542186_pir__JQ2268
                   O-methyltransferase (EC 2.1.1.-) - maize \overline{>}gi \overline{40}4070
                   (L14063) O-methyltransferase [Zea mays]
Seq. No.
                   311428
Seq. ID
                   vux700160269.h1
Method
                   BLASTX
NCBI GI
                   g4115915
BLAST score
                   263
E value
                   2.0e-23
Match length
                   77
% identity
                   62
NCBI Description
                   (AF118222) contains similarity to Helix pomatia br-1
                   protein (GB: X96994) [Arabidopsis thaliana]
Seq. No.
                   311429
Seq. ID
                   vux700160276.h1
                   BLASTX
Method
NCBI GI
                   q2624383
BLAST score
                   246
E value
                   6.0e-24
Match length
                   71
% identity
                   76
NCBI Description (Y09447) cinnamate 4-hydroxylase [Phaseolus vulgaris]
```

Seq. No.

Seq. ID

Method

311435

BLASTX

vux700160372.h1

```
311430
Seq. No.
Seq. ID
                   vux700160279.h1
Method
                  BLASTN
                   g507770
NCBI GI
BLAST score
                   65
E value
                   3.0e-28
Match length
                  133
                   88
% identity
NCBI Description Zea mays D3L H(+)-transporting ATPase (Mha1) gene, complete
Seq. No.
                   311431
Seq. ID
                   vux700160319.h1
Method
                  BLASTX
                   g3759184
NCBI GI
BLAST score
                   143
E value
                   5.0e-16
Match length
                   57
% identity
                   77
NCBI Description (AB018441) phi-1 [Nicotiana tabacum]
Seq. No.
                   311432
Seq. ID
                   vux700160325.h1
Method
                  BLASTN
NCBI GI
                   g1244652
BLAST score
                   33
E value
                   4.0e-09
Match length
                   61
% identity
                   89
NCBI Description Zea mays copia-type retroelement PREM-2 gag gene, complete
Seq. No.
                   311433
                   vux700160331.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q2252844
BLAST score
                   430
E value
                   8.0e-43
Match length
                   93
                   85
% identity
NCBI Description
                   (AF013293) belongs to the cytochrome p450 family
                   [Arabidopsis thaliana]
Seq. No.
                   311434
Seq. ID
                   vux700160362.h1
Method
                   BLASTN
NCBI GI
                   g22646
BLAST score
                   169
E value
                   2.0e-90
Match length
                   177
% identity
                   99
NCBI Description Z.mays MFS18 mRNA
```

E value

Match length

% identity

4.0e-11

41

59

```
NCBI GI
                  q4190952
BLAST score
                  228
E value
                  3.0e-19
Match length
                  72
                  58
% identity
NCBI Description (AB022689) similar to hsr203J [Lycopersicon esculentum]
                  311436
Seq. No.
Seq. ID
                  vux700160380.h1
Method
                  BLASTX
NCBI GI
                  q3337367
BLAST score
                  240
E value
                  1.0e-20
                  67
Match length
% identity
                  61
NCBI Description (AC004481) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  311437
                  vux700160414.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4415942
BLAST score
                  211
E value
                  8.0e-20
Match length
                  77
% identity
                  66
NCBI Description (AC006418) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  311438
Seq. ID
                  vux700160416.h1
Method
                  BLASTX
NCBI GI
                  q2853081
BLAST score
                  325
E value
                  1.0e-30
Match length
                  81
                  77
% identity
NCBI Description (AL021768) ATP binding protein-like [Arabidopsis thaliana]
Seq. No.
                  311439
Seq. ID
                  vux700160419.h1
Method
                  BLASTX
NCBI GI
                  q3924594
BLAST score
                  165
E value
                  8.0e-12
Match length
                  84
% identity
                  45
NCBI Description
                  (AF069442) putative ribonucleoprotein [Arabidopsis
                  thaliana] >gi 4262139 gb AAD14439 (AC005275) putative
                  ribonucleoprotein [Arabidopsis thaliana]
Seq. No.
                  311440
Seq. ID
                  vux700160490.h1
Method
                  BLASTX
NCBI GI
                  g114270
BLAST score
                  157
```



```
NCBI Description
                  L-ASCORBATE OXIDASE PRECURSOR (ASCORBASE) (ASO)
                  >gi_66291_pir__KSKVAO L-ascorbate oxidase (EC 1.10.3.3)
                  precursor - cucumber >gi_167513 (J04494) ascorbate oxidase
                  precursor (EC 1.10.3.3) [Cucumis sativus]
                  311441
Seq. No.
Seq. ID
                  vux700160566.h1
Method
                  BLASTX
NCBI GI
                  q4371296
BLAST score
                  157
                  2.0e-22
E value
Match length
                  80
% identity
                  67
NCBI Description
                  (AC006260) putative receptor protein kinase [Arabidopsis
                  thaliana]
                  311442
Seq. No.
                  vux700160583.h1
Seq. ID
Method
                  BLASTX
                  g136140
NCBI GI
BLAST score
                  304
                  3.0e-28
E value
Match length
                  80
% identity
                  68
NCBI Description PUTATIVE AC9 TRANSPOSASE >gi_72973_pir__TQZMCA probable
                  transposase - maize transposon Ac9
Seq. No.
                  311443
Seq. ID
                  vux700160587.h1
                  BLASTN
Method
                  g2668749
NCBI GI
                  43
BLAST score
                  4.0e-15
E value
Match length
                  63
                  92
% identity
NCBI Description
                  Zea mays ribosomal protein L30 (rpl30) mRNA, complete cds
                  311444
Seq. No.
Seq. ID
                  vux700160602.h1
Method
                  BLASTX
NCBI GI
                  q1280434
BLAST score
                  147
E value
                  9.0e-10
Match length
                  59
% identity
                  56
NCBI Description (U42014) hemomucin [Drosophila melanogaster]
Seq. No.
                  311445
Seq. ID
                  vux700160686.h1
Method
                  BLASTX
                  q2865177
NCBI GI
```

Method BLASTX
NCBI GI g2865177
BLAST score 362
E value 5.0e-35
Match length 76
% identity 87

NCBI Description (AB010946) AtRer1B [Arabidopsis thaliana]

BLAST score

E value Match length 222 1.0e-18

48

```
Seq. No.
                  311446
                  vux700160804.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2832697
BLAST score
                  186
E value
                  3.0e-14
Match length
                  62
                  60
% identity
                  (AL021713) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  311447
Seq. ID
                  vux700160946.h1
Method
                  BLASTX
NCBI GI
                  q2408009
BLAST score
                  154
                  2.0e-10
E value
                  30
Match length
                  87
% identity
                  (Z99161) ubiquitin [Schizosaccharomyces pombe]
NCBI Description
                  311448
Seq. No.
                  vux700161008.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4514634
BLAST score
                  122
                  1.0e-62
E value
Match length
                  122
% identity
                  100
NCBI Description Zea mays ZmRCP1 mRNA for root cap protein 1, complete cds
                  311449
Seq. No.
Seq. ID
                  vux700161075.h1
Method
                  BLASTN
NCBI GI
                  g3452305
BLAST score
                  116
E value
                  1.0e-58
Match length
                   180
                   91
% identity
NCBI Description Zea mays retrotransposon Opie-3 3' LTR, partial sequence
Seq. No.
                   311450
Seq. ID
                   vux700161087.h1
Method
                  BLASTX
NCBI GI
                   g3269288
BLAST score
                   256
                  1.0e-22
E value
Match length
                   61
% identity
                  74
                  (AL030978) putative protein [Arabidopsis thaliana]
NCBI Description
                   311451
Seq. No.
Seq. ID
                   vux700161105.h1
                  BLASTX
Method
NCBI GI
                  g3135543
```

```
% identity
NCBI Description (AF062393) aquaporin [Oryza sativa]
                  311452
Seq. No.
                  vux700161158.hl
Seq. ID
Method
                  BLASTX
                  g2655295
NCBI GI
                  325
BLAST score
                  1.0e-30
E value
Match length
                  68
% identity
                  88
NCBI Description (AF032976) germin-like protein 6 [Oryza sativa]
Seq. No.
                  311453
                  vux700161172.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g600115
BLAST score
                  72
E value
                  2.0e-32
Match length
                  149
                  97
% identity
NCBI Description
                  Z.mays apx gene encoding cytosolic ascorbate peroxidase
Seq. No.
                  311454
Seq. ID
                  vux700161183.h1
Method
                  BLASTN
NCBI GI
                  q2735839
BLAST score
                  57
                  2.0e-23
E value
Match length
                  162
% identity
                  85
                  Sorghum bicolor ADP-glucose pyrophosphorylase subunit SH2,
NCBI Description
                  transcriptional regulator, NADPH-dependent reductase A1-a
                  and NADPH-dependent reductase A1-b genes, complete cds
                  311455
Seq. No.
                  vux700161192.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3292824
BLAST score
                  212
                  2.0e-17
E value
                  76
Match length
                  62
% identity
NCBI Description (AL031018) putative protein [Arabidopsis thaliana]
Seq. No.
                  311456
                  vux700161209.h1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4539660
```

Method BLASTX
NCBI GI g4539660
BLAST score 335
E value 1.0e-31
Match length 87
% identity 72

NCBI Description (AF061282) polyprotein [Sorghum bicolor]

Seq. No. 311457

Seq. ID vux700161222.h1

```
BLASTX
Method
                  q1762144
NCBI GI
                  315
BLAST score
                  2.0e-29
E value
                  85
Match length
% identity
                  62
                  (U48435) putative cytochrome P450 [Solanum chacoense]
NCBI Description
Seq. No.
                  311458
Seq. ID
                  vux700161263.h1
Method
                  BLASTN
NCBI GI
                  g141961
BLAST score
                  50
                  2.0e-19
E value
Match length
                  86
% identity
                  90
NCBI Description
                  Alcaligenes eutrophus protein H (phbH) and protein I (phbI)
                  genes, complete cds
Seq. No.
                  311459
Seq. ID
                  vux700161264.h1
Method
                  BLASTN
NCBI GI
                  g550433
BLAST score
                  103
E value
                   6.0e-51
Match length
                  143
% identity
                  93
NCBI Description Z.mays CYP71C1 gene for cytochrome P-450
Seq. No.
                  311460
                  vux700161304.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g459169
BLAST score
                  131
E value
                   6.0e-68
Match length
                  131
% identity
                  100
                  Zea mays B73 antifungal zeamatin-like protein mRNA,
NCBI Description
                  complete cds
Seq. No.
                  311461
Seq. ID
                  vux700161348.h1
Method
                  BLASTX
NCBI GI
                  q3913192
BLAST score
                  172
E value
                   4.0e-17
                  85
Match length
% identity
                  52
NCBI Description
                  CYTOCHROME P450 93A1 >gi 2129824 pir S62899 cytochrome
                  P450 (CYP93 A1) - soybean >gi 1232111 dbj BAA12159
                   (D83968) Cytochrome P-450 (CYP93A1) [Glycine max]
                  >gi 1588679 prf 2209281A cytochrome P450 [Glycine max]
                  311462
```

Seq. No.

Seq. ID vux700161373.h1

BLASTN Method NCBI GI g2832242



BLAST score 98
E value 6.0e-48
Match length 226
% identity 86

NCBI Description Zea mays 22-kDa alpha zein gene cluster, complete sequence

Seq. No. 311463

Seq. ID vux700161424.h1

Method BLASTX
NCBI GI g130718
BLAST score 205
E value 1.0e-16
Match length 78
% identity 58

NCBI Description ACID PHOSPHATASE PRECURSOR 1 >gi 170370 (M83211) acid

phosphatase type 1 [Lycopersicon esculentum] >gi_170372 (M67474) acid phosphatase type 5 [Lycopersicon esculentum] >gi_445121_prf__1908427A acid phosphatase 1 [Lycopersicon

esculentum]

Seq. No. 311464

Seq. ID vux700161441.h1

Method BLASTX
NCBI GI g3142293
BLAST score 149
E value 3.0e-13
Match length 75
% identity 57

NCBI Description (AC002411) Contains similarity to myosin IB heavy chain

gb_X70400 from Gallus gallus. [Arabidopsis thaliana]

Seq. No. 311465

Seq. ID vux700161458.h1

Method BLASTX
NCBI GI g2369766
BLAST score 169
E value 3.0e-12
Match length 41
% identity 73

NCBI Description (AJ001304) hypothetical protein [Citrus x paradisi]

Seq. No. 311466

Seq. ID vux700161507.h1

Method BLASTX
NCBI GI g3335060
BLAST score 153
E value 2.0e-10
Match length 45
% identity 62

NCBI Description (AF025842) plasma membrane-type calcium ATPase [Arabidopsis

thaliana] >gi_4468989_emb_CAB38303 (AL035605) plasma

membrane-type calcium ATPase (ACA2) [Arabidopsis thaliana]

Seq. No. 311467

Seq. ID vux700161592.h1

Method BLASTX NCBI GI g1171429

```
BLAST score
E value
                  5.0e-40
Match length
                  82
% identity
                   49
                  (U44028) CKC [Arabidopsis thaliana]
NCBI Description
                  311468
Seq. No.
Seq. ID
                  vux700161671.h1
Method
                  BLASTX
                  g3445397
NCBI GI
BLAST score
                  188
E value
                  1.0e-14
                  59
Match length
% identity
                  59
NCBI Description
                  (AJ010166) S-domain receptor-like protein kinase [Zea mays]
Seq. No.
                  311469
Seq. ID
                  vux700161672.h1
Method
                  BLASTN
NCBI GI
                  g4185305
BLAST score
                  107
E value
                  2.0e-53
Match length
                  158
% identity
                   47
NCBI Description
                  Zea mays cosmid IV.1E1 22-kDa alpha zein protein 21
                   (sz22-21) gene, complete cds; retrotransposon Opie-2 gag
                  protein, polyprotein, and copia protein genes, complete
                  cds; and unknown genes
                  311470
Seq. No.
Seq. ID
                  vux700161687.h1
Method
                  BLASTN
NCBI GI
                  g3218547
BLAST score
                  40
E value
                  2.0e-13
Match length
                  92
                  86
% identity
NCBI Description
                  Oryza sativa AOX1b mRNA for alternative oxidase, complete
                  cds
Seq. No.
                  311471
Seq. ID
                  vux700161721.h1
Method
                  BLASTX
NCBI GI
                  g1085973
BLAST score
                  187
E value
                  2.0e-14
Match length
                  37
                  92
```

% identity

isopentyl pyrophosphate isomerase - Clarkia breweri
(fragment) >gi_572635_emb_CAA57947_ (X82627) isopentenyl NCBI Description

pyrophosphate isomerase [Clarkia breweri]

Seq. No. 311472

Seq. ID vux700161735.h1

Method BLASTX NCBI GI g2435521 BLAST score 195



```
2.0e-15
E value
Match length
                  60
% identity
                  57
                   (AF024504) contains similarity to Nicotiana tabacum
NCBI Description
                  membrane-associated salt-inducible protein (GB:U08285)
                   [Arabidopsis thaliana]
Seq. No.
                  311473
Seq. ID
                  vux700161737.h1
Method
                  BLASTX
NCBI GI
                  q3341695
BLAST score
                  263
E value
                  2.0e-23
                  82
Match length
% identity
                   (AC003672) putative thiamin pyrophosphokinase [Arabidopsis
NCBI Description
                  thaliana]
                   311474
Seq. No.
                  vux700161739.h1
Seq. ID
Method
                  BLASTX
                  g731058
NCBI GI
BLAST score
                  233
                  5.0e-20
E value
Match length
                   69
% identity
                   61
                  URACIL-DNA GLYCOSYLASE (UDG) >gi_2118057_pir__S39712
NCBI Description
                  probable uracil-DNA glycosylase - Bacillus subtilis
                  >gi 580875 emb CAA51613 (X73124) ipa-57d [Bacillus
                   subtilis] >gi 2636332 emb CAB15823 (Z99123) uracil-DNA
                  glycosylase [Bacillus subtilis]
Seq. No.
                   311475
Seq. ID
                   vux700161783.h1
Method
                  BLASTX
NCBI GI
                   g123688
                                       ....
BLAST score
                   151
E value
                   2.0e-10
                   60
Match length
% identity
                   50
                  DNAJ PROTEIN HOMOLOG HSJ1 (HSJ-1) >qi 284069 pir S23508
NCBI Description
                   dnaJ protein homolog - human >gi 32469 emb CAA44968
                   (X63368) HSJ1b [Homo sapiens]
Seq. No.
                   311476
Seq. ID
                   vux700161785.h1
Method
                  BLASTX
NCBI GI
                   g4574406
BLAST score
                   138
```

E value 7.0e-09 Match length 47 % identity 53

(AF121139) RIM2 protein [Oryza sativa] NCBI Description

Seq. No. 311477

Seq. ID vux700161792.h1

Method BLASTX

% identity

```
q1255951
NCBI GI
                  260
BLAST score
                  5.0e-23
E value
                  70
Match length
% identity
                  70
NCBI Description
                  (X96932) PS60 [Nicotiana tabacum]
Seq. No.
                  311478
Seq. ID
                  vux700161819.h1
Method
                  BLASTN
NCBI GI
                  q2832242
BLAST score
                  98
E value
                  6.0e - 48
Match length
                  198
                  87
% identity
NCBI Description Zea mays 22-kDa alpha zein gene cluster, complete sequence
Seq. No.
                  311479
Seq. ID
                  vux700161851.h1
Method
                  BLASTX
NCBI GI
                  q4587997
BLAST score
                  160
E value
                  3.0e-11
Match length
                  80
% identity
                  45
NCBI Description
                  (AF085279) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  311480
Seq. ID
                  vux700161992.h1
Method
                  BLASTX
NCBI GI
                  g3264605
BLAST score
                  153
E value
                  1.0e-10
Match length
                  30
% identity
                  100
NCBI Description (AF061508) ribosomal protein L25 [Zea mays]
                  311481
Seq. No.
Seq. ID
                  vux700162047.hl
Method
                  BLASTX
                  g4249391
NCBI GI
                  162
BLAST score
E value
                  1.0e-11
Match length
                  48
                  60
% identity
                  (ACO05966) Similar to gi 3249076 T13D8.16 beta glucosidase
NCBI Description
                  from Arabidopsis thaliana BAC gb AC004473. [Arabidopsis
                  thaliana]
                  311482
Seq. No.
Seq. ID
                  vux700162059.h1
Method
                  BLASTX
NCBI GI
                  g3377517
BLAST score
                  262
                  3.0e-23
E value
                  79
Match length
```

```
NCBI Description (AF073361) nitrate transporter NTL1 [Arabidopsis thaliana]
Seq. No.
                  311483
                  vux700162176.h1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g4185305
BLAST score
                  79
E value
                  1.0e-36
Match length
                  161
% identity
                  88
NCBI Description
                  Zea mays cosmid IV.1E1 22-kDa alpha zein protein 21
                  (sz22-21) gene, complete cds; retrotransposon Opie-2 gag
                  protein, polyprotein, and copia protein genes, complete
                  cds; and unknown genes
Seq. No.
                  311484
Seq. ID
                  vux700162177.h1
Method
                  BLASTX
NCBI GI
                  q1781326
BLAST score
                  181
E value
                  8.0e-14
Match length
                  74
% identity
                  47
NCBI Description
                  (Y10464) peroxidase [Spinacia oleracea]
Seq. No.
                  311485
Seq. ID
                  vux700162226.h1
Method
                  BLASTX
NCBI GI
                  g130940
                  320
                  5.0e-30
                  57
% identity
                  100
NCBI Description
                  PATHOGENESIS-RELATED PROTEIN PRMS PRECURSOR
```

BLAST score E value Match length

>gi 100906 pir S14969 pathogenesis-related protein - maize

>gi 22454 emb CAA38223 (X54325) pathogenesis-related

protein [Zea mays]

Seq. No. 311486

Seq. ID vux700162229.h1

Method BLASTX NCBI GI g3402682 BLAST score 195 E value 3.0e-15 Match length 87 % identity 40

NCBI Description (AC004697) unknown protein [Arabidopsis thaliana]

Seq. No. 311487

Seq. ID vux700162261.h1

Method BLASTX NCBI GI g3878119 BLAST score 173 E value 8.0e-13 Match length 60 % identity 53

NCBI Description (Z49068) similar to GTP-binding protein; cDNA EST



EMBL:M89111 comes from this gene; cDNA EST EMBL:D27709 comes from this gene; cDNA EST EMBL:D27708 comes from this gene; cDNA EST EMBL:D73788 comes from this gene; cDNA EST yk353

 Seq. No.
 311488

 Seq. ID
 vux700162318.h1

 Method
 BLASTX

 NCBI GI
 g3377941

 BLAST score
 146

 E value
 9.0e-10

 Match length
 43

NCBI Description (AL021960) putative protein (fragment) [Arabidopsis

thaliana]

58

Seq. No. 311489

% identity

Seq. ID vux700162339.h1

Method BLASTX
NCBI GI g3218543
BLAST score 225
E value 5.0e-19
Match length 50
% identity 84

NCBI Description (AB004813) alternative oxidase [Oryza sativa]

>gi 3218548 dbj BAA28774 (AB004865) alternative oxidase

[Oryza sativa]

Seq. No. 311490

Seq. ID vux700162420.h1

Method BLASTN
NCBI GI g170813
BLAST score 33
E value 4.0e-09
Match length 49
% identity 92

NCBI Description Candida albicans ADP-ribosylation factor (YCaARF1) gene,

complete cds

Seq. No. 311491

Seq. ID vux700162427.h1

Method BLASTX
NCBI GI g118104
BLAST score 365
E value 3.0e-35
Match length 79
% identity 89

NCBI Description PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE)

(CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN)

>gi_68408_pir__CSZM peptidylprolyl isomerase (EC 5.2.1.8) -

maize >gi_168461 (M55021) cyclophilin [Zea mays]

>gi $82914\overline{8}$ emb CAA48638 (X68678) cyclophilin [Zea mays]

Seq. No. 311492

Seq. ID vux700162471.h1

Method BLASTX NCBI GI g3548808

44431

. . .

```
BLAST score
                  3.0e-13
E value
                  73
Match length
                   47
% identity
                  (AC005313) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  311493
                  vux700162541.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2623247
BLAST score
                   64
E value
                  1.0e-27
Match length
                  76
% identity
                   96
NCBI Description
                  Zea mays SU1 isoamylase (sugary1) gene, complete cds
Seq. No.
                   311494
                  vux700162563.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g542179
BLAST score
                   433
E value
                   2.0e-43
Match length
                  79
% identity
                  100
NCBI Description
                  alpha tubulin - maize >gi 629837 pir S39998 tubulin alpha
                  chain - maize (fragment) >gi 393401 emb CAA52158 (X73980)
                  alpha tubulin [Zea mays]
Seq. No.
                   311495
Seq. ID
                  vvh700281911.h1
Method
                  BLASTN
NCBI GI
                  g22275
BLAST score
                   45
E value
                  1.0e-16
Match length
                  94
                  91
% identity
NCBI Description Maize mRNA for ferritin (clone FM1)
                  311496
Seq. No.
Seq. ID
                  vvh700281922.h2
Method
                  BLASTX
NCBI GI
                  g2961378
BLAST score
                   283
                   2.0e-25
E value
                  74
Match length
                  34
% identity
NCBI Description
                  (AL022141) putative protein [Arabidopsis thaliana]
Seq. No.
                  311497
Seq. ID
                  wen700331857.h1
Method
                  BLASTX
NCBI GI
                  g4314371
BLAST score
                  286
                  7.0e-26
E value
                  96
Match length
                   55
% identity
```

NCBI Description (AC006340) putative G9a protein [Arabidopsis thaliana]

```
Seq. No.
                   311498
Seq. ID
                   wen700331895.h1
Method
                   BLASTX
NCBI GI
                   q4580022
BLAST score
                   172
E value
                   1.0e-12
                   49
Match length
                   59
% identity
                  (AF061981) CCCH zinc finger protein C3H-2 [Xenopus laevis]
NCBI Description
Seq. No.
                   311499
Seq. ID
                   wen700331905.h1
Method
                   BLASTX
NCBI GI
                   g1314711
BLAST score
                   219
                   5.0e-18
E value
Match length
                   47
% identity
                   87
NCBI Description
                   (U54615) calcium-dependent protein kinase [Arabidopsis
                   thaliana] >gi_3068712 (AF049236) calcium dependent protein
                   kinase [Arabidopsis thaliana]
Seq. No.
                   311500
                   wen700331917.hl
Seq. ID
Method
                   BLASTX
                   q4505917
NCBI GI
BLAST score
                   168
E value
                   3.0e-12
                   55
Match length
% identity
                   56
                   autoantigen PM-SCL >gi_417499_sp_Q01780_PMSC_HUMAN
AUTOANTIGEN PM-SCL >gi_284357_pir_A43920 nucleolar 100K
NCBI Description
                   polymyositis-scleroderma protein 2 - human >gi_179283
                   (L01457) PM-Scl autoantigen [Homo sapiens]
Seq. No.
                   311501
                   wen700331933.hl
Seq. ID
Method
                   BLASTX
NCBI GI
                   q730843
BLAST score
                   177
E value
                   2.0e-13
Match length
                   69
                   42
% identity
NCBI Description
                   SHUTTLE CRAFT PROTEIN >gi 487400 (U09306) shuttle craft
                   protein [Drosophila melanogaster]
Seq. No.
                   311502
Seq. ID
                   wen700331934.h1
Method
                   BLASTN
NCBI GI
                   g57656
BLAST score
                   111
E value
                   9.0e-56
Match length
                   203
% identity
                   89
```

NCBI Description R.rattus pyruvate dehydrogenase El alpha form 1 subunit



```
311503
Seq. No.
Seq. ID
                  wen700331951.h1
                  BLASTX
Method
NCBI GI
                  g2500543
BLAST score
                  176
                  3.0e-23
E value
                  89
Match length
                  63
% identity
                  PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA
NCBI Description
                  HELICASE EEED8.5 >gi 733602 (U23484) similar to S.
                  cerevisiae pre-mRNA splicing factor RNA helicase PRP22
                  (SP:PR22 YEAST, P24384) and other DEAH subfamily members of
                  the DEAD box family helicases [Caenorhabditis elegans]
Seq. No.
                  311504
Seq. ID
                  wen700331978.h1
Method
                  BLASTX
NCBI GI
                  g1353193
BLAST score
                  214
E value
                  2.0e-17
Match length
                  102
% identity
                  37
NCBI Description
                  O-METHYLTRANSFERASE ZRP4 (OMT) >gi_542186_pir__JQ2268
                  O-methyltransferase (EC 2.1.1.-) - maize >gi 404070
                  (L14063) O-methyltransferase [Zea mays]
                  311505
Seq. No.
Seq. ID
                  wen700332055.h1
                  BLASTN
Method
NCBI GI
                  g177865
BLAST score
                  142
E value
                  3.0e-74
Match length
                  251
                  88
% identity
NCBI Description
                  Human tumor necrosis factor alpha inducible protein A20
                  mRNA, complete cds
Seq. No.
                  311506
Seq. ID
                  wen700332068.h1
                  BLASTX
Method
NCBI GI
                  g3097244
BLAST score
                  228
E value
                  1.0e-25
Match length
                  83
                  80
% identity
                  (Y08307) ribosomal protein S14 [Mus musculus]
NCBI Description
Seq. No.
                  311507
                  wen700332130.h1
```

Seq. ID

Method BLASTN NCBI GI g4506692 BLAST score 58 E value 2.0e-24 Match length 98 90

% identity

NCBI Description Homo sapiens ribosomal protein S17 (RPS17) mRNA

>gi_337500_gb_M13932_HUMRPS17 Human ribosomal protein S17



```
mRNA, complete cds
                   311508
Seq. No.
Seq. ID
                   wen700332132.h1
                   BLASTX
Method
                   g1176658
NCBI GI
BLAST score
                   153
                   2.0e-10
E value
Match length
                   44
% identity
                   61
NCBI Description
                  HYPOTHETICAL 200.6 KD PROTEIN B0228.2 IN CHROMOSOME II
                   >gi 726363 (U23168) No definition line found
                   [Caenorhabditis elegans]
Seq. No.
                   311509
Seq. ID
                   wen700332146.h1
Method
                  BLASTN
NCBI GI
                   g4507616
BLAST score
                   72
                   8.0e-33
E value
Match length
                   92
% identity
                   95
                  Homo sapiens troponin C2, fast (TNNC2) mRNA
NCBI Description
                   >gi_36728_emb_X07898 HSTC2 Human mRNA for fast skeletal
                   troponin C
Seq. No.
                   311510
Seq. ID
                  wen700332166.h1
Method
                  BLASTX
NCBI GI
                   g2496930
BLAST score
                   157
E value
                   1.0e-10
Match length
                   89
                   39
% identity
NCBI Description
                  HYPOTHETICAL 84.2 KD PROTEIN C44B7.11 IN CHROMOSOME II
                   >gi_861310 (U28928) C44B7.11 gene product [Caenorhabditis
                   elegans]
Seq. No.
                   311511
Seq. ID
                  wen700332192.h1
Method
                  BLASTN
NCBI GI
                   g416263
BLAST score
                  53
E value
                   4.0e-21
Match length
                  89
% identity
                  90
NCBI Description Rice mRNA for ribosomal protein S28, partial sequence
Seq. No.
                  311512
Seq. ID
                  wen700332255.h1
```

BLASTX Method NCBI GI g1814405 BLAST score 184 E value 6.0e-14 Match length 50 76 % identity

NCBI Description (U84890) putative phosphate permease [Mesembryanthemum



crystallinum]

```
Seq. No.
                       311513
Seq. ID
                       wen700332274.h1
Method
                       BLASTX
NCBI GI
                       g4506663
BLAST score
                       230
E value
                       4.0e-27
Match length
                       90
% identity
                       83
                       ribosomal protein L8 >gi_133027_sp_P25120_RL8_HUMAN 60S
RIBOSOMAL PROTEIN L8 >gi_71075_pir__R5RTL8 ribosomal
protein L8 - rat >gi_478326_pir__JN0923 ribosomal protein
L8 - human >gi_57704_emb_CAA44071_ (X62145) ribosomal
NCBI Description
                       protein L8 [Rattus rattus] >gi_433899 emb_CAA82248 (Z28407) ribosomal protein L8 [Homo sapiens] >gi_1527178
                        (U67771) ribosomal protein L8 [Mus musculus]
Seq. No.
                       311514
Seq. ID
                       wen700332277.h1
Method
                       BLASTX
NCBI GI
                       g113217
BLAST score
                       183
E value
                       4.0e-14
Match length
                       34
                       100
% identity
NCBI Description ACTIN 1 > gi 100149 pir S07002 actin 1 - carrot
Seq. No.
                       311515
Seq. ID
                       wen700332321.h1
Method
                       BLASTX
NCBI GI
                       g4220474
BLAST score
                       208
E value
                       8.0e-17
Match length
                       60
% identity
                       68
NCBI Description
                       (AC006069) putative myosin heavy chain [Arabidopsis
                       thaliana]
Seq. No.
                       311516
Seq. ID
                       wen700332331.h1
Method
                       BLASTX
NCBI GI
                       g3461813
BLAST score
                       384
E value
                       2.0e-37
Match length
                       88
```

% identity NCBI Description (AC004138) putative sucrose/H+ symporter [Arabidopsis

thaliana]

Seq. No. 311517

Seq. ID wen700332334.h1

Method BLASTX NCBI GI g487123 BLAST score 239 E value 1.0e-20 Match length 48

% identity 90

NCBI Description u-plasminogen activator receptor form 2 precursor - human

>gi 433901 emb CAA52191 (X74039) urokinase plasminogen

activator receptor [Homo sapiens]

Seq. No. 311518

Seq. ID wen700332396.h1

Method BLASTN
NCBI GI g4506008
BLAST score 196
E value 1.0e-106
Match length 256

NCBI Description Homo sapiens protein phosphatase 1, regulatory subunit 10

(PPP1R10) mRNA >gi 2117158 emb Y13247 HSFB19 Homo sapiens

fb19 mRNA

94

Seq. No. 311519

% identity

Seq. ID wen700332446.h1

Method BLASTN
NCBI GI g204490
BLAST score 50
E value 2.0e-19
Match length 54
% identity 98

NCBI Description Rat glutathione S-transferase mRNA, complete cds

Seq. No. 311520

Seq. ID wen700332463.h1

Method BLASTX
NCBI GI g2827656
BLAST score 233
E value 1.0e-21
Match length 73
% identity 73

NCBI Description (AL021637) DAG-like protein [Arabidopsis thaliana]

Seq. No. 311521

Seq. ID wen700332474.h1

Method BLASTN
NCBI GI g179276
BLAST score 88
E value 2.0e-42
Match length 124
% identity 94

NCBI Description Human ATP synthase beta subunit gene, exons 1-7

Seq. No. 311522

Seq. ID wen700332483.h1

Method BLASTN
NCBI GI g535741
BLAST score 133
E value 5.0e-69
Match length 176
% identity 95

NCBI Description Rattus norvegicus palmitoyl-protein thioesterase mRNA,

complete cds

```
311523
Seq. No.
Seq. ID
                    wen700332487.hl
Method
                    BLASTN
NCBI GI
                    g587519
BLAST score
                    47
                    6.0e-18
E value
Match length
                    55
% identity
                    96
NCBI Description
                    R.norvegicus mRNA for keratin
Seq. No.
                    311524
Seq. ID
                    wen700332519.hl
Method
                    BLASTN
NCBI GI
                    q4589659
BLAST score
                    216
                  ~1.0e-118
E value
Match length
                    256
                    96
% identity
NCBI Description Homo sapiens mRNA for KIAA1008 protein, complete cds
                                                                 ×. .
Seq. No.
                    311525
Seq. ID
                    wen700332520.h1
Method
                    BLASTX
NCBI GI
                    q115454
BLAST score
                    256
                    2.0e-22
E value
                    74
Match length
% identity
                    62
                    CARBONIC ANHYDRASE II (CARBONATE DEHYDRATASE II)
NCBI Description
                    >gi_1079389_pir__JC2580 carbonate dehydratase (EC 4.2.1.1)
II - chicken >gi_65332_emb_CAA78681_ (Z14957) carbonic
                    anhydrase [Gallus gallus]
Seq. No.
                    311526
Seq. ID
                    wen700332538.hl
Method
                    BLASTX
                    q481452
NCBI GI
BLAST score
                    157
                    4.0e-20
E value
                    94
Match length
                    59
% identity
                    Ig kappa chain V region - human (fragment)
>gi_415956_emb_CAA81694_ (Z27170) IG light chain variable
NCBI Description
                    region (VJ) [Homo sapiens]
Seq. No. Seq. ID
                    311527
                    wen700332554.hl
                    BLASTN
Method
NCBI GI
                    q4505612
BLAST score
                    174
                    3.0e-93
E value
                    282
Match length
% identity
                    91
                    Homo sapiens PRKC, apoptosis, WT1, regulator (PAWR) mRNA
NCBI Description
                    >gi 3282204 gb U63809 HSU63809 Homo sapiens prostate
                    apoptosis response protein par-4 mRNA, complete cds
```

Seq. No.

```
311528
Seq. No.
Seq. ID
                  wen700332563.h1
Method
                  BLASTN
NCBI GI
                  g57656
BLAST score
                  236
                  1.0e-130
E value
Match length
                  268
% identity
                  97
NCBI Description R.rattus pyruvate dehydrogenase E1 alpha form 1 subunit
Seq. No.
                  311529
                  wen700332576.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4506617
BLAST score
                  315
E value
                  7.0e-31
Match length
                  90
% identity
                  79
NCBI Description
                  ribosomal protein L17 >gi_132799_sp_P18621_RL17_HUMAN 60S
                  RIBOSOMAL PROTEIN L17 (L23) >gi_71281_pir__R5HU22 ribosomal
                  protein L17 - human >gi_34199_emb_CAA37793_ (X53777)
                  putative ribosomal protein (AA 1-184) [Homo sapiens]
Seq. No.
                  311530
Seq. ID
                  wen700332579.h1
Method
                  BLASTN
NCBI GI
                  g2213812
BLAST score
                  106
                  6.0e-53
E value
Match length
                  158
% identity
                  92
NCBI Description Homo sapiens podocalyxin-like protein mRNA, complete cds
Seq. No.
                  311531
Seq. ID
                  wen700332596.h1
Method
                  BLASTX
NCBI GI
                  q3402697
BLAST score
                  364
                  4.0e-35
E value
                  88
Match length
                  80
% identity
NCBI Description
                  (AC004261) putative phosphatidylinosito1-4-phosphate
                  5-kinase [Arabidopsis thaliana]
                  311532
Seq. No.
Seq. ID
                  wen700332606.h1
Method
                  BLASTN
NCBI GI
                  g37995
BLAST score
                  105
                  2.0e-52
E value
Match length
                  133
% identity
                  95
NCBI Description
                  H.sapiens mRNA for xeroderma pigmentosum group C
```

44439

complementing factor (XP-C)



```
wen700332630.h1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2077942
BLAST score
                   105
                   2.0e-52
E value
Match length
                   113
                   98
% identity
NCBI Description
                  Rattus norvegicus mRNA for phospholipase D, complete cds
Seq. No.
                   311534
Seq. ID
                   wen700332664.h1
Method
                   BLASTX
NCBI GI
                   q1350662
BLAST score
                   176
                   3.0e-13
E value
Match length
                   37
% identity
                   86
NCBI Description
                   60S RIBOSOMAL PROTEIN L13 (A52) >gi_899445 (U28917) 60S
                   ribosomal protein [Mus musculus]
Seq. No.
                   311535
Seq. ID
                  wen700332684.hl
Method
                  BLASTN
NCBI GI
                  g533946
BLAST score
                  176
E value
                  2.0e-94
Match length
                  240
                  94
% identity
NCBI Description H.sapiens (xs31) mRNA, 835bp
Seq. No.
                  311536
Seq. ID
                  wen700332708.h1
Method
                  BLASTN
NCBI GI
                  g1916228
BLAST score
                  297
E value
                  1.0e-166
Match length
                  313
% identity
                  99
NCBI Description
                  Human line-1 reverse transcriptase gene, partial cds, and
                  granulocyte chemotactic protein-2 (GCP-2) gene, complete
                  cds
Seq. No.
                  311537
Seq. ID
                  wen700332741.h1
Method
                  BLASTN
NCBI GI
                  q4406704
BLAST score
                  140
E value
                  4.0e-73
Match length
                  188
% identity
                  94
NCBI Description
                  Homo sapiens clone 24870 mRNA sequence
```

Seq. No. 311538

Seq. ID wen700332786.h1

Method BLASTX
NCBI GI g3873807
BLAST score 143

```
4.0e-09
E value
Match length
                    45
                    60
% identity
                    (Z49907) B0491.1 [Caenorhabditis elegans]
NCBI Description
Seq. No.
                    311539
Seq. ID
                    wen700332792.h1
Method
                    BLASTN
                                                                              .3
NCBI GI
                    g505037
BLAST score
                    110
E value
                    2.0e-55
Match length
                    162
% identity
                    92
NCBI Description H.sapiens polyA site DNA sequence
                    311540
Seq. No.
Seq. ID
                    wen700332839.h1
Method
                    BLASTX
NCBI GI
                    g4506655
BLAST score
                    479
E value
                    2.0e-48
Match length
                    96
% identity
                    94
                    ribosomal protein L5 >gi_1173054_sp_P46777_RL5_HUMAN 60S
RIBOSOMAL PROTEIN L5 >gi_1362932_pir__S55912 ribosomal
protein L5 - human >gi_550013 (U14966) ribosomal protein L5
NCBI Description
                     [Homo sapiens] >gi_1096938_prf__2113200A ribosomal protein
                    L5 [Homo sapiens]
                    311541
Seq. No.
Seq. ID
                    wen700332847.h1
Method
                    BLASTN
NCBI GI
                    g4506750
BLAST score
                    86
                    3.0e-41
E value
Match length
                    113
% identity
                    96
NCBI Description
                    Homo sapiens restin (Reed-Steinberg cell-expressed
                    intermediate filament-associated protein) (RSN) mRNA
                    >gi 35998 emb X64838 HSRESTIN H.sapiens mRNA for restin
Seq. No.
                    311542
Seq. ID
                    wen700332849.h1
Method
                    BLASTX
NCBI GI
                    g2894106
BLAST score
                    300
E value
                    7.0e-28
Match length
                    59
% identity
NCBI Description
                    (Z78279) Collagen alphal [Rattus norvegicus]
```

Seq. No. 311543

Seq. ID wen700332858.hl Method BLASTN

NCBI GI g1518112 BLAST score 41 E value 5.0e-14

Match length 87 % identity Brassica napus S locus-linked gene two (SLL2) mRNA, NCBI Description complete cds Seq. No. 311544 wen700332873.hl Seq. ID Method BLASTN NCBI GI q1666699 BLAST score 88 E value 2.0e-42 Match length 100 % identity 97 Mus musculus Btk locus, alpha-D-galactosidase A (Ags), NCBI Description ribosomal protein (L44L), and Bruton's tyrosine kinase (Btk) genes, complete cds Seq. No. 311545 Seq. ID wen700332881.h1

 Seq. ID
 wen700332881

 Method
 BLASTN

 NCBI GI
 g2731598

 BLAST score
 137

 E value
 2.0e-71

 Match length
 169

NCBI Description Homo sapiens chromosome 5, Pl clone 1029A7 (LBNL H15),

complete sequence [Homo sapiens]

Seq. No. 311546

% identity

Seq. ID wen700332924.h1

95

Method BLASTN
NCBI GI g341979
BLAST score 222
E value 1.0e-122
Match length 261
% identity 97

NCBI Description Homo sapiens NADH-cytochrome b5 reductase (b5R) gene, exon

9

Seq. No. 311547

Seq. ID wen700332930.h1

Method BLASTN
NCBI GI 94406702
BLAST score 114
E value 2.0e-57
Match length 232
% identity 97

NCBI Description Homo sapiens clone 24856 mRNA sequence, complete cds

Seq. No. 311548

Seq. ID wen700332949.h1

Method BLASTX
NCBI GI g4165488
BLAST score 425
E value 3.0e-42
Match length 94
% identity 90



NCBI Description (AJ132399) alpha-tubulin 3 [Hordeum vulgare]

Seq. No. 311549

Seq. ID wen700332973.h1

Method BLASTX
NCBI GI g3169828
BLAST score 243
E value 7.0e-21
Match length 61
% identity 82

NCBI Description (AF030454) epithelial V-like antigen precursor [Mus

musculus]

Seq. No. 311550

Seq. ID wen700332986.h1

Method BLASTN
NCBI GI g1124883
BLAST score 196
E value 1.0e-106
Match length 251
% identity 96

NCBI Description Rattus norvegicus small proline-rich protein (spr) gene,

complete cds

Seq. No. 311551

Seq. ID wen700333013.h1

Method BLASTX
NCBI GI g4415941
BLAST score 143
E value 4.0e-09
Match length 36
% identity 69

NCBI Description (AC006418) putative arginine-serine rich splicing factor

[Arabidopsis thaliana]

Seq. No. 311552

Seq. ID wen700333019.h1

Method BLASTN
NCBI GI g3341647
BLAST score 34
E value 1.0e-09
Match length 70
% identity 87

NCBI Description Zea mays Ama gene encoding single-subunit RNA polymerase

Seq. No. 311553

Seq. ID wen700333024.h1

Method BLASTX
NCBI GI g4503135
BLAST score 332
E value 3.0e-31
Match length 80
% identity 81

NCBI Description chymotrypsinogen B1 >gi_117617_sp_P17538_CTRB_HUMAN CHYMOTRYPSINOGEN B PRECURSOR >gi_105619_pir__A31299 chymotrypsin (EC 3.4.21.1) precursor - human >gi_181190 (M24400) preprochymotrypsinogen (EC 3.4.21.1) [Homo

(M24400) preprochymotrypsinogen (EC 3.4.21.1) [Homo



sapiens]

```
311554
Seq. No.
Seq. ID
                  wen700333028.h1
Method
                  BLASTX
NCBI GI
                  g3402682
BLAST score
                  178
E value
                  3.0e-13
Match length
                  97
% identity
                  13
NCBI Description
                  (AC004697) unknown protein [Arabidopsis thaliana]
Seq. No.
                  311555
Seq. ID
                  wen700333048.h1
Method
                  BLASTN
NCBI GI
                  q4003383
BLAST score
                  203
E value
                  1.0e-110
Match length
                  275
                  93
% identity
NCBI Description
                  Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of
                  hepatocellular colorectal and non-small cell lung cancer ,
                  segment 6/11
Seq. No.
                  311556
Seq. ID
                  wen700333062.h1
Method
                  BLASTX
NCBI GI
                  q4512688
BLAST score
                  262
E value
                  4.0e-23
Match length
                  92
                  60
% identity
NCBI Description
                  (AC006931) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  311557
Seq. ID
                  wen700333072.h1
Method
                  BLASTX
NCBI GI
                  g2351097
BLAST score
                  260
                  7.0e-23
E value
Match length
                  60
% identity
                  80
                  (AB006810) ATMRK1 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  311558
Seq. ID
                  wen700333173.h1
Method
                  BLASTX
NCBI GI
                  q1703380
BLAST score
                  175
                  7.0e-13
E value
Match length
                  37
                  97
% identity
                  ADP-RIBOSYLATION FACTOR >qi 1132483 dbj BAA04607 (D17760)
NCBI Description
                  ADP-ribosylation factor [Oryza sativa]
```

Seq. No. 311559

Seq. ID wen700333180.h1

Seq. ID

Method

NCBI GI

```
Method
                   BLASTX
NCBI GI
                   q3169158
BLAST score
                   217
E value
                   2.0e-22
Match length
                   68
% identity
                   73
NCBI Description
                   (AC004770) BC269730 2 [Homo sapiens]
Seq. No.
                   311560
Seq. ID
                   wen700333188.h1
Method
                   BLASTX
NCBI GI
                   q118104
BLAST score
                   252
E value
                   6.0e-22
Match length
                   74
% identity
                   69
NCBI Description
                   PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE)
                   (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN)
                   >gi_68408_pir__CSZM peptidylprolyl isomerase (EC 5.2.1.8) -
                   maize >gi_168\overline{461} (M55021) cyclophilin [Zea mays]
                   >gi_829148_emb_CAA48638_ (X68678) cyclophilin [Zea mays]
Seq. No.
                   311561
Seq. ID
                   wen700333240.h1
Method
                   BLASTN
NCBI GI
                   q4416300
BLAST score
                   90
E value
                   4.0e-43
Match length
                   132
                   99
% identity
                  Zea mays chromosome 4 22 kDa zein-associated intercluster
NCBI Description
                  region, complete sequence
Seq. No.
                  311562
Seq. ID
                  wen700333301.h1
Method
                  BLASTX
NCBI GI
                  g4220529
BLAST score
                  268
E value
                  9.0e-24
Match length
                  92
% identity
                  54
NCBI Description
                  (AL035356) putative protein [Arabidopsis thaliana]
Seq. No.
                  311563
Seq. ID
                  wen700333305.h1
Method
                  BLASTX
NCBI GI
                  g2959781
BLAST score
                  145
E value
                  1.0e-13
Match length
                  75
% identity
NCBI Description
                  (AJ223508) Zwille protein [Arabidopsis thaliana]
Seq. No.
                  311564
```

44445

wen700333330.h1

BLASTX

q4206209



BLAST score E value 1.0e-18 Match length 100 % identity 38

(AF071527) putative glucan synthase component [Arabidopsis NCBI Description

thaliana] >gi_4263042_gb_AAD15311_ (AC005142) putative

glucan synthase component [Arabidopsis thaliana]

Seq. No. 311565

Seq. ID wen700333394.hl

Method BLASTN NCBI GI g21800 BLAST score 85 E value 4.0e-40 Match length 215 % identity 78

NCBI Description T.aestivum L mRNA for histone H2B

Seq. No. 311566

Seq. ID wen700333417.h1

Method BLASTX NCÉI GI q417103 BLAST score 401 E value 2.0e-39 Match length 80 % identity 100

NCBI Description HISTONE H3.2, MINOR >gi_282871_pir__S24346 histone

H3.3-like protein - Arabidopsis thaliana

>gi_16324_emb_CAA42957_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_404825_emb_CAA42958_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_488563 (U09458) histone H3.2 [Medicago sativa] $>gi_488567$ ($\overline{U}09460$) histone H3.2 [Medicago sativa] >gi_488569 (U09461) histone H3.2 [Medicago sativa] >gi_488575 (U09464) histone H3.2

[Medicago sativa] >gi_488577 (U09465) histone H3.2 [Medicago sativa] >gi_510911 emb_CAA56153 (X79714) histone H3 [Lolium temulentum] >gi_1435157 emb_CAA58445 (X83422)

histone H3 variant H3.3 [Lycopersicon esculentum] >gi_2558944 (AF024716) histone 3 [Gossypium hirsutum]

>gi 3273350_dbj BAA31218 (AB015760) histone H3 [Nicotiana tabacum] >gi_3885890 (AF093633) histone H3 [Oryza sativa] >gi_4038469_gb_AAC97380_ (AF109910) histone H3 [Porteresia coarctata] >gi_4490754_emb_CAB38916.1_ (AL035708) histone H3.3 [Arabidopsis thaliana] >gi_4490755_emb_CAB38917.1_

(AL035708) Histon H3 [Arabidopsis thaliana]

Seq. No. 311567

Seq. ID wen700333418.h1

Method BLASTN NCBI GI q4504486 BLAST score 35 E value 2.0e-10

Match length 75 % identity 87

NCBI Description Homo sapiens histidine-rich calcium-binding protein (HRC)

mRNA >gi_183918_gb_M60052 HUMHCPB Human histidine-rich

calcium binding protein (HRC) mRNA, complete cds

```
Seq. No.
                   311568
Seq. ID
                  wen700333451.hl
Method
                  BLASTN
NCBI GI
                   g4505740
BLAST score
                   128
E value
                   4.0e-66
Match length
                   132
                   99
% identity
NCBI Description
                  Homo sapiens prefoldin 4 (PFDN4) mRNA
                  >gi_1620560_gb_U41816_HSU41816 Human C-1 mRNA, complete cds
Seq. No.
                   311569
Seq. ID
                  wen700333457.hl
Method
                  BLASTN
NCBI GI
                   g4506606
BLAST score
                   40
E value
                   1.0e-13
Match length
                   40
                   100
% identity
NCBI Description
                  Homo sapiens ribosomal protein L18 (RPL18) mRNA
                  >gi_337492 gb L11566 HUMRPL18A Homo sapiens ribosomal
                  protein L18 (RPL18) mRNA, complete cds
Seq. No.
                  311570
Seq. ID
                  wen700333502.h1
Method
                  BLASTX
NCBI GI
                  g493066
BLAST score
                   419
E value
                  1.0e-41
Match length
                  89
                  90
% identity
NCBI Description
                  (U09510) glycyl-tRNA synthetase [Homo sapiens]
Seq. No.
                  311571
Seq. ID
                  wen700333508.h1
Method
                  BLASTN
NCBI GI
                  g4557532
BLAST score
                  213
E value
                  1.0e-116
Match length
                  280
                  94
%_identity
NCBI Description
                  Homo sapiens diptheria toxin resistance protein required
                  for diphthamide biosynthesis (Saccharomyces)-like 2(DPH2L2)
                  mRNA >gi_3170457_gb AF053003 AF053003 Homo sapiens
                  diphthamide biosynthesis protein-2 (DPH2) mRNA, complete
                  cds
Seq. No.
                  311572
Seq. ID
                  wen700333512.h1
Method
                  BLASTN
NCBI GI
                  g56056
BLAST score
                  158
E value
                  1.0e-83
Match length
                  257
% identity
                  90
```

NCBI Description R.norvegicus DCN mRNA for decorin



Seq. No. 311573 Seq. ID wen700333535.h1 Method BLASTN NCBI GI q205381 BLAST score 210 E value 1.0e-115 Match length 238 97 % identity NCBI Description rat metallothionein-i (mt-1) mrna Seq. No. 311574 Seq. ID wen700333558.hl Method BLASTN NCBI GI q188542 BLAST score 242 E value 1.0e-134 Match length 266 % identity NCBI Description Human MIC2 mRNA, complete cds Seq. No. 311575 Seq. ID wen700333559.h1 Method BLASTX NCBI GI g2967678 BLAST score 304 E value 6.0e-41 Match length 92 % identity 95 NCBI Description (AF012348) smooth muscle gamma actin [Gallus gallus] Seq. No. 311576 Seq. ID wen700333570.h1 Method BLASTN NCBI GI g4587711 BLAST score 112 2.0e-56 E value Match length 142 % identity 95 Homo sapiens mu-adaptin-related protein 2 (HSMU4) mRNA, NCBI Description complete cds 311577 Seq. No. Seq. ID wen700333572.h1 Method BLASTX NCBI GI g3738319 BLAST score 310 9.0e-29 E value Match length 90 % identity 62 NCBI Description (AC005170) hypothetical protein [Arabidopsis thaliana]

Seq. No. 311578

Seq. ID wen700333573.h1

Method BLASTX NCBI GI g3766236 BLAST score 297



```
E value
                    3.0e-27
Match length
                    82
% identity
                    76
NCBI Description
                    (AF095287) pituitary tumor transforming gene protein 1
                    [Homo sapiens] >gi_3819182_emb_CAA11683.1_ (AJ223953) hPTTG
[Homo sapiens] >gi_4377993_gb_AAD19335_ (AF075242) tumor
                    transforming protein 1 [Homo sapiens]
Seq. No.
                    311579
Seq. ID
                   wen700333578.h1
Method
                   BLASTN
NCBI GI
                    q35183
BLAST score
                    51
                    4.0e-20
E value
Match length
                   123
% identity
NCBI Description
                   H.sapiens p27 mRNA
Seq. No.
                    311580
Seq. ID
                   wen700333589.h1
Method
                   BLASTN
NCBI GI
                   g2813964
BLAST score
                    57
E value
                   1.0e-23
Match length
                    113
                    88
% identity
NCBI Description
                   Human DNA sequence from PAC 179M20 on chromosome
                    20q12-13.1. Contains adenosine deaminase (ADA), placental
                   protein Diff33, CA repeat, ESTs, STS
Seq. No.
                    311581
Seq. ID
                   wen700333613.h1
Method
                   BLASTN
NCBI GI
                   g34469
BLAST score
                    204
E value
                   1.0e-111
                   298
Match length
% identity
                    92
NCBI Description H.sapiens max gene
Seq. No.
                   311582
Seq. ID
                   wen700333618.h1
Method
                   BLASTX
NCBI GI
                   g1154954
BLAST score
                   238
E value
                   3.0e-20
Match length
                   57
                   89
% identity
NCBI Description
                   (X94693) histone H2A [Triticum aestivum]
```

Seq. No. 311583 Seq. ID wen700333672.h1

Method BLASTN NCBI GI g183622 BLAST score 196 E value 1.0e-106 Match length 220

% identity

NCBI Description Human gro (growth regulated) gene

Seq. No.

311584

Seq. ID

wen700333684.hl

Method NCBI GI BLASTN g1594283

BLAST score

220

E value

1.0e-120

Match length

276

% identity NCBI Description

Human transcription factor E2F1 (E2F1) gene, exons 4-7 and

complete cds

Seq. No.

311585

Seq. ID

wen700333686.h1

Method

BLASTN

NCBI GI

g3150089

BLAST score

93

E value

6.0e-45

Match length

165

% identity

89

NCBI Description

Homo sapiens DNA sequence from PAC 418A9 on chromosome

6q21. Contains the first (5') two exons of a CDK8 (Cell Division Protein Kinase 8) LIKE gene, a Neutral Calponin LIKE pseudogene, ESTs and STSs, complete sequence [Hom

Seq. No.

311586

Seq. ID Method · wen700333727.h1

NCBI GI

BLASTX g113609

BLAST score

E value

422

8.0e-42

Match length

88

% identity

93

NCBI Description

FRUCTOSE-BISPHOSPHATE ALDOLASE A (MUSCLE-TYPE ALDOLASE)

>gi 202835 (M12919) aldolase A (EC 4.1.2.13) [Rattus

norvegicus] >gi_1619605_emb_CAA27815_ (X04261) aldolase A

[Rattus norvegicus]

Seq. No.

311587

Seq. ID

wen700333731.h1

Method

BLASTX

NCBI GI

g4531444

BLAST score

257

E value

2.0e-22

Match length

% identity

95 55

NCBI Description

(AC006224) putative protein kinase [Arabidopsis thaliana]

Seq. No.

311588

Seq. ID Method

wen700333740.h1

NCBI GI

BLASTX

g108463

BLAST score

359

E value

1.0e-34

Match length

77

Seq. No.

311594



```
% identity
 NCBI Description
                    25K FK506/rapamycin-binding protein - bovine (fragment)
                    311589
 Seq. No.
                    wen700333759.h1
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g3347848
 BLAST score
                    310
 E value
                    1.0e-28
 Match length
                    64
 % identity
                    94
 NCBI Description
                    (AF055666) kinesin light chain 2 [Mus musculus]
 Seq. No.
                    311590
                    wen700333829.h1
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g1213442
 BLAST score
                    231
                    2.0e-19
 E value
 Match length
                    50
 % identity
                    84
 NCBI Description
                    (U48961) isopentenyl pyrophosphate isomerase [Arabidopsis
                    thaliana]
 Seq. No.
                    311591
 Seq. ID
                    wen700333904.hl
 Method
                    BLASTX
 NCBI GI
                    g2335108
 BLAST score
                    182
 E value
                    1.0e-13
 Match length
                    61
 % identity
                    54
 NCBI Description
                   (AC002339) putative isulinase [Arabidopsis thaliana]
 Seq. No.
                    311592
 Seq. ID
                    wen700333906.h1
 Method
                    BLASTX
 NCBI GI
                    q1345588
 BLAST score
                    265
 E value
                    3.0e-25
 Match length
                    68
 % identity
                    94
 NCBI Description
                    14-3-3-LIKE PROTEIN GF14-12 >qi 998432 bbs 164524
                    GF14-12=GRF2 product/14-3-3 protein homolog [Zea mays,
                    XL80, Peptide, 261 aa]
 Seq. No.
                    311593
 Seq. ID
                    wen700333908.hl
 Method
                    BLASTX
 NCBI GI
                    g4454478
BLAST score
                    193
 E value
                    4.0e-15
 Match length
                    68
 % identity
                    56
 NCBI Description
                   (AC006234) hypothetical protein [Arabidopsis thaliana]
```



Seq. ID wen700334095.h1 Method BLASTX q3859982 NCBI GI 155 BLAST score 1.0e-22 E value Match length 59 % identity 82 NCBI Description (AF091072) unknown [Homo sapiens] Seq. No. 311595 Seq. ID wen700334109.h1 Method BLASTN NCBI GI g3273244 BLAST score 43 E value 2.0e-15 Match length 59 93 % identity NCBI Description Oryza sativa DNA for NLS receptor, complete cds Seq. No. 311596 wen700334116.h1 Seq. ID Method BLASTX NCBI GI g1632755 BLAST score 223 8.0e-19 E value Match length 54 % identity 87 NCBI Description (D83585) proteasome Z subunit precursor [Mus musculus] >gi_2062107_emb_CAA71824_ (Y10874) proteasome subunti MC14 [Mus musculus] >gi_2547068 dbj BAA22857 (D85570) PSMB7 [Mus musculus] Seq. No. 311597 Seq. ID wen700334133.h1 Method BLASTN NCBI GI q4325179 BLAST score 127 1.0e-65 E value Match length 135 % identity 99 NCBI Description Homo sapiens tetraspan NET-6 mRNA, complete cds Seq. No. 311598 Seq. ID wen700334146.h1 Method BLASTX NCBI GI g627339 BLAST score 155 E value 8.0e-11 Match length 39 77 % identity NCBI Description tensin, cardiac muscle - chicken Seq. No. 311599

Seq. ID wen700334172.h1

Method BLASTN NCBI GI g168460 BLAST score 256

311600

1.0e-142 E value Match length 276 % identity 98

NCBI Description Zea mays cyclophilin (CyP) mRNA, complete cds

Seq. No.

Seq. ID wen700334184.h1

Method BLASTX NCBI GI q3386606 BLAST score 268 4.0e-24 E value Match length 60 % identity 75

NCBI Description (AC004665) putative beta-amylase [Arabidopsis thaliana]

311601 Seq. No.

Seq. ID wen700334187.hl

Method BLASTX NCBI GI g231443 178 BLAST score 2.0e-27 E value Match length 89 % identity 79

NCBI Description PROTEIN PHOSPHATASE PP2A, 65 KD REGULATORY SUBUNIT, ALPHA

ISOFORM (PROTEIN PHOSPHATASE PP2A SUBUNIT A, ALPHA ISOFORM)

(PR65-ALPHA) >gi_107300_pir__A34541 phosphoprotein phosphatase (EC 3.1.3.16) 2A-alpha 65K regulatory chain human >gi 189428 (J02902) phosphatase 2A regulatory subunit

[Homo sapiens]

Seq. No. 311602

wen700334209.h1 Seq. ID

Method BLASTN NCBI GI g3483435 BLAST score 166 E value 1.0e-88 Match length 209 % identity 95

NCBI Description Homo sapiens full length insert cDNA clone YZ86H11

Seq. No. 311603

Seq. ID wen700334250.h1

Method BLASTX NCBI GI g106468 BLAST score 220 E value 3.0e-18 Match length 85 % identity 55

Ig heavy chain V region precursor - human NCBI Description

>gi_37725_emb_CAA39626_ (X56158) immunoglobulin from VH4

family [Homo sapiens]

Seq. No. 311604

Seq. ID wen700334259.hl

Method BLASTX NCBI GI g4103635 BLAST score 174



```
6.0e-13
E value
Match length
                     64
% identity
                     45
                     (AF026538) ABA-responsive protein [Hordeum vulgare]
NCBI Description
Seq. No.
                     311605
Seq. ID
                     wen700334269.h1
Method
                     BLASTX
                     g4506681
NCBI GI
BLAST score
                     189
                     8.0e-15
E value
Match length
                     49
% identity
                     80
                     ribosomal protein S11 >gi_133723_sp_P04643_RS11_HUMAN 40S
RIBOSOMAL PROTEIN S11 >gi_71004_pir__R3HU11 ribosomal
protein S11 - human >gi_71005_pir__R3RT11 ribosomal protein
S11 - rat >gi_36144_emb_CAA29834__(X06617) ribosomal
NCBI Description
                     protein S11 (AA 1 - 158) [Homo sapiens] >gi 206739 (K03250)
                     ribosomal protein S11 [Rattus norvegicus] >gi 1938406
                     (U93864) ribosomal protein S11 [Mus musculus]
Seq. No.
                     311606
Seq. ID
                     wen700334270.h1
Method
                     BLASTX
NCBI GI
                     q1800217
BLAST score
                     223 🛷
E value
                     8.0e-19
Match length
                     50
% identity
                     (U56730) Phytochrome B [Sorghum bicolor]
NCBI Description
Seq. No.
                     311607
Seq. ID
                     wen700334275.hl
Method
                     BLASTN
NCBI GI
                     g3253129
BLAST score
                     105
                     2.0e-52
E value
Match length
                     149
                     93
% identity
NCBI Description
                     Homo sapiens chromosome 17, clone HRPC837J1, complete
                     sequence [Homo sapiens]
                     311608
Seq. No.
Seq. ID
                     wen700334280.h1
Method
                     BLASTN
NCBI GI
                     g473948
BLAST score
                     83
E value
                     5.0e-39
Match length
                     211
% identity
                     85
NCBI Description Human mRNA for KIAA0116 gene, partial cds
```

Seq. No. 311609

Seq. ID wen700334294.h1

Method BLASTX NCBI GI g4506761 BLAST score 282



E value 2.0e-25 Match length 57 % identity 93

NCBI Description S100 calcium-binding protein A10 (annexin II ligand,

calpactin I, light polypeptide (p11))

>gi_116486_sp_P08206_S110_HUMAN_CALPACTIN_I LIGHT_CHAIN (P10_PROTEIN) (P11) (CELLULAR LIGAND_OF_ANNEXIN_II) >gi_89438_pir__B28489_calpactin_I light_chain - bovine >gi_107251_pir__JC1139_calpactin_I light_chain_- human >gi_162785_(M16464)_calpactin_I light_chain_[Bos_taurus] >gi_179875_(M81457)_calpactin_I light_chain_[Homo_sapiens] >gi_180596_(M38591)_cellular_ligand_of_annexin_II_[Homo_

sapiens]

Seq. No. 311610

Seq. ID wen700334319.h1

Method BLASTN
NCBI GI g1724101
BLAST score 54
E value 5.0e-22
Match length 58
% identity 98

NCBI Description Mesembryanthemum crystallinum S-adenosyl-L-homocystein

hydrolase mRNA, complete cds

Seq. No. 311611

Seq. ID wen700334330.h1

Method BLASTX
NCBI GI g132540
BLAST score 194
E value 2.0e-15
Match length 37
% identity 95

NCBI Description TRANSFORMING PROTEIN RHOA (H12) >gi_68960_pir__TVHU12

GTP-binding protein rhoA - human >gi 2144596_pir _TVB012 GTP-binding protein rhoA - bovine >gi 36030 emb CAA28690 (X05026) ORF (AA 1-193) [Homo sapiens] >gi 162743 (M27278)

rho (Gb) protein [Bos taurus] $>gi_407697$ ($\overline{L}25080$)

GTP-binding protein [Homo sapiens]

Seq. No. 311612

Seq. ID wen700334343.h1

Method BLASTX
NCBI GI g3063653
BLAST score 263
E value 2.0e-23
Match length 54
% identity 94

NCBI Description (AF057356) calcyclin binding protein [Homo sapiens]

>gi_4200224_emb_CAA22910_ (AL035305) hypothetical protein

[Homo sapiens]

Seq. No. 311613

Seq. ID wen700334381.hl

Method BLASTN NCBI GI g7382486

BLAST score 78



2.0e-36 E value Match length 102 94 % identity

NCBI Description Homo sapiens chloride intracellular channel 1 (CLIC1) mRNA,

and translated products

Seq. No. 311614

Seq. ID wen700334385.h1

Method BLASTN NCBI GI g4504328 BLAST score 88 E value 2.0e-42 Match length 104 % identity 96

NCBI Description Homo sapiens hepatocyte growth factor activator inhibitor

(HAI) mRNA >gi_2924600_dbj_AB000095_AB000095 Homo sapiens mRNA for hepatocyte growth factor activator inhibitor,

complete cds

Seq. No. 311615

Seq. ID wen700334438.hl

Method BLASTN NCBI .GI q313141 BLAST score 45 E value 2.0e-16 Match length 61 % identity 93

NCBI Description Z.mays ZmPRO3 mRNA for profilin

Seq. No. 311616

Seq. ID wen700334455.h1

Method BLASTX NCBI GI g4504549 BLAST score 424 E value 4.0e-42 Match length 75

% identity 96

NCBI Description hexabrachion (tenascin C, cytotactin)

>gi_3915888_sp_P24821_TENA_HUMAN TENASCIN PRECURSOR (TN) (HEXABRACHION) (CYTOTACTIN) (NEURONECTIN) (GMEM) (JI) (MIOTENDINOUS ANTIGEN) (GLIOMA-ASSOCIATED-EXTRACELLULAR

MATRIX ANTIGEN) (GP 150-225) (TENASCIN-C) >gi_2119620_pir__A32160 tenascin-C - huma A32160 tenascin-C - human

>gi 556845 emb CAA55309 (X78565) human tenascin-C [Homo

sapiens]

Seq. No. 311617

Seq. ID wen700334477.h1

Method BLASTX NCBI GI q91322 BLAST score 141 E value 3.0e-09 Match length 38 % identity 74

NCBI Description SURF-1 protein - mouse

Seq. No. 311618

```
wen700334482.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3914006
BLAST score
                  235
                  3.0e-20
E value
Match length
                  50
% identity
                  94
NCBI Description
                  MITOCHONDRIAL LON PROTEASE HOMOLOG 2 PRECURSOR >gi 1816588
                  (U85495) LON2 [Zea mays]
Seq. No.
                  311619
Seq. ID
                  wen700334561.hl
Method
                  BLASTX
NCBI GI
                  q4503841
BLAST score
                  215
```

7.0e-18 E value Match length 50 % identity 84

NCBI Description thyroid autoantigen 70kD (Ku antigen)

>gi_125729 sp P12956 KU70 HUMAN ATP-DEPENDENT DNA HELICASE II, 70 KD SUBUNIT (LUPUS KU AUTOANTIGEN PROTEIN P70) (70 KD SUBUNIT OF KU ANTIGEN) (THYROID-LUPUS AUTOANTIGEN) (TLAA) (KU70) (CTC BOX BINDING FACTOR 75 KD SUBUNIT) (CTCBF) (CTC75) >gi_105163_pir__A30894 70K thyroid autoantigen human $>gi_178650$ ($\overline{J}046\overline{11}$) p70 autoantigen [Homo sapiens] $>gi_250497$ bbs_107206 (S38729) Ku autoantigen p70 subunit [human, Peptide, 609 aa] [Homo sapiens] >gi_307095 (M32865) Ku protein subunit [Homo sapiens] >gi 339667 (J04607)

thyroid autoantigen [Homo sapiens]

Seq. No. 311620

Seq. ID wen700334646.hl

Method BLASTX NCBI GI g4587533 BLAST score 231 2.0e-19 E value Match length 87 % identity 56

(AC007060) EST gb AA721821 comes from this gene. NCBI Description

[Arabidopsis thaliana]

Seq. No. 311621

Seq. ID wen700334725.h1

Method BLASTX NCBI GI q4432822 BLAST score 174 E value 8.0e-13 Match length 88 % identity 42

NCBI Description (AC006593) hypothetical protein [Arabidopsis thaliana]

Seq. No. 311622

wen700334805.h1 Seq. ID

Method BLASTX NCBI GI g401161 BLAST score 458 E value 4.0e-46



```
Match length 86
% identity 100
NCBI Description TUBULIN ALPHA-5 CHAIN >gi_322879_pir__S28982 tubulin alpha-5 chain - maize >gi_22156_emb_CAA44862 (X63177) alpha-tubulin #5 [Zea mays] >gi_450293 (L27815) alpha-tubulin [Zea mays] >gi_452474 (U05258) alpha-tubulin [Zea mays]

Seq. No. 311623
Seq. ID wen700334813.h1
```

Method BLASTN
NCBI GI g1575504
BLAST score 65
E value 2.0e-28
Match length 65

Match length 65 % identity 100

NCBI Description Mus musculus Tera (Tera) mRNA, complete cds

 Seq. No.
 311624

 Seq. ID
 wen700334830.h1

 Method
 BLASTX

 NCBI GI
 g4581164

 BLAST score
 181

BLAST score 181 E value 7.0e-14 Match length 55 % identity 62

NCBI Description (AC006220) putative polyprotein [Arabidopsis thaliana]

Seq. No. 311625

Seq. ID wen700334835.h1

Method BLASTX
NCBI GI g4262186
BLAST score 175
E value 3.0e-13
Match length 65
% identity 55

% identity 55
NCBI Description (AC005508) Highly similar to cullin 3 [Arabidopsis

thaliana]

Seq. No. 311626

Seq. ID wen700334844.h1

Method BLASTX
NCBI GI g2459436
BLAST score 137
E value 9.0e-09
Match length 55
% identity 47

NCBI Description (AC002332) unknown protein [Arabidopsis thaliana]

Seq. No. 311627

Seq. ID wen700334939.h1

Method BLASTX
NCBI GI g4587589
BLAST score 234
E value 9.0e-20
Match length 99
% identity 45

```
NCBI Description (AC007232) hypothetical protein [Arabidopsis thaliana]
```

```
Seq. No.
                   311628
Seq. ID
                   wen700334978.hl
Method
                   BLASTX
NCBI GI
                   g3461817
BLAST score
                   169
E value
                   2.0e-12
Match length
                   64
% identity
                   56
NCBI Description
                   (AC004138) unknown protein [Arabidopsis thaliana]
Seq. No.
                   311629
Seq. ID
                   wen700334992.h1
Method
                   BLASTN
NCBI GI
                   q643596
BLAST score
                   82
                   1.0e-38
E value
Match length
                   125
% identity
                   91
NCBI Description
                  Corn mRNA for cysteine proteinase, clone CCP, complete cds
Seq. No.
                   311630
Seq. ID
                   wen700335044.h1
Method
                   BLASTX
NCBI GI
                   q1709970
BLAST score
                   304
E value
                   5.0e-28
Match length
                   82
% identity
                   71
                  60S RIBOSOMAL PROTEIN L10A
NCBI Description
Seq. No.
                   311631
Seq. ID
                   wen700335081.h1
Method
                   BLASTX
NCBI GI
                   g2809481
BLAST score
                   319
E value
                   4.0e-30
Match length
                   62
                   100
% identity
NCBI Description
                  (AF042839) calmodulin [Oryza sativa]
                   311632
Seq. No.
Seq. ID
                   wen700335104.h1
Method
                  BLASTX
NCBI GI
                   g133021
BLAST score
                   292
E value
                   6.0e-38
Match length
                   93
% identity
                   81
                  60S RIBOSOMAL PROTEIN L7 >gi 71120 pir R5HU7 ribosomal
NCBI Description
                  protein L7 - human >gi 36140 emb CAA37139 (X52967)
                  ribosomal protein L7 [Homo sapiens]
Seq. No.
                  311633
```

Method BLASTX

wen700335110.h1

Seq. ID

Seq. ID

Method

NCBI GI

```
q445615
NCBI GI
BLAST score
                  274
                  1.0e-24
E value
                  59
Match length
                  90
% identity
NCBI Description ribosomal protein L27 [Pisum sativum]
Seq. No.
                  311634
                  wen700335147.hl
Seq. ID
Method
                  BLASTX
                  g127170
NCBI GI
BLAST score
                  196
E value
                  2.0e-15
Match length
                  42
% identity
                  90
NCBI Description
                  MYOSIN REGULATORY LIGHT CHAIN 2-A, SMOOTH MUSCLE ISOFORM
                  (MYOSIN RLC-A) >gi_112008_pir__A37100 myosin regulatory
                  light chain A, smooth muscle - rat >gi_57087_emb_CAA29080_
                  (X05566) RCL (AA 1-172) [Rattus norvegīcus]
Seq. No.
                  311635
                  wen700335188.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3687201
BLAST score
                  155
E value
                  6.0e-82
Match length
                  270
                  90
% identity
NCBI Description
                  Homo sapiens Xp22 bins 16-17 BAC GSHB-531I17 (Genome
                  Systems Human BAC Library) complete sequence [Homo sapiens]
Seq. No.
                  311636
Seq. ID
                  wen700335234.h1
Method
                  BLASTX
NCBI GI
                  g2492518
BLAST score
                  223
E value
                  1.0e-18
Match length
                  49
% identity
                  92
NCBI Description
                  26S PROTEASE REGULATORY SUBUNIT 7 (MSS1 PROTEIN)
                  >gi_1395179 dbj BAA09339 (D50694) proteasomal ATPase
                  (MSS1) [Rattus norvegicus]
Seq. No.
                  311637
Seq. ID
                  wen700335254.h1
Method
                  BLASTN
NCBI GI
                  g309514
BLAST score
                  110
                  3.0e-55
E value
Match length
                  206
% identity
                  88
NCBI Description
                  Mouse cysteine proteinase inhibitor (MS3) mRNA sequence
Seq. No.
                  311638
```

44460

wen700335261.h1

BLASTX

g400396

NCBI GI

E value

BLAST score

g4006829

2.0e-26

289



```
BLAST score
                    156
                    7.0e-11
E value
Match length
                    40
                   72
% identity
NCBI Description
                   NADH-UBIQUINONE OXIDOREDUCTASE B17 SUBUNIT (COMPLEX I-B17)
                    (CI-B17) >gi_346537_pir__S28246 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain CI-B17 - bovine
                   >gi_242_emb_CAA44897 (X63212) NADH dehydrogenase [Bos
                    taurus]
Seq. No.
                   311639
Seq. ID
                   wen700335272.h1
Method
                   BLASTX
NCBI GI
                   q554565
BLAST score
                   262
E value
                    4.0e-23
Match length
                   56
% identity
                   89
NCBI Description
                   (M24889) glutathione S-transferase [Artificial gene]
Seq. No.
                   311640
Seq. ID
                   wen700335368.h1
Method
                   BLASTN
NCBI GI
                   q1657762
BLAST score
                   82
E value
                   2.0e-38
Match length
                   293
% identity
                   44
NCBI Description
                   Zea mays retrotransposon Huck-2 5' LTR and primer binding
                   site DNA sequence
Seq. No.
                   311641
Seq. ID
                   wen700335463.h1
Method
                   BLASTX
NCBI GI
                   g3618320
BLAST score
                   212
                   3.0e-17
E value
Match length
                   76
% identity
                   62
NCBI Description
                   (AB001888) zinc finger protein [Oryza sativa]
Seq. No.
                   311642
Seq. ID
                   wen700335576.h1
Method
                   BLASTX
NCBI GI
                   g4314378
BLAST score
                   214
E value
                   2.0e-17
Match length
                   87
% identity
                   47
NCBI Description
                   (AC006232) putative lipase [Arabidopsis thaliana]
Seq. No.
                   311643
Seq. ID
                   wen700335586.h1
Method
                   BLASTX
```



Match length % identity 92

NCBI Description (AC005970) putative protein kinase [Arabidopsis thaliana]

Seq. No. 311644

Seq. ID wen700335594.h1

Method BLASTX NCBI GI g2494111 BLAST score 157 E value 5.0e-11 Match length 36 % identity 78

NCBI Description (AC002376) Contains similarity to Glycine protein kinase 6

(gb M67449). [Arabidopsis thaliana]

Seq. No. 311645

Seq. ID wen700335601.h1

Method BLASTN NCBI GI g4034056 BLAST score 78 E value 2.0e-36

Match length 98 % identity 95

NCBI Description Human DNA sequence from clone 108K11 on chromosome 6p21

> Contains SRP20 (SR protein family member), Ndr protein kinase gene similar to yeast suppressor protein SRP40, EST

and GSS, complete sequence [Homo sapiens]

Seq. No. 311646

Seq. ID wen700335613.h1

Method BLASTX NCBI GI g1352830 BLAST score 376 2.0e-36 E value Match length 77 % identity 97

NCBI Description VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A (V-ATPASE 69 KD

SUBUNIT) >gi_1049253 (U36436) vacuolar ATPase 69 kDa

subunit [Zea mays]

Seq. No. 311647

Seq. ID wen700335644.h1

Method BLASTX NCBI GI g135417 BLAST score 289 E value 3.0e-26 Match length 51 100 % identity

NCBI Description

TUBULIN ALPHA-3 CHAIN >gi_100946_pir__JN0105 tubulin alpha-3 chain - maize >gi_22150_emb_CAA44861_ (X63176) Alpha-tubulin #3 [Zea mays] >gi_485377 (M60171) alpha-3

tubulin [Zea mays]

Seq. No. 311648

Seq. ID wen700335662.h1

Method BLASTX NCBI GI "~ g4455350

```
BLAST score
                   2.0e-18
E value
Match length
                   60
                   67
% identity
NCBI Description
                  (AL035524) putative protein [Arabidopsis thaliana]
                  311649
Seq. No.
                  wen700335679.h1
Seq. ID
```

Method BLASTX g3927830 NCBI GI BLAST score 268 E value 8.0e-24 Match length 93

% identity 60

NCBI Description (AC005727) hypothetical protein [Arabidopsis thaliana]

Seq. No. 311650

Seq. ID wen700335728.h1

Method BLASTX NCBI GI g4503453 BLAST score 236 E value 2.0e-20 Match length 53 % identity 89

NCBI Description endothelial differentiation-related factor 1

>gi_3043445_emb_CAA06446_ (AJ005259) homologous to Bombyx mori multiprotein bridging factor (EMBL: AB001078) [Homo

sapiens]

Seq. No. 311651

Seq. ID wen700335754.h1

Method BLASTX NCBI GI g4506013 BLAST score 300 E value 5.0e-35 Match length 97 % identity

NCBI Description protein phosphatase 1, regulatory subunit 7

>gi_2136139_pir__S68209 sds22 protein homolog - human >gi_1085028_emb_CAA90626_ (Z50749) yeast sds22 homolog [Homo sapiens] >gi_4633067_gb_AAD26611.1_ (AF067136) protein phosphatase-1 regulatory subunit 7 alpha1 [Homo sapiens] >gi_1585165_prf _2124310A sds22 gene [Homo

sapiens]

Seq. No. 311652

Seq. ID wen700335838.h1

Method BLASTN NCBI GI g2133879 BLAST score 105 E value 3.0e-52 Match length 212 % identity

NCBI Description Genomic sequence from Mouse 9, complete sequence [Mus

musculus]

Seq. No. 311653

BLAST score

E value

97

2.0e-47

```
Seq. ID
                  wen700335862.h1
Method
                  BLASTN
                  q1101883
NCBI GI
BLAST score
                  104
E value
                   7.0e-52
Match length
                  116
% identity
                   97
NCBI Description
                  Rattus norvegicus muscle Y-box protein YB2 mRNA, complete
                  cds
Seq. No.
                  311654
Seq. ID
                  wen700335869.h1
Method
                  BLASTN
NCBI GI
                  q3769548
BLAST score
                  86
E value
                  6.0e-41
Match length
                  181
% identity
                  Mus musculus ubiquitin-conjugating enzyme HR6A mRNA,
NCBI Description
                  complete cds
Seq. No.
                  311655
Seq. ID
                  wen700335886.h1
Method
                  BLASTX
NCBI GI
                  g1354510
BLAST score
                  153
E value
                  1.0e-10
Match length
                  56
% identity
                  54
NCBI Description
                  (U55205) HAL2-like protein [Arabidopsis thaliana]
Seq. No.
                  311656
Seq. ID
                  wen700335889.h1
Method
                  BLASTX
NCBI GI
                  g4336325
BLAST score
                  187
E value
                  1.0e-14
Match length
                  36
% identity
                  92
                  (AF081282) small membrane protein 1 [Homo sapiens]
NCBI Description
Seq. No.
                  311657
Seq. ID
                  wen700336042.hl
Method
                  BLASTX
                  g55675
NCBI GI
BLAST score
                  141
                  3.0e-09
E value
Match length
                  25
                  100
% identity
                  (V01224) reading frame [Rattus norvegicus]
NCBI Description
                  311658
Seq. No.
Seq. ID
                  wen700336074.hl
                  BLASTN
Method
NCBI GI
                  g4506386
```

Match length % identity 87

Homo sapiens RAD23 (S. cerevisiae) homolog B (RAD23B) mRNA NCBI Description >gi 498147 dbj D21090 HUMHHR23B Human mRNA for XP-C repair

complementing protein (p58/HHR23B), complete cds

Seq. No. 311659

Seq. ID wen700336077.h1

Method BLASTX NCBI GI q2880042 BLAST score 142 E value 4.0e-09 Match length 57

% identity 54

(AC002340) putative 3-hydroxyisobutyryl-coenzyme A NCBI Description

hydrolase [Arabidopsis thaliana]

Seq. No. 311660

Seq. ID wen700336084.h1

Method BLASTX NCBI GI g1730519 BLAST score 481 E value 9.0e-49 Match length 98 % identity

PHOSPHOGLYCERATE KINASE >gi_2117894_pir__I48074 NCBI Description

phosphoglycerate kinase - Chinese hamster

>gi_987048_emb_CAA86028_ (Z37974) phosphoglycerate kinase

[Cricetulus griseus]

Seq. No. 311661

Seq. ID wen700336123.h1

Method BLASTX NCBI GI g312179 BLAST score 305 E value 3.0e-28 Match length 64 91 % identity

(X73151) glyceraldehyde 3-phosphate dehydrogenase NCBI Description

(phosphorylating) [Zea mays] >gi 1184772 (U45855) cytosolic glyceroldehyde-3-phosphate dehydrogenase GAPC2 [Zea mays]

>gi 1185554 (U45858) glyceraldehyde-3-phosphate

dehydrogenase [Zea mays]

Seq. No. 311662

Seq. ID wen700336140.h1

Method BLASTN NCBI GI g34342 BLAST score 102 E value 1.0e-50 Match length 142 % identity 93

NCBI Description Human mRNA for beta-galactoside-binding lectin

Seq. No. 311663

wen700336151.h1 Seq. ID

Method BLASTN

Method

NCBI GI BLAST score BLASTX g1518540

361

```
NCBI GI
                   q3413891
BLAST score
                   84
E value
                   1.0e-39
Match length
                   164
% identity
                   87
NCBI Description Homo sapiens mRNA for KIAA0465 protein, partial cds
Seq. No.
                   311664
Seq. ID
                   wen700336152.h1
Method
                   BLASTN
NCBI GI
                   q56669
BLAST score
                   165
E value
                   7.0e-88
Match length
                   257
% identity
                   92
NCBI Description Rat mRNA for ventricular myosin light chain
Seq. No.
                   311665
Seq. ID
                   wen700336170.h1
Method
                   BLASTX
NCBI GI
                   q1083700
BLAST score
                   270
E value
                   4.0e-24
Match length
                   57
% identity
                   91
NCBI Description
                   insulin-stimulated phosphoprotein PHAS-I - rat >gi 468024
                    (U05014) PHAS-I [Rattus norvegicus]
Seq. No.
                   311666
Seq. ID
                   wen700336235.h1
Method
                   BLASTN
NCBI GI
                   g3483442
BLAST score
                   96
E value
                   4.0e-47
Match length
                   116
% identity
                   96
NCBI Description Homo sapiens full length insert cDNA clone YZ88E05
Seq. No.
                   311667
Seq. ID
                   wen700336238.h1
Method
                   BLASTX
NCBI GI
                   g4502163
BLAST score
                   203
E value
                   2.0e-16
Match length
                   37
% identity
                   97
                   apolipoprotein D >gi_114034_sp_P05090_APD_HUMAN APOLIPOPROTEIN D PRECURSOR >gi_72088_pir_LPHUD
NCBI Description
                   apolipoprotein D precursor - human >gi_178841 (J02611)
                   apolipoprotein D precursor [Homo sapiens] >gi 178847
                   (M16696) apolipoprotein D precursor [Homo sapiens]
Seq. No.
                   311668
Seq. ID
                   wen700336343.h1
```

```
E value
                  1.0e-34
Match length
                  79
% identity
                  90
NCBI Description
                  (U53418) UDP-glucose dehydrogenase [Glycine max]
                  311669
Seq. No.
Seq. ID
                  wen700336346.h1
Method
                  BLASTX
                  g548770
NCBI GI
BLAST score
                  307
E value
                  1.0e-28
Match length
                  64
% identity
                  88
NCBI Description
                  60S RIBOSOMAL PROTEIN L3 >gi_481228_pir___S38359 ribosomal
                  protein L3 - rice >gi 303853 dbj BAA02155 (D12630)
                  ribosomal protein L3 [Oryza sativa]
Seq. No.
                  311670
Seq. ID
                  wen700336375.h1
Method
                  BLASTX
NCBI GI
                  g4507523
BLAST score
                  183
E value
                  4.0e-14
Match length
                  38
% identity
                  92
NCBI Description
                  transducin-like enhancer of split 2, homolog of Drosophila
                  E(sp1) >gi 464897 sp Q04725 TLE2 HUMAN TRANSDUCIN-LIKE
                  ENHANCER PROTEIN 2 (ESG2) >gi 1082865 pir C56695
                  transducin-like enhancer-of-split homolog TLE-2 - human
                  >gi 307512 (M99436) transducin-like enhancer protein [Homo
                  sapiens]
Seq. No.
                  311671
Seq. ID
                  wen700336381.h1
Method
                  BLASTN
NCBI GI
                  g35631
BLAST score
                  93
E value
                  2.0e-45
Match length
                  113
% identity
                  96
NCBI Description
                  Human PRAD1 mRNA for cyclin
                  311672
Seq. ID
                  wen700336390.h1
Method
                  BLASTN
```

Seq. No.

NCBI GI g4455409 BLAST score 100 E value 2.0e-49 Match length 165 % identity 89

NCBI Description Human DNA sequence from clone 1049G16 on chromosome

20q12-13.2 Contains gene similar to

GLUCOSAMINE-6-SULFATASE, a nuclear receptor coactivator gene, ESTs, STSs, GSSs, complete sequence [Homo sapiens]

Seq. No. 311673

Seq. ID wen700336394.h1

```
Method
                  BLASTX
NCBI GI
                  q2160694
BLAST score
                  288
E value
                  2.0e-26
Match length
                  71
% identity
                  75
NCBI Description
                  (U73528) B' regulatory subunit of PP2A [Arabidopsis
                  thaliana]
Seq. No.
                  311674
Seq. ID
                  wen700336416.h1
Method
                  BLASTN
NCBI GI
                  q2648017
BLAST score
                  176
E value
                  1.0e-94
Match length
                  187
                  99
% identity
NCBI Description
                  Human DNA sequence from cosmid F0811 on chromosome 6.
                  Contains Daxx, BING1, Tapasin, RGL2, KE2, BING4, BING5,
                  ESTs and CpG islands
Seq. No.
                  311675
Seq. ID
                  wen700336417.h1
Method
                  BLASTX
NCBI GI
                  q4519623
BLAST score
                  365
                  4.0e-39
E value
Match length
                  96
% identity
                  86
                  (AB017616) homologous to the yeast YGR163 gene [Mus
NCBI Description
                  musculus]
Seq. No.
                  311676
Seq. ID
                  wen700336449.h1
Method
                  BLASTN
NCBI GI
                  q3319676
BLAST score
                  231
E value
                  1.0e-127
Match length
                  298
% identity
                  52
NCBI Description
                  Human DNA sequence from clone 323P24 on chromosome
                  Xp11.21-11.23 Contains SPIN (spindlin homolog (PROTEIN
                  DXF34), hypothetical protein EST, STS, GSS, complete
                  sequence [Homo sapiens]
Seq. No.
                  311677
Seq. ID
                  wen700336508.hl
Method
                  BLASTX
NCBI GI
                  g1519249
BLAST score
                  193
E value
                  4.0e-15
```

Match length 56 70 % identity

NCBI Description (U65956) GF14-b protein [Oryza sativa]

Seq. No.

311678

wen700336529.h1 Seq. ID



```
BLASTN
Method
NCBI GI
                  q3288442
                  236
BLAST score
                  1.0e-130
E value
Match length
                  273
                  96
% identity
NCBI Description
                  Homo sapiens DNA sequence from clone 511B24 on chromosome
                  20q11.2-12. Contains the TOP1 gene for Topoisomerase I, the
                  PLCG1 gene for 1-Phosphatidylinositol-4,5-Bisphosphate
```

Phosphodiesterase Gamma 1 (EC 3.1.4.11, PLC-Ga Seq. No. 311679

 Seq. ID
 wen700336554.h1

 Method
 BLASTN

 NCBI GI
 g3851208

 BLAST score
 64

 E value
 4.0e-28

E value 4.0 Match length 80 % identity 95

NCBI Description Homo sapiens chromosome 4 clone B366024 map 4q25, complete

sequence [Homo sapiens]

Seq. No. 311680

Seq. ID wen700336633.h1

Method BLASTX
NCBI GI g1345588
BLAST score 307
E value 1.0e-31
Match length 80
% identity 97

NCBI Description 14-3-3-LIKE PROTEIN GF14-12 >gi_998432_bbs_164524

GF14-12=GRF2 product/14-3-3 protein homolog [Zea mays,

XL80, Peptide, 261 aa]

Seq. No. 311681

Seq. ID wen700336683.h1

Method BLASTX
NCBI GI g2358275
BLAST score 424
E value 4.0e-42
Match length 91
% identity 92

NCBI Description (AF004368) UDP-glucose pyrophosphorylase [Cricetulus

griseus]

Seq. No. 311682

Seq. ID wen700336762.h1

Method BLASTN
NCBI GI g22292
BLAST score 78
E value 4.0e-36
Match length 191
% identity 90

NCBI Description Z.mays mRNA for glycine-rich protein

Seq. No. 311683

Seq. ID wen700336772.h1



```
Method
                  BLASTX
NCBI GI
                  g113621
BLAST score
                  476
                  3.0e-48
E value
Match length
                  93
% identity
                  100
NCBI Description
                  FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME
                  >gi_68196_pir__ADZM fructose-bisphosphate aldolase (EC
                  4.1.2.13), cytosolic - maize >gi_168420 (M16220) aldolase
                  [Zea mays] >gi_295850_emb_CAA31366_ (X12872) fructose
                  bisphosphate aldolase [Zea mays] >gi_225624_prf__1307278A
                  cytoplasmic aldolase [Zea mays]
Seq. No.
                  311684
Seq. ID
                  wen700336787.h1
Method
                  BLASTN
NCBI GI
                  q1006784
```

BLAST score 116
E value 1.0e-58
Match length 140
% identity 96

NCBI Description Rattus norvegicus B/K protein mRNA, complete cds

Seq. No. 311685

Seq. ID wen700336793.h1

Method BLASTN
NCBI GI g32708
BLAST score 173
E value 1.0e-92
Match length 240
% identity 94

NCBI Description H.sapiens mRNA for IFP53

Seq. No. 311686

Seq. ID wen700336915.h1

Method BLASTX
NCBI GI g1351974
BLAST score 301
E value 1.0e-27
Match length 61
% identity 100

NCBI Description ADP-RIBOSYLATION FACTOR >gi_1076788_pir__S49325

ADP-ribosylation factor - maize >gi_1076789_pir__S53486 ADP-ribosylation factor - maize >gi_556686_emb_CAA56351_

(X80042) ADP-ribosylation factor [Zea mays]

Seq. No. 311687

Seq. ID wen700336986.h1

Method BLASTX
NCBI GI g3319212
BLAST score 251
E value 8.0e-22
Match length 67
% identity 69

NCBI Description (U84140) self-pruning protein [Lycopersicon esculentum]

Seq. No. 311688

```
Seq. ID
                   wev700404949.h1
Method
                  BLASTX
                   q2983819
NCBI GI
BLAST score
                   189
E value
                   2.0e-15
Match length
                   76
% identity
                   54
NCBI Description
                  (AE000739) valyl-tRNA synthetase [Aquifex aeolicus]
Seq. No.
                   311689
Seq. ID
                  wev700405044.h1
Method
                   BLASTX
NCBI GI
                   g2293566
BLAST score
                   366
E value
                   3.0e-35
Match length
                  73
% identity
                   99
NCBI Description
                  (AF012896) ADP-ribosylation factor 1 [Oryza sativa]
Seq. No.
                   311690
Seq. ID
                  wev700405046.h1
Method
                  BLASTX
NCBI GI
                  g3702327
BLAST score
                   204
                   3.0e-16
E value
Match length
                  56
% identity
                   62
NCBI Description
                  (AC005397) unknown protein [Arabidopsis thaliana]
Seq. No.
                   311691
Seq. ID
                  wty700162623.h1
Method
                  BLASTX
NCBI GI
                  g4455171
BLAST score
                  152
E value
                  2.0e-10
Match length
                  77
% identity
                   43
NCBI Description
                  (AL035521) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  311692
Seq. ID
                  wty700162711.h1
Method
                  BLASTX
NCBI GI
                  g3935170
BLAST score
                  254
E value
                  2.0e-22
Match length
                  49
% identity
                  88
NCBI Description
                  (AC004557) F17L21.13 [Arabidopsis thaliana]
```

Seq. No. 311693

Seq. ID wty700162720.h1

Method BLASTN
NCBI GI g4105718
BLAST score 124
E value 2.0e-63
Match length 164
% identity 94

BLAST score

Match length

% identity

E value

173

62

48

7.0e-13

```
NCBI Description Zea mays cell wall invertase Incw2 gene, complete cds
                  311694
Seq. No.
Seq. ID
                  wty700162754.h1
Method
                  BLASTX
NCBI GI
                  g4588906
BLAST score
                  155
E value
                  1.0e-10
Match length
                  36
% identity
                  83
NCBI Description
                  (AF118149) ribosomal protein S7 [Secale cereale]
Seq. No.
                  311695
Seq. ID
                  wty700162769.h1
Method
                  BLASTX
NCBI GI
                  q113621
BLAST score
                  403
E value
                  8.0e-40
Match length
                  79
                  100
% identity
                  FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME
NCBI Description
                  >gi_68196_pir__ADZM fructose-bisphosphate aldolase (EC
                  4.1.2.13), cytosolic - maize >gi_168420 (M16220) aldolase
                   [Zea mays] >gi_295850_emb_CAA31366_ (X12872) fructose
                  bisphosphate aldolase [Zea mays] >gi_225624_prf__1307278A
                  cytoplasmic aldolase [Zea mays]
                  311696
Seq. No.
Seq. ID
                  wty700162819.hl
Method
                  BLASTX
NCBI GI
                  g1351856
BLAST score
                  275
E value
                  2.0e-30
Match length
                  78
% identity
                  67
NCBI Description
                  ACONITATE HYDRATASE, CYTOPLASMIC (CITRATE HYDRO-LYASE)
                   (ACONITASE) >gi_868003_dbj BAA06108 (D29629) aconitase
                   [Cucurbita sp.]
Seq. No.
                  311697
Seq. ID
                  wty700162820.h1
Method
                  BLASTX
NCBI GI
                  g4455350
BLAST score
                  150
E value
                  1.0e-10
Match length
                  59
% identity
                  63
NCBI Description
                  (AL035524) putative protein [Arabidopsis thaliana]
Seq. No.
                  311698
Seq. ID
                  wty700162852.h1
Method
                  BLASTX
NCBI GI
                  g2674203
```



```
(AF036328) CLP protease regulatory subunit CLPX
NCBI Description
                   [Arabidopsis thaliana]
                   311699
Seq. No.
Seq. ID
                  wty700162917.h1
Method
                  BLASTX
NCBI GI
                  g629602
BLAST score
                 - 173
E value
                  8.0e-13
Match length
                  51
% identity
                   61
NCBI Description
                  probable imbibition protein - wild cabbage
                  >gi 488787 emb CAA55893 (X79330) putative imbibition
                  protein [Brassica oleracea]
                  311700
Seq. No.
Seq. ID
                  wty700162937.h1
Method
                  BLASTN
NCBI GI
                  g2062705
BLAST score
                  35
                  2.0e-10
E value
Match length
                  35
% identity
                  100
NCBI Description
                  Human butyrophilin (BTF5) mRNA, complete cds
Seq. No.
                  311701
Seq. ID
                  wty700163007.h1
Method
                  BLASTX
NCBI GI
                  g4467115
                  157
BLAST score
E value
                  5.0e-11
Match length
                  54
% identity
                   65
NCBI Description
                  (AL035538) putative protein [Arabidopsis thaliana]
Seq. No.
                  311702
Seq. ID
                  wty700163012.h1
Method
                  BLASTX
NCBI GI
                  q3953477
BLAST score
                  151
E value
                  4.0e-10
Match length
                  80
% identity
                  40
NCBI Description (AC002328) F2202.22 [Arabidopsis thaliana]
                  311703
Seq. No.
Seq. ID
                  wty700163016.hl
Method
                  BLASTX
                  g1495366
```

NCBI GI BLAST score 288 E value 4.0e-26 Match length 93 % identity 63

NCBI Description (Z69370) nitrite transporter [Cucumis sativus]

Seq. No. 311704

wty700163111.h1 Seq. ID



```
Method
                   BLASTN
NCBI GI
                   g2665839
BLAST score
                   53
                   2.0e-21
E value
Match length
                   97
                   98
% identity
NCBI Description
                   Zea mays putative histone deacetylase RPD3 mRNA, complete
Seq. No.
                   311705
Seq. ID
                   wty700163118.h1
Method
                   BLASTX
NCBI GI
                   q1213536
BLAST score
                   190
E value
                   8.0e-15
Match length
                   71
                   54
% identity
NCBI Description
                   (U50193) the above GenBank entry begins at aa 120
                   [Caenorhabditis elegans]
Seq. No.
                   311706
Seq. ID
                   wty700163129.h1
Method
                   BLASTX
                   g2098575
NCBI GI
BLAST score
                   190
E valme
                   6.0e-15
Match length
                   45
                   76
% identity
NCBI Description
                   (AC002115) F25451 2 [Homo sapiens]
Seq. No.
                   311707
Seq. ID
                   wty700163147.h1
Method
                   BLASTN
NCBI GI
                   g1906603
BLAST score
                   44
                   4.0e-16
E value
Match length
                   68
% identity
                   91
NCBI Description
                   Zea mays ACCase gene, intron containing colonist1 and
                   colonist2 retrotransposons and reverse transcriptase
                   pseudogene, complete sequence
Seq. No.
                   311708
Seq. ID
                   wty700163232.h1
Method
                   BLASTX
NCBI GI
                   g2827631
BLAST score
                   190
                   9.0e-15
E value
                   53
Match length
% identity
                   64
                  (AL021636) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   311709
Seq. ID
                   wty700163258.h1
```

44474

BLASTN

44

g2331140

Method NCBI GI

BLAST score

E value

Match length

% identity

4.0e-12

45

67

```
E value
                  9.0e-16
Match length
                  88
% identity
                  88
NCBI Description
                  Oryza sativa water-stress inducible protein (WSI) mRNA,
                  complete cds
Seq. No.
                  311710
Seq. ID
                  wty700163260.h1
Method
                  BLASTN
NCBI GI
                  g2062705
BLAST score
                  36
E value
                  5.0e-11
Match length
                  36
% identity
                  100
NCBI Description Human butyrophilin (BTF5) mRNA, complete cds
Seq. No.
                  311711
Seq. ID
                  wty700163301.h1
Method
                  BLASTN
NCBI GI
                  g2286152
BLAST score
                  127
E value
                  3.0e-65
Match length
                  156
% identity
                  94
NCBI Description
                  Zea mays cytoplasmic malate dehydrogenase mRNA, complete
Seq. No.
                  311712
Seq. ID
                  wty700163326.h1
Method
                  BLASTN
NCBI GI
                  g2062705
BLAST score
                  36
                  6.0e-11
E value
Match length
                  36
                  100
% identity
NCBI Description
                  Human butyrophilin (BTF5) mRNA, complete cds
                  311713
Seq. No.
Seq. ID
                  wty700163364.h1
Method
                  BLASTX
NCBI GI
                  g2894598
BLAST score
                  196
E value
                  2.0e-15
Match length
                  62
% identity
                  61
NCBI Description
                  (AL021889) putative protein [Arabidopsis thaliana]
Seq. No.
                  311714
Seq. ID
                  wty700163477.h1
Method
                  BLASTX
NCBI GI
                  g3004565
BLAST score
                  166
```

NCBI Description (AC003673) putative protein kinase [Arabidopsis thaliana]

Seq. ID

311720

wty700163695.h1

```
311715
Seq. No.
Seq. ID
                  wty700163543.h1
Method
                  BLASTX
                  g3415115
NCBI GI
BLAST score
                   221
                  2.0e-18
E value
Match length
                  58
% identity
                   66
                  (AF081202) villin 2 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  311716
Seq. ID
                  wty700163562.h1
Method
                  BLASTX
NCBI GI
                  g3885882
BLAST score
                   145
                   3.0e-17
E value
Match length
                  51
% identity
                   96
NCBI Description
                  (AF093629) inorganic pyrophosphatase [Oryza sativa]
Seq. No.
                  311717
Seq. ID
                  wty700163566.hl
Method
                  BLASTX
NCBI GI
                  q4106515
BLAST score
                  256
E value
                  2.0e-22
Match length
                  84
% identity
                  57
NCBI Description
                   (AF092743) CAK associated cyclinH homolog [Populus tremula
                  x Populus tremuloides]
                  311718
Seq. No.
Seq. ID
                  wty700163655.h1
Method
                  BLASTX
NCBI GI
                  g120670
BLAST score
                  437
                  1.0e-43
E value
Match length
                  83
% identity
                  100
NCBI Description
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
                  >gi 100879 pir S06879 glyceraldehyde-3-phosphate
                  dehydrogenase (EC 1.2.1.12) C - maize
                  >gi_295853 emb CAA33620 (X15596) GAPDH [Zea mays]
Seq. No.
                  311719
Seq. ID
                  wty700163663.h1
Method
                  BLASTX
NCBI GI
                  g3128224
BLAST score
                  190
                  9.0e-15
E value
                  79
Match length
                  48
% identity
                   (AC004077) putative protein serine/threonine kinase
NCBI Description
                   [Arabidopsis thaliana]
```



```
Method
                  BLASTX
NCBI GI
                  g2130121
BLAST score
                  402
E value
                  7.0e-40
Match length
                  79
% identity
                  100
NCBI Description
                  cyclin II - maize >gi 516550 (U10077) cyclin IIZm [Zea
Seq. No.
                  311721
Seq. ID
                  wty700163704.h1
Method
                  BLASTN
NCBI GI
                  q1667388
BLAST score
                  57
E value
                  2.0e-23
Match length
                  65
% identity
                  Z.mays gene encoding 3-hydroxy-3-methylglutaryl-CoA
NCBI Description
                  reductase
Seq. No.
                  311722
Seq. ID
                  wty700163773.h1
Method
                  BLASTX
                  q3850585
NCBI GI
BLAST score
                  153
E value
                  1.0e-10
Match length
                  74
% identity
                  46
                  (AC005278) ESTs gb_H36966, gb_R65511, gb_T42324 and
NCBI Description
                  gb T20569 come from this gene. [Arabidopsis thaliana]
Seq. No.
                  311723
Seq. ID
                  wty700163806.h1
Method
                  BLASTX
NCBI GI
                  q4115913
BLAST score
                  242
E value
                  7.0e-21
Match length
                  81
% identity
NCBI Description
                  (AF118222) contains similarity to Iron/Ascorbate family of
                  oxidoreductases (Pfam: PF00671, Score=307.1, E=2.2e-88,
                  N=1) [Arabidopsis thaliana] >gi 4539409 emb CAB40042.1
                  (AL049524) putative flavanone 3-beta-hydroxylase
                  [Arabidopsis thaliana]
Seq. No.
                  311724
Seq. ID
                  wty700163813.h1
Method
                  BLASTN
NCBI GI
                  g563926
BLAST score
                  149
E value
                  2.0e-78
Match length
                  197
% identity
                  95
NCBI Description
                  Zea mays xyloglucan endo-transglycosylase homolog mRNA,
```

44477

complete cds

```
wty700163822.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1001478
BLAST score
                   186
E value
                   2.0e-14
Match length
                   76
% identity
                   49
NCBI Description
                  (D63999) hypothetical protein [Synechocystis sp.]
Seq. No.
                   311726
                   wty700163835.hl
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1839188
BLAST score
                   159
E value
                   4.0e-11
Match length
                   37
% identity
                   81
NCBI Description
                  (U86081) root hair defective 3 [Arabidopsis thaliana]
Seq. No.
                   311727
Seq. ID
                   wty700163847.h1
Method
                   BLASTX
NCBI GI
                   g4008006
BLAST score
                   161
E value
                   2.0e-11
Match length
                   52
% identity
NCBI Description
                   (AF084034) receptor-like protein kinase [Arabidopsis
                   thaliana]
Seq. No.
                   311728
Seq. ID
                   wty700163873.h1
Method
                   BLASTX
NCBI GI
                   g2058284
BLAST score
                   163
                                                                ٠<u>٠</u>
E value
                   1.0e-11
Match length
                   60
% identity
                   52
NCBI Description
                  (X97378) atranbp1b [Arabidopsis thaliana]
Seq. No.
                   311729
Seq. ID
                   wty700163910.h1
Method
                   BLASTN
NCBI GI
                   q3821780
BLAST score
                   36
E value
                   5.0e-11
Match length
                   36
% identity
                   100
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                   311730
Seq. ID
                   wty700163914.h1
Method
                   BLASTN
NCBI GI
                   g3821780
BLAST score
                   36
E value
                   6.0e-11
Match length
                   48
```

```
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                   311731
Seq. ID
                   wty700163918.hl
Method
                   BLASTX
NCBI GI
                   q4467134
BLAST score
                   252
                   4.0e-22
E value
Match length
                   66
% identity
                   71
NCBI Description
                   (AL035540) protein kinase like protein [Arabidopsis
                   thaliana]
                   311732
Seq. No.
Seq. ID
                   wty700163922.h1
Method
                   BLASTX
NCBI GI
                   g1519251
BLAST score
                   233
E value
                   5.0e-20
                   49
Match length
% identity
                   98
NCBI Description
                   (U65957) GF14-c protein [Oryza sativa]
Seq. No.
                   311733
                   wty700163970.hl
Seq. ID
Method
                   BLASTN
NCBI GI
                   q3821780
BLAST score
                   34
                   8.0e-10
E value
Match length
                   34
                   100
% identity
NCBI Description
                   Xenopus laevis cDNA clone 27A6-1
Seq. No.
                   311734
Seq. ID
                   wty700163975.h1
Method
                   BLASTX
NCBI GI
                   q3335366
BLAST score
                   153
E value
                   2.0e-10
Match length
                   46
% identity
                   59
NCBI Description
                   (AC003028) unknown protein [Arabidopsis thaliana]
Seq. No.
                   311735
Seq. ID
                   wty700163993.h1
Method
                   BLASTX
NCBI GI
                   g4588906
BLAST score
                   217
E value
                   4.0e-18
Match length
                   44
                   95
% identity
                   (AF118149) ribosomal protein S7 [Secale cereale]
NCBI Description
Seq. No.
                   311736
Seq. ID
                   wty700164057.h1
- Method
                   BLASTN
```

, ept

```
NCBI GI
                  q3821780
BLAST score
                  36
                  5.0e-11
E value
                  36
Match length
                  100
% identity
                  Xenopus laevis cDNA clone 27A6-1
NCBI Description
                  311737
Seq. No.
                  wty700164059.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4263710
BLAST score
                  237
E value
                  2.0e-20
Match length
                  62
                  77
% identity
                  (AC006223) putative pur-alpha transcriptional activator
NCBI Description
                  protein [Arabidopsis thaliana]
Seq. No.
                  311738
                  wty700164115.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3980410
BLAST score
                  148
E value
                  6.0e-10
Match length
                  45
% identity
                  58
                   (AC004561) putative receptor-like protein kinase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  311739
Seq. ID
                  wty700164138.h1
Method
                  BLASTX
                  g1345719
NCBI GI
BLAST score
                  228
                  2.0e-19
E value
Match length
                  49
% identity
                  92
                  CALCIUM-DEPENDENT PROTEIN KINASE 2 (CDPK 2) >qi 886821
NCBI Description
                   (U28376) calcium-dependent protein kinase [Zea mays]
                  311740
Seq. No.
Seq. ID
                  wty700164162.h1
Method
                  BLASTX
NCBI GI
                  q4490310
BLAST score
                  159
E value
                  2.0e-11
Match length
                  37
                  84
% identity
                  (AL035678) somatic embryogenesis receptor-like kinase-like
NCBI Description
                  protein [Arabidopsis thaliana]
Seq. No.
                  311741
Seq. ID
                  wty700164211.h1
```

Method BLASTN
NCBI GI g3550435
BLAST score 33
E value 4.0e-09

```
Match length
                  41
% identity
                  95
NCBI Description
                  Hordeum vulgare Hotr1 gene
                  311742
Seq. No.
                  wty700164220.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4587556
BLAST score
                  162
                  2.0e-11
E value
Match length
                  46
                  70
% identity
NCBI Description
                  (AC006577) Similar to gi_1653162 (p)ppGpp
                  3-pyrophosphohydrolase from Synechocystis sp genome
                  gb D90911. EST gb W43807 comes from this gene.
                  [Arabidopsis thaliana]
Seq. No.
                  311743
Seq. ID
                  wty700164227.h1
Method
                  BLASTX
                  g232033
NCBI GI
BLAST score
                  265
                  1.0e-23
E value
Match length
                  58
% identity
                  88
                  ELONGATION FACTOR 1 BETA' >gi_479830_pir__$35501
NCBI Description
                  translation elongation factor eEF-1 beta chain - wheat
                  >gi 218341 dbj BAA02436 (D13147) elongation factor 1 beta'
                  [Triticum aestivum]
Seq. No.
                  311744
                  wty700164269.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3927830
BLAST score
                  143
E value
                  2.0e-09
Match length
                  62
% identity
                  52
NCBI Description
                  (AC005727) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  311745
                  wty700164317.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g459267
BLAST score
                  111
E value
                  7.0e-56
                  151
Match length
% identity
NCBI Description Z.mays gene for HMG protein
Seq. No.
                  311746
Seq. ID
                  wty700164347.h1
Method
                  BLASTX
NCBI GI
                  q122007
BLAST score
                  172
```

1.0e-12

36

E value Match length

```
% identity
                   <code>HISTONE H2A >gi_100161_pir__S11498 histone H2A - parsley >gi_20448_emb_CAA37828_ (X53831) H2A histone protein (AA 1</code>
NCBI Description
                    - 149) [Petroselinum crispum]
Seq. No.
                    311747
Seq. ID
                    wty700164362.h1
Method
                    BLASTX
NCBI GI
                    g2565275
                    248
BLAST score
                    1.0e-21
E value
Match length
                    56
% identity
                    75
                   (AF023611) Dim1p homolog [Homo sapiens]
NCBI Description
                    311748
Seq. No.
                    wty700164411.hl
Seq. ID
Method
                    BLASTX
NCBI GI
                    g3641870
BLAST score
                    144
                    1.0e-09
E value
Match length
                    52
                    52
% identity
NCBI Description (AJ011013) hypothetical protein [Cicer arietinum]
Seq. No.
                    311749
Seq. ID
                    wty700164414.hl
Method
                    BLASTX
NCBI GI
                    q3036807
BLAST score
                    176
                    2.0e-13
E value
Match length
                    62
% identity
                    56
NCBI Description
                   (AL022373) putative protein [Arabidopsis thaliana]
Seq. No.
                    311750
Seq. ID
                    wty700164418.h1
Method
                    BLASTN
NCBI GI
                    q433040
BLAST score
                    77
                    2.0e-35
E value
Match length
                    129
% identity
                    90
NCBI Description
                    Zea mays W-22 clone PREM-1A retroelement PREM-1, partial
                    sequence
Seq. No.
                    311751
Seq. ID
                    wty700164457.h1
Method
                    BLASTX
NCBI GI
                    g3068713
BLAST score
                    161
E value
                    2.0e-11
Match length
                    60
% identity
                    55
```

44482

NCBI Description (AF049236) unknown [Arabidopsis thaliana]

```
Seq. ID
                  wty700164485.hl
Method
                  BLASTX
NCBI GI
                  q3850573
BLAST score
                  174
E value
                  5.0e-13
Match length
                  62
% identity
                  47
NCBI Description
                  (AC005278) Similar to gi_1652733 glycogen operon protein
                  GlgX from Synechocystis sp. genome gb_D90908. ESTs
                  gb_H36690, gb_AA712462, gb_AA651230 and gb_N95932 come from
                  this gene. [Arabidopsis thaliana]
Seq. No.
                  311753
                  wty700164561.h1
Seq. ID
Method
                  BLASTN
                  q3821780
NCBI GI
BLAST score
                  36
                  6.0e-11
E value
Match length
                  36
% identity
                  100
NCBI Description
                  Xenopus laevis cDNA clone 27A6-1
Seq. No.
                  311754
Seq. ID
                  wty700164589.h1
Method
                  BLASTX
                  g541920
NCBI GI
BLAST score
                  288
E value
                  2.0e-26
Match length
                  60
                  88
% identity
NCBI Description Acetoacyl-CoA-thiolase - radish
Seq. No.
                  311755
Seq. ID
                  wty700164668.h1
Method
                  BLASTX
NCBI GI
                  g1173257
BLAST score
                  188
E value
                  1.0e-14
Match length
                  40
% identity
                  88
NCBI Description
                  40S RIBOSOMAL PROTEIN S4 >gi 1076674 pir S47642 ribosomal
                  protein S4 - potato >gi 457803 emb CAA54095 (X76651)
                  ribosomal protein S4 [Solanum tuberosum]
Seq. No.
                  311756
Seq. ID
                  wty700164673.h1
Method
                  BLASTX
                  q2827699
                  162
                  2.0e-11
Match length
                  39
```

NCBI GI BLAST score E value

72 % identity

NCBI Description (AL021684) predicted protein [Arabidopsis thaliana]

Seq. No.

311757

Seq. ID wty700164686.h1

Method

BLASTN

BLAST score

Match length

E value

194

2.0e-15 41

```
NCBI GI
                  g3821780
BLAST score
                  37
E value
                  1.0e-11
Match length
                  37
                  100
% identity
NCBI Description
                  Xenopus laevis cDNA clone 27A6-1
                  311758
Seq. No.
                  wty700164760.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1076641
BLAST score
                  157
                  4.0e-11
E value
Match length
                  32
% identity
                  94
NCBI Description
                  tau-protein kinase (EC 2.7.1.135) homolog - common tobacco
                  >gi_456356_emb_CAA54803_ (X77763) shaggy like protein
                  kinase [Nicotiana tabacum] >gi 1094395 prf 2106142A
                  Ser/Thr protein kinase [Nicotiana tabacum]
Seq. No.
                  311759
Seq. ID
                  wty700164825.h1
Method
                  BLASTX
NCBI GI
                  g3776029
BLAST score
                  292
                  9.0e-27
E value
Match length
                  82
% identity
                  67
NCBI Description
                  (AJ010476) RNA helicase [Arabidopsis thaliana]
Seq. No.
                  311760
Seq. ID
                  wty700164866.h1
Method
                  BLASTN
NCBI GI
                  q2062705
BLAST score
                  35
E value
                  2.0e-10
Match length
                  35
% identity
                  100
NCBI Description Human butyrophilin (BTF5) mRNA, complete cds
                  311761
Seq. No.
Seq. ID
                  wty700164920.h1
Method
                  BLASTX
NCBI GI
                  g4585972
BLAST score
                  143
E value
                  2.0e-09
Match length
                  47
% identity
                  62
                  (AC005287) Putative ATPase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  311762
Seq. ID
                  wty700164934.h1
Method
                  BLASTX
NCBI GI
                  g1362091
```

NCBI Description

```
% identity
NCBI Description
                  cellulase (EC 3.2.1.4) precursor - tomato >gi 924622
                   (U20590) endo-1,4-beta-glucanase precursor [Solanum
                   lycopersicum]
                   311763
Seq. No.
                  wty700164974.hl
Seq. ID
Method
                  BLASTX
                  g3004950
NCBI GI
BLAST score
                  195
E value
                   2.0e-15
Match length
                  47
% identity
                  83
                  (AF037061) tonoplast intrinsic protein; ZmTIP1 [Zea mays]
NCBI Description
                   311764
Seq. No.
                  wty700164982.hl
Seq. ID
Method
                  BLASTX
NCBI GI
                   q2160175
BLAST score
                   300
                   9.0e-28
E value
                   72
Match length
% identity
                   76
NCBI Description
                   (AC000132) Strong similarity to Dianthus cysteine
                  proteinase (gb_U17135). [Arabidopsis thaliana]
                   311765
Seq. No.
                   wty700165039.h1
Seq. ID
Method
                   BLASTX
                   q4249382
NCBI GI
                   233
BLAST score
                   9.0e-20
E value
Match length
                   86
% identity
                   52
                   (AC005966) Strong similarity to gi_3337350 F13P17.3
NCBI Description
                   putative permease from Arabidopsis thaliana BAC
                   gb AC004481. [Arabidopsis thaliana]
                   311766
Seq. No.
Seq. ID
                   wty700165104.hl
Method
                   BLASTX
NCBI GI
                   g2654870
BLAST score
                   189
                   8.0e-15
E value
Match length
                   41
                   88
% identity
NCBI Description
                  (AF015302) RbohAOsp [Oryza sativa]
Seq. No.
                   311767
Seq. ID
                   wty700165253.hl
Method
                   BLASTX
NCBI GI
                   g1895084
BLAST score
                   395
                   9.0e-39
E value
Match length
                   84
% identity
                   86
```

44485

(U89897) golgi associated protein se-wap41 [Zea mays]

Seq. ID

```
311768
Seq. No.
                  wty700165263.hl
Seq. ID
Method
                  BLASTX
                  g1946364
NCBI GI
                  237
BLAST score
                  3.0e-20
E value
Match length
                  80
                  59
% identity
NCBI Description (U93215) lipase isolog [Arabidopsis thaliana]
                  311769
Seq. No.
                  wty700165265.h1
Seq. ID
                  BLASTX
Method
                  g2274859
NCBI GI
                  271
BLAST score
                  2.0e-24
E value
                  73
Match length
                  68
% identity
                  (AJ000016) Cks1 protein [Arabidopsis thaliana]
NCBI Description
                  >gi 4510420_gb_AAD21506.1_ (AC006929) putative
                  cyclin-dependent kinase regulatory subunit [Arabidopsis
                  thaliana]
Seq. No.
                  311770
                  wty700165387.h1
Seq. ID
Method
                 BLASTX
                  g1419758
NCBI GI
                  184
BLAST score
                  3.0e-14
E value
Match length
                  66
                  62
% identity
                  (X98795) geranylgeranyl pyrophosphate synthase [Sinapis
NCBI Description
                  alba]
                  311771
Seq. No.
                  wty700165408.h1
Seq. ID
Method
                  BLASTX
                  g3063701
NCBI GI
BLAST score
                  265
                  9.0e-24
E value
                  58
Match length
% identity
                  81
NCBI Description (AL022537) putative protein [Arabidopsis thaliana]
                  311772
Seq. No.
                  wty700165464.h1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2827497
                  200
BLAST score
E value
                   6.0e-16
Match length
                   51
                   75
% identity
                  (AL009195) EG:30B8.2 [Drosophila melanogaster]
NCBI Description
Seq. No.
                   311773
```

44486

wty700165481.hl



```
Method
                  BLASTX
NCBI GI
                  q3047109
BLAST score -
                  218
                  4.0e-18
E value
                  75
Match length
                  60
% identity
                  (AF058919) No definition line found [Arabidopsis thaliana]
NCBI Description
                  311774
Seq. No.
                  wty700165505.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3023751
BLAST score
                   249
E value
                  7.0e-22
                  60
Match length
                  75
% identity
                  70 KD PEPTIDYLPROLYL ISOMERASE (PEPTIDYLPROLYL CIS-TRANS
NCBI Description
                   ISOMERASE) (CYCLOPHILIN) (PPIASE) >gi_1076772_pir__S55383
                  peptidylprolyl isomerase (EC 5.2.1.8) - wheat
                   >gi 854626 emb CAA60505 (X86903) peptidylprolyl isomerase
                   [Triticum aestivum]
                   311775
Seq. No.
                  wty700165551.h1
Seq. ID
Method
                  BLASTX
                   g1524383
NCBI GI
                   296
BLAST score
                   3.0e-27
E value
                   78
Match length
% identity
                   79
                   (X63374) 3-phosphoshikimate 1-carboxyvinyltransferase [Zea
NCBI Description
                  mays]
                   311776
Seq. No.
                   wty700165570.hl
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2499803
BLAST score
                   166
                   5.0e-12
E value
Match length
                   53
                   60
% identity
                   PROTEIN ARGININE N-METHYLTRANSFERASE 1 (INTERFERON RECEPTOR
NCBI Description
                   1-BOUND PROTEIN 4) >gi 1808646 emb CAA71764 (Y10806)
                   arginine methyltransferase [Homo sapiens]
                   311777
Seq. No.
                   wty700165603.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2500497
BLAST score
                   224
E value
                   6.0e-19
Match length
                   43
% identity
                   100
```

NCBI Description 40S RIBOSOMAL PROTEIN S21 >gi_1419372_emb_CAA67225_

(X98656) ribosomal protein S21 [Zea mays]

Seq. No. 311778

Seq. ID

311783

wty700165809.hl

```
Seq. ID
                  wty700165616.h1
Method
                  BLASTX
NCBI GI
                  q1173327
BLAST score
                  343
                  6.0e-33
E value
Match length
                  69
% identity
                  96
NCBI Description
                  U2 SMALL NUCLEAR RIBONUCLEOPROTEIN A' (U2 SNRNP-A')
                  >gi_322619_pir__S30580 U2 snRNP protein A' - Arabidopsis
                  thaliana >gi_17669_emb_CAA48890_ (X69137) U2 small nuclear
                  ribonucleoprotein A' [Arabidopsis thaliana]
Seq. No.
                  311779
                  wty700165624.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2245066
BLAST score
                  235
E value
                  3.0e-20
Match length
                  50
                  82
% identity
                  (Z97342) Beta-Amylase [Arabidopsis thaliana]
NCBI Description
                  311780
Seq. No.
Seq. ID
                  wty700165712.hl
Method
                  BLASTX
NCBI GI
                  g2244865
BLAST score
                  175
E value
                  3.0e-13
Match length
                  58
% identity
                  64
NCBI Description
                  (Z97337) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  311781
                  wty700165751.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1170434
BLAST score
                   308
E value
                  8.0e-29
Match length
                   60
% identity
                  100
                  HOMEOBOX PROTEIN HOX1A >gi 283057 pir S25237 homeotic
NCBI Description
                  protein Hoxla - maize >gi_22331_emb_CAA47859_ (X67561)
                  Zmhoxla homeobox protein [Zea mays]
Seq. No.
                  311782
Seq. ID
                  wty700165761.h1
Method
                  BLASTN
NCBI GI
                  g609289
BLAST score
                  125
E value
                   4.0e-64
Match length
                  173
% identity
                  93
                  Z.mays cultivar (LG11) ROA mRNA for replication origin
NCBI Description
                  activator protein
```

44488

Hill



```
BLASTX
Method
                   q4105772
NCBI GI
                   153
BLAST score
                   2.0e-10
E value
                   38
Match length
% identity
                   71
                   (AF049917) PGP9B [Petunia x hybrida]
NCBI Description
                   311784
Seq. No.
Seq. ID
                   wty700165810.h1
Method
                   BLASTX
NCBI GI
                   q2246625
BLAST score
                   197
E value
                   1.0e-15
Match length
                   82
% identity
                   61
NCBI Description
                   (AF004947) protein kinase [Oryza sativa]
Seq. No.
                   311785
Seq. ID
                   wty700165819.h1
Method
                   BLASTN
NCBI GI
                   q1060934
BLAST score
                   111
E value
                   4.0e-56
Match length
                   123
% identity
                   98
NCBI Description Maize mRNA for mLIP15 (DNA-binding factor), complete cds
Seq. No.
                   311786
Seq. ID
                   wty700165829.h1
Method
                   BLASTN
NCBI GI
                   g3821780
BLAST score
                   36
                   5.0e-11
E value
Match length
                   36
                   100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                   311787
Seq. No.
Seq. ID
                   wty700165908.h1
Method
                   BLASTX
NCBI GI
                   g4218007
BLAST score
                   141
                   3.0e-09
E value
                   71
Match length
% identity
                   42
                   (AC006135) putative membrane-associated salt-inducible
NCBI Description
                   protein [Arabidopsis thaliana]
                   311788
Seq. No.
Seq. ID
                   wty700165915.h1
Method
                   BLASTX
NCBI GI
                   g2499946
BLAST score
                   226
```

3.0e-19

48

90

E value Match length

% identity



```
NCBI Description

URIDINE 5'-MONOPHOSPHATE SYNTHASE (UMP SYNTHASE) (OROTATE PHOSPHORIBOSYLTRANSFERASE AND OROTIDINE 5'-PHOSPHATE DECARBOXYLASE >gi_747980 (U22260) UMP synthase [Nicotiana tabacum]

Seq. No. 311789
Seq. ID wty700165931.h1
Method BLASTN
NCBI GI G1420923
BLAST score 48
```

BLAST score 48
E value 3.0e-18
Match length 76
% identity 91

NCBI Description Zea mays repressor-like protein (in1) gene, complete cds

Seq. No. 311790

Seq. ID wty700165947.h1

Method BLASTX
NCBI GI g3047123
BLAST score 295
E value 3.0e-27
Match length 65
% identity 80

NCBI Description (AF058919) similar to the family of glycosyl hydrolases

[Arabidopsis thaliana]

Seq. No. 311791

Seq. ID wty700165963.h1

Method BLASTX
NCBI GI g82696
BLAST score 227
E value 5.0e-19
Match length 59
% identity 78

NCBI Description glycine-rich protein - maize >gi 22293 emb CAA43431

(X61121) glycine-rich protein [Zea mays]

Seq. No. 311792

Seq. ID wty700166004.h1

Method BLASTX
NCBI GI g2129578
BLAST score 359
E value 1.0e-34
Match length 74
% identity 89

NCBI Description dTDP-glucose 4-6-dehydratases homolog - Arabidopsis

thaliana >gi_928932_emb_CAA89205_ (Z49239) homolog of dTDP-glucose 4-6-dehydratases [Arabidopsis thaliana] >gi_1585435_prf__2124427B diamide resistance gene

[Arabidopsis thaliana]

Seq. No. 311793

Seq. ID wty700166021.h1

Method BLASTX NCBI GI g464367 BLAST score 176 E value 3.0e-13



```
Match length
  % identity
                     44
                     POLYGALACTURONASE INHIBITOR PRECURSOR
  NCBI Description
                     (POLYGALACTURONASE-INHIBITING PROTEIN)
                     >gi 543660 pir JQ2262 Polygalacturonase inhibitor
                     precursor - Pyrus communis >gi_169684 (L09264)
                     polygalacturonase inhibitor [Pyrus communis]
  Seq. No.
                     311794
  Seq. ID
                     wty700166028.h1
  Method
                     BLASTN
  NCBI GI
                     q3452291
  BLAST score
                     129
  E value
                     2.0e-66
  Match length
                     221
                     90
  % identity
  NCBI Description Zea mays retrotransposon Huck-2 3' LTR, partial sequence
  Seq. No.
                     311795
  Seq. ID
                     wty700166038.h1
  Method
                     BLASTN
  NCBI GI
                     q3821780
  BLAST score
                     37
  E value
                     1.0e-11
  Match length
                     49
  % identity
                     67
  NCBI Description Xenopus laevis cDNA clone 27A6-1
  Seq. No.
                     311796
  Seq. ID
                     wty700166041.h1
  Method
                     BLASTX
  NCBI GI
                     g4038056
  BLAST score
                     178
                     2.0e-13
  E value
  Match length
                     74
  % identity
                     41
NCBI Description (AC005897) putative transposon [Arabidopsis thaliana]
  Seq. No.
                     311797
  Seq. ID
                     wty700166046.h1
  Method
                     BLASTX
  NCBI GI
                     g3548802
```

BLAST score 265 1.0e-23 E value Match length 76 68 % identity

NCBI Description (AC005313) axi 1-like protein [Arabidopsis thaliana]

>gi 4335769 gb AAD17446 (AC006284) putative axi1 protein

[Nicotiana tabacum] [Arabidopsis thaliana]

311798 Seq. No.

Seq. ID wty700166055.h1

Method BLASTX NCBI GI g1076289 BLAST score 197 E value 1.0e-15 Match length 56

```
% identity
NCBI Description
                  amino acid permease AAP5 - Arabidopsis thaliana
                  >gi_608673_emb_CAA54632_ (X77501) amino acid permease
                   [Arabidopsis thaliana]
Seq. No.
                  311799
Seq. ID
                  wty700166066.h1
Method
                  BLASTN
NCBI GI
                  q1667388
BLAST score
                  119
E value
                  8.0e-61
Match length
                  130
% identity
                  98
NCBI Description
                  Z.mays gene encoding 3-hydroxy-3-methylglutaryl-CoA
                  reductase
Seq. No.
                  311800
Seq. ID
                  wty700166120.h1
Method
                  BLASTN
NCBI GI
                  q1845194
BLAST score
                  104
E value
                  9.0e-52
Match length
                  104
% identity
                  100
NCBI Description Z.mays mRNA for HMGc1 protein
Seq. No.
                  311801
Seq. ID
                  wty700166156.hl
Method
                  BLASTX
NCBI GI
                  q2909781
BLAST score
                  257
E value
                  1.0e-22
Match length
                  78
```

% identity 71

NCBI Description (AF020288) MgATP-energized glutathione S-conjugate pump

[Arabidopsis thaliana]

Seq. No. 311802

Seq. ID wty700166227.h1

Method BLASTX NCBI GI q4539351 BLAST score 184 3.0e-14 E value Match length 73 % identity 45

NCBI Description (AL035539) putative protein [Arabidopsis thaliana]

Seq. No. 311803

Seq. ID wty700166248.h1

Method BLASTN NCBI GI q2232016 BLAST score 100 E value 3.0e-49 Match length 131 93 % identity

NCBI Description Zea mays viviparous-14 (vp14) mRNA, complete cds



```
Seq. No.
                   311804
Seq. ID
                   wty700166257.h1
Method
                   BLASTN
                   q3821780
NCBI GI
BLAST score
                   36
E value
                   5.0e-11
Match length
                   48
% identity
                   67
NCBI Description
                  Xenopus laevis cDNA clone 27A6-1
Seq. No.
                   311805
Seq. ID
                   wty700166286.h1
Method
                   BLASTX
NCBI GI
                   g3123270
BLAST score
                   212
                  .1.0e-17
E value
Match length
                   40
% identity
                   97
NCBI Description
                   40S RIBOSOMAL PROTEIN S4 (SCAR PROTEIN SS620)
                   >gi 2463335 emb CAA75242 (Y15009) ribosomal protein S4
                   [Oryza sativa]
Seq. No.
                   311806
Seq. ID
                   wty700166304.h1
Method
                   BLASTX
NCBI GI
                   q3688173
BLAST score
                   352
E value
                   8.0e-34
Match length
                   77
% identity
                   84
NCBI Description
                   (AL031804) putative protein [Arabidopsis thaliana]
Seq. No.
                   311807
Seq. ID
                   wty700166326.h1
Method
                   BLASTX
NCBI GI
                   q4589981
BLAST score
                   271
                   2.0e-24
E value
Match length
                   80
% identity
                   70
                   (AC007195) amidophosphoribosyltransferase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   311808
Seq. ID
                   wty700166352.h1
Method
                   BLASTX
                   g4558665
NCBI GI
BLAST score
                   283
E value
                   1.0e-25
Match length
                   81
% identity
                   72
NCBI Description
                   (AC007063) putative white protein [Arabidopsis thaliana]
```

Seq. ID wty700166376.h1

Method BLASTX NCBI GI g3236238



```
BLAST score
E value
                  1.0e-10
Match length
                  30
                  93
% identity
                   (AC004684) putative ARF1 GTPase activating protein
NCBI Description
                   [Arabidopsis thaliana] >gi 4519792 dbj_BAA75744.1_
                   (AB017876) Aspl [Arabidopsis thaliana]
Seq. No.
                  311810
                  wty700166383.hl
Seq. ID
Method
                  BLASTX
NCBI GI
                   g538607
BLAST score
                  187
E value
                   2.0e-14
Match length
                  38
                  100
% identity
                  superoxide dismutase (EC 1.15.1.1) (Cu-Zn) 4A - maize
NCBI Description
                  >gi 1885354 (U34727) superoxide dismutase 4A [Zea mays]
Seq. No.
                   311811
                  wty700166411.hl
Seq. ID
Method
                  BLASTX
                   g3445397
NCBI GI
                   298
BLAST score
E value
                   3.0e-27
                   83
Match length
                   67
% identity
                   (AJ010166) S-domain receptor-like protein kinase [Zea mays]
NCBI Description
                   311812
Seq. No.
                  wty700166415.hl
Seq. ID
Method
                  BLASTX
NCBI GI
                   g113682
BLAST score
                   151
E value
                   3.0e-10
Match length
                   31
                   90
% identity
                  ALPHA-AMYLASE ISOZYME 3D PRECURSOR (1,4-ALPHA-D-GLUCAN
NCBI Description
                   GLUCANOHYDROLASE) >gi_82457_pir__S12625 alpha-amylase (EC
                   3.2.1.1) 3D - rice >gi_169771 (\overline{M5}9351) alpha-amylase [Oryza
                   sativa]
Seq. No.
                   311813
                   wty700166432.h1
Seq. ID
Method
                   BLASTN
                   g4140643
NCBI GI
BLAST score
                   33
                   4.0e-09
E value
Match length
                   61
                   89
% identity
NCBI Description
                  Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster,
                   complete sequence
```

Seq. ID wty700166452.h1

Method BLASTX NCBI GI g3746060

% identity

NCBI Description

56

```
BLAST score
E value
                  5.0e-12
Match length
                  42
                  69
% identity
                  (AC005311) unknown protein [Arabidopsis thaliana]
NCBI Description
                  311815
Seq. No.
                  wty700166461.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1800216
BLAST score
                  41
                  6.0e-14
E value
Match length
                  134
% identity
                  90
NCBI Description Sorghum bicolor phytochrome B (PHYB) gene, partial cds
                  311816
Seq. No.
                  wty700166464.h1
Seq. ID
Method
                  BLASTX
                  g2443886
NCBI GI
BLAST score
                  179
                  1.0e-13
E value
Match length
                  42
% identity
                  88
                  (AC002294) Unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  311817
                  wty700166470.hl
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3004565
BLAST score
                   274
                  1.0e-24
E value
                  79
Match length
% identity
                   65
                  (AC003673) putative protein kinase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   311818
                  wty700166586.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                   a3859547
BLAST score
                   35
E value
                   1.0e-10
Match length
                   71
                   87
% identity
NCBI Description
                  Oryza sativa protein phosphatase 2A catalytic subunit
                   (Pp2a) gene, complete cds
Seq. No.
                   311819
Seq. ID
                  wty700166603.hl
Method
                   BLASTX
NCBI GI
                   g2258336
BLAST score
                   212
                   2.0e-17
E value
                   72
Match length
```

. . .

[Reclinomonas americana]

(AF007261) component involved in Haem biosynthesis

Method

BLASTX

```
Seq. No.
                  311820
Seq. ID
                  wty700166606.h1
Method
                  BLASTN
                  q4468791
NCBI GI
                  96
BLAST score
E value
                  4.0e-47
Match length
                  121
                  94
% identity
NCBI Description
                  Zea mays mRNA for glutathione transferase III(a)
                  311821
Seq. No.
                  wty700166609.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g22392
BLAST score
                  39
                  8.0e-13
E value
Match length
                  51
% identity
                  94
NCBI Description
                  Maize phosphoenolpyruvate carboxylase gene 5'flanking
                  region (EC 4.1.1.31) clone M91
Seq. No.
                  311822
Seq. ID
                  wty700166623.h1
Method
                  BLASTN
                  g3821780
NCBI GI
BLAST score
                  36
                  5.0e-11
E value
Match length
                  36
% identity
                  100
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                  311823
Seq. ID
                  wty700166669.h1
Method
                  BLASTN
                  g1628481
NCBI GI
BLAST score
                  191
E value
                  1.0e-103
Match length
                  199
% identity
                  99
NCBI Description
                  Z.mays dek34 gene
Seq. No.
                  311824
Seq. ID
                  wty700166671.h1
Method
                  BLASTX
NCBI GI
                  g1076809
BLAST score
                  301
E value
                  6.0e-28
Match length
                  58
% identity
                  98
NCBI Description
                  H+-transporting ATPase (EC 3.6.1.35) - maize
                  >gi_758355_emb_CAA59800 (X85805) H(+)-transporting ATPase
                   [Zea mays]
Seq. No.
                  311825
Seq. ID
                  wty700166742.h1
```

```
a2766450
NCBI GI
                  154
BLAST score
                  1.0e-10
E value
                  44
Match length
                   64
% identity
                  (AF029857) cytochrome P450 CYP99A1 [Sorghum bicolor]
NCBI Description
                  311826
Seq. No.
                  wty700166756.hl
Seq. ID
Method
                  BLASTX
                  g3885882
NCBI GI
BLAST score
                   402
                  1.0e-39
E value
Match length
                   84
                   89
% identity
                  (AF093629) inorganic pyrophosphatase [Oryza sativa]
NCBI Description
                   311827
Seq. No.
                  wty700166814.h1
Seq. ID
                  BLASTX
Method
                  g584825
NCBI GI
                   187
BLAST score
                   2.0e-14
E value
Match length
                   74
% identity
                   50
                  B2 PROTEIN >gi_322726_pir__S32124 B2 protein - carrot
NCBI Description
                   >gi 297889 emb CAA51078 (X72385) B2 protein [Daucus
                   carota]
Seq. No.
                   311828
                   wty700166824.h1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3645985
BLAST score
                   314
E value
                   2.0e-29
Match length
                   69
% identity
                   74
                   (AL031581) 1-evidence-predicted by content;
NCBI Description
                   1-method=genefinder;084; 1-method score=23.36;
                   1-evidence_end; 2-evidence=predicted by match;
                   2-match_accession=AA141041;
                   2-match_description=CK01110.3prime CK Drosophila
                   melanogaster
Seq. No.
                   311829
                   wty700166849.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q135398
BLAST score
                   270
E value
                   3.0e-24
Match length
                   76
                   72
% identity
                   TUBULIN ALPHA-1 CHAIN >gi 82731 pir S15773 tubulin alpha-1
NCBI Description
                   chain - maize >gi 22147 emb CAA33734 (X15704)
                   alpha1-tubulin [Zea mays]
```



```
Seq. ID
                  wty700166873.h1
Method
                  BLASTX
NCBI GI
                  q3218550
BLAST score
                  234
E value
                   5.0e-20
Match length
                  77
% identity
                   52
NCBI Description
                  (AB009399) Cdk-activating kinase 1At [Arabidopsis thaliana]
                   311831
Seq. No.
Seq. ID
                  wty700166963.h1
Method
                  BLASTX
NCBI GI
                   q4539676
                   148
BLAST score
                   4.0e-14
E value
                   53
Match length
                  83
% identity
                  (AF061282) patatin-like protein [Sorghum bicolor]
NCBI Description
                   311832
Seq. No.
                  wty700167027.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                   g3821780
BLAST score
                   36
                   5.0e-11
E value
Match length
                   36
                   100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                   311833
Seq. ID
                   wty700167036.h1
Method
                   BLASTX
NCBI GI
                   g4490325
BLAST score
                   199
E value
                   6.0e-16
Match length
                   46
% identity
                   87
                  (AL035656) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   311834
Seq. No.
Seq. ID
                   wty700167056.hl
Method
                   BLASTX
NCBI GI
                   g3335378
BLAST score
                   175
                   5.0e-13
E value
Match length
                   36
% identity
                   89
NCBI Description
                   (AC003028) Myb-related transcription activator [Arabidopsis
                   thaliana]
Seq. No.
                   311835
Seq. ID
                   wty700167112.h1
Method
                   BLASTX
NCBI GI
                   g1532169
BLAST score
                   364
```

3.0e-35

78

E value Match length



% identity (U63815) similar to a E. coli hypothetical protein F402 NCBI Description encoded by GenBank Accession Number S47768 [Arabidopsis thaliana]

311836 Seq. No.

Seq. ID wty700167129.hl

Method BLASTX NCBI GI q1781336 255 BLAST score E value 3.0e-22 Match length 70 % identity

(Y10469) peroxidase [Spinacia oleracea] NCBI Description

311837 Seq. No.

wty700167168.h1 Seq. ID

Method BLASTX g4454466 NCBI GI 149 BLAST score 6.0e-10 E value 38 Match length % identity

(AC006234) unknown protein [Arabidopsis thaliana] NCBI Description

311838 Seq. No.

wty700167218.h1 Seq. ID

BLASTX Method NCBI GI q1703129 198 BLAST score 8.0e-16 E value 38 Match length 97 % identity

ACTIN 11 >gi_2129522_pir__S68109 actin 11 - Arabidopsis thaliana >gi_1002533 (U27981) actin-11 [Arabidopsis NCBI Description

thaliana]

311839 Seq. No.

Seq. ID wty700167221.hl

Method BLASTX q3176669 NCBI GI BLAST score 168 2.0e-12 E value Match length 42 % identity 76

(AC004393) End is cut off. [Arabidopsis thaliana] NCBI Description

Seq. No. 311840

wty700167259.hl Seq. ID

Method BLASTX g1360090 NCBI GI 189 BLAST score 1.0e-14 E value 73 Match length 49 % identity

(X95576) C1C-Nt1 [Nicotiana tabacum] NCBI Description

```
Seq. No.
                  311841
                  wty700167260.hl
Seq. ID
Method
                  BLASTX
                  g1174745
NCBI GI
BLAST score
                  279
                  3.0e-25
E value
Match length
                  64
% identity
                  TRIOSEPHOSPHATE ISOMERASE, CHLOROPLAST PRECURSOR (TIM)
NCBI Description
                  >gi_1363523_pir__S53761 triose-phosphate isomerase (EC
                  5.3.1.1) precursor, chloroplast - rye
                  >qi 609262 emb CAA83533 (Z32521) triosephosphate isomerase
                  [Secale cereale] >gi 1095494 prf 2109226B triosephosphate
                  isomerase [Secale cereale]
                  311842
Seq. No.
                  wty700167266.hl
Seq. ID
Method
                  BLASTX
                  q3193316
NCBI GI
                  217
BLAST score
                  2.0e-24
E value
                  76
Match length
% identity
                  78
                  (AF069299) contains similarity to nucleotide sugar
NCBI Description
Seq. No.
                  311843
                  wty700167344.h1
Seq. ID
Method
                  BLASTX
```

epimerases [Arabidopsis thaliana]

q1709000 NCBI GI BLAST score 205 1.0e-16 E value Match length 40 % identity 97

S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE NCBI Description ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)

>gi 960357 dbj BAA09895 (D63835) S-adenosylmethionine

synthetase [Hordeum vulgare]

311844 Seq. No.

Seq. ID wty700167361.hl

Method BLASTX g2191144 NCBI GI BLAST score 258 9.0e-23 E value 57 Match length % identity

(AF007269) A IG002N01.24 gene product [Arabidopsis NCBI Description

thaliana]

311845 Seq. No.

Seq. ID wty700167387.h1

BLASTX Method g3413500 NCBI GI 163 BLAST score 1.0e-11 E value Match length



```
% identity
                  (AJ005589) protein tyrosine phosphatase [Pisum sativum]
NCBI Description
                  311846
Seq. No.
                  wty700167395.h1
Seq. ID
                  BLASTX
Method
                  g3097271
NCBI GI
                  251
BLAST score
                   4.0e-22
E value
                   49
Match length
                  100
% identity
                   (AJ005802) ferrochelatase [Solanum tuberosum]
NCBI Description
                   311847
Seq. No.
                   wty700167405.hl
Seq. ID
                   BLASTX
Method
                   g1084481
NCBI GI
                   364
BLAST score
                   4.0e-35
E value
                   84
Match length
                   86
% identity
                  heat shock protein 70 - Maize
NCBI Description
                   311848
Seq. No.
                   wty700167407.hl
Seq. ID
                   BLASTX
Method
                   g2055374
NCBI GI
                   309
BLAST score
                   1.0e-28
E value
                   62
Match length
                   92
% identity
                   (U29095) serine-threonine protein kinase [Triticum
NCBI Description
                   aestivum]
                   311849
Seq. No.
                   wty700167418.hl
Seq. ID
                   BLASTX
Method
                   g3043430
NCBI GI
BLAST score
                   157
                   6.0e-11
E value
Match length
                   73
                   45
% identity
                   (AJ005347) annexin [Cicer arietinum]
NCBI Description
                   311850
Seq. No.
                   wty700167451.h1
Seq. ID
                   BLASTX
Method
                   q3540195
NCBI GI
BLAST score
                   156
                   6.0e-11
E value
Match length
                   39
                   37
 % identity
                   (AC004260) Unknown protein [Arabidopsis thaliana]
NCBI Description
```

wty700167464.hl Seq. ID

Method BLASTN

NCBI GI BLAST score

E value

Match length

```
g3821780
NCBI GI
                  36
BLAST score
                  5.0e-11
E value
Match length
                  36
                  100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                  311852
Seq. No.
                  wty700167480.hl
Seq. ID
                  BLASTX
Method
                  g66009
NCBI GI
                   353
BLAST score
                   8.0e-34
E value
Match length
                   67
                   100
% identity
                  glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) C,
NCBI Description
                   cytosolic - maize >gi_22238_emb_CAA30151_ (X07156) GADPH
                   (AA 1-337) [Zea mays]
                   311853
Seq. No.
                   wty700167496.hl
Seq. ID
                   BLASTX
Method
                   g129591
NCBI GI
                   306
BLAST score
E value
                   2.0e-28
                   63
Match length
                   89
% identity
                   PHENYLALANINE AMMONIA-LYASE >gi 295824 emb_CAA34226_
NCBI Description
                   (X16099) phenylalanine ammonia-lyase [Oryza sativa]
                   311854
Seq. No.
                   wty700167505.h1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g3821780
                   36
BLAST score
E value
                   5.0e-11
Match length
                   48
                   67
% identity
                  Xenopus laevis cDNA clone 27A6-1
NCBI Description
                   311855
Seq. No.
                   wty700167508.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4567304
BLAST score
                   247
                   1.0e-21
E value
Match length
                   60
                   73
% identity
                   (AC005956) unknown protein [Arabidopsis thaliana]
NCBI Description
                   311856
Seq. No.
                   wty700167512.h1
Seq. ID
Method
                   BLASTX
```

44502

g1699053

213 1.0e-17



```
% identity
                   (U78868) putative aspartate-arginine-rich mRNA binding
NCBI Description
                  protein [Arabidopsis thaliana]
                   311857
Seq. No.
Seq. ID
                  wty700167520.h1
Method
                  BLASTX
NCBI GI
                   g2760839
BLAST score
                   184
                   3.0e-14
E value
Match length
                   70
% identity
                   63
                   (AC003105) putative receptor kinase [Arabidopsis thaliana]
NCBI Description
                   311858
Seq. No.
                   wty700167535.h1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g4582786
                   77
BLAST score
                   2.0e-35
E value
Match length
                   77
                   100
% identity
NCBI Description
                   Zea mays mRNA for adenosine kinase, putative
                   311859
Seq. No.
                   wty700167618.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3176707
BLAST score
                   170
                   2.0e-12
E value
                   82
Match length
                   44
% identity
                   (AC002392) putative proline-rich protein APG [Arabidopsis
NCBI Description
                   thaliana]
                   311860
Seq. No.
                   wty700167620.h1 💰
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2264369
BLAST score
                   150
                   4.0e-10
E value
Match length
                   82
% identity
                   46
                   (AC002354) predicted protein of unknown function
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   311861
                   wty700167629.h1
Seq. ID
Method
                   BLASTX
                   g3319212
NCBI GI
                   343
BLAST score
                   1.0e-32
E value
                   74
Match length
                   82
% identity
                   (U84140) self-pruning protein [Lycopersicon esculentum]
NCBI Description
```

311862

Seq. No.

```
wty700167655.hl
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3549678
                  348
BLAST score
                  2.0e-33
E value
                  73
Match length
% identity
                  (ALO31394) putative aspartate--tRNA ligase [Arabidopsis
NCBI Description
                  thaliana]
                  311863
Seq. No.
                  wty700167748.h1
Seq. ID
Method
                  BLASTX
                  g3548802
NCBI GI
BLAST score
                  263
                  2.0e-23
E value
Match length
                  79
                  66
% identity
                   (ACO05313) axi 1-like protein [Arabidopsis thaliana]
NCBI Description
                  >gi_4335769_gb_AAD17446_ (AC006284) putative axi1 protein
                   [Nicotiana tabacum] [Arabidopsis thaliana]
                   311864
Seq. No.
                  wty700167767.h1
Seq. ID
                  BLASTN
Method
                   q2655097
NCBI GI
BLAST score
                   33
                   2.0e-09
E value
                   41
Match length
                   95
% identity
                  Hordeum vulgare peptide transporter (ptr1) mRNA, complete
NCBI Description
Seq. No.
                   311865
                   wty700167768.h1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2944039
BLAST score
                   44
                   6.0e-16
E value
Match length
                   64
                   92
% identity
                  Zea mays indeterminate spikelet 1 (ids1) mRNA, complete cds
NCBI Description
Seq. No.
                   311866
                   wty700167786.h1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3821780
BLAST score
                   36
                   4.0e-11
E value
Match length
                   36
                   100
% identity
                  Xenopus laevis cDNA clone 27A6-1
NCBI Description
                   311867
Seq. No.
                   wty700167807.h1
Seq. ID
                   BLASTX
Method
```

g4138137

NCBI GI

```
BLAST score
                  2.0e-25
E value
Match length
                  79
                  66
% identity
                  (AJ012796) ss-galactosidase [Lycopersicon esculentum]
NCBI Description
Seq. No.
                  311868
                  wty700167878.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1617470
BLAST score
                  104
E value
                  1.0e-51
                  230
Match length
                  87
% identity
NCBI Description Z.diploperennis DNA for Grandel-4 retrotransposon
                  311869
Seq. No.
                  wty700167883.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1084481
BLAST score
                   259
                   6.0e-23
E value
Match length
                   62
% identity
                   82
NCBI Description heat shock protein 70 - Maize
                   311870
Seq. No.
                   wty700167886.hl
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3367523
BLAST score
                   234
                   5.0e-20
E value
Match length
                   75
% identity
                   55
                   (AC004392) ESTs gb_AA728658 and gb_N95943 come from this
NCBI Description
                   gene. [Arabidopsis thaliana]
                   311871
Seq. No.
                   wty700167912.h1
Seq. ID
Method
                   BLASTX
                   g2505870
NCBI GI
                   238
BLAST score
                   1.0e-20
E value
                   63
Match length
                   75
% identity
                  (Y12227) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   311872
Seq. No.
Seq. ID
                   wty700167927.h1
                   BLASTX
Method
                   g2809385
NCBI GI
```

BLAST score 326 9.0e-31 E value 78 Match length 85 % identity

(AF024634) NADPH cytochrome P450 reductase [Petroselinum NCBI Description

crispum]

```
311873
Seq. No.
                  wty700167939.hl
Seq. ID
                  BLASTX
Method
                  g3152587
NCBI GI
                  318
BLAST score
                  6.0e-30
E value
Match length
                  63
                  84
% identity
                  (AC002986) Similar to CREB-binding protein homolog
NCBI Description
                  gb_U88570 from D. melanogaster and contains similarity to
                  callus-associated protein gb_U01961 from Nicotiana tabacum.
                  EST gb_W43427 comes from this gene. [Arabidopsis thaliana]
                  311874
Seq. No.
                  wty700168044.h1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1149569
BLAST score
                  198
                  6.0e-16
E value
                  56
Match length
                   66
% identity
                  (Z50851) HD-zip [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   311875
                  wty700168109.hl
Seq. ID
                  BLASTX
Method
                   g2979542
NCBI GI
BLAST score
                   344
                   1.0e-32
E value
Match length
                   80
                   78
% identity
                   (AC003680) putative Ser/Thr kinase [Arabidopsis thaliana]
NCBI Description
                   311876
Seq. No.
                   wty700168115.h1
Seq. ID
Method
                   BLASTX
                   q3386613
NCBI GI
                   323
BLAST score
E value
                   2.0e-30
                   73
Match length
                   86
% identity
                   (AC004665) putative ATP-dependent RNA helicase [Arabidopsis
NCBI Description
                   thaliana]
                   311877
Seq. No.
                   wty700168215.h1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1703199
```

Method NCBI GI BLAST score E value

Match length 84 % identity 54

* identity
NCBI Description

ription PROTEIN KINASE AFC1 >gi_601787 (U16176) protein kinase

[Arabidopsis thaliana]

Seq. No.

311878

228

3.0e-19

```
wty700168310.hl
Seq. ID
                  BLASTX
Method
                  g4309734
NCBI GI
                  320
BLAST score
                   6.0e-30
E value
                  71
Match length
                   89
% identity
                   (AC006439) putative 26S proteosome regulatory subunit 8
NCBI Description
                   [Arabidopsis thaliana]
                   311879
Seq. No.
                  wty700168315.hl
Seq. ID
                  BLASTX
Method
                   g4263547
NCBI GI
BLAST score
                   168
                   4.0e-12
E value
Match length
                   88
                   42
% identity
                   (AC006250) putative retrotransposon pol protein
NCBI Description
                   [Arabidopsis thaliana]
                   311880
Seq. No.
                   wty700168332.h1
Seq. ID
                   BLASTX
Method
                   g2191168
NCBI GI
BLAST score
                   148
                   5.0e-10
E value
Match length
                   48
% identity
                   56
                   (AF007270) contains similarity to myosin heavy chain
NCBI Description
                   [Arabidopsis thaliana]
                   311881
Seq. No.
                   wty700168361.h1
Seq. ID
                   BLASTX
Method
                   g4262162
NCBI GI
                   208
BLAST score
                   7.0e-17
E value
                   80
Match length
                   47
% identity
                   (AC005275) putative glycosylation enzyme [Arabidopsis
NCBI Description
                   thaliana]
                   311882
Seq. No.
                   wty700168415.hl
Seq. ID
                   BLASTX
Method
                   g3821793
NCBI GI
                   330
BLAST score
                   4.0e-31
E value
Match length
                   64
 % identity
                   (Y11526) casein kinase II alpha subunit [Zea mays]
NCBI Description
                   311883
 Seq. No.
                   wty700168432.hl
 Seq. ID
Method
                   BLASTX
NCBI GI
                   g1082337
```

```
BLAST score
                  1.0e-25
E value
Match length
                  85
% identity
                  64
                  DNA helicase Q1 - human >gi 531243 dbj BAA07200 (D37984)
NCBI Description
                  DNA helicase Q1 [Homo sapiens]
                  311884
Seq. No.
                  wty700168508.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2499708
BLAST score
                  225
E value
                  6.0e-19
Match length
                  74
                  69
% identity
                  PHOSPHOLIPASE D PRECURSOR (PLD) (CHOLINE PHOSPHATASE)
NCBI Description
                   (PHOSPHATIDYLCHOLINE-HYDROLYZING PHOSPHOLIPASE D)
                  >gi 1020409_dbj_BAA11135_ (D73410) phospholipase D [Zea
                  mays]
Seq. No.
                  311885
                  wty700168514.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g642624
BLAST score
                  222
                  1.0e-33
E value
Match length
                  73
% identity
                  99
                  (L39266) phytoene desaturase [Zea mays]
NCBI Description
                  311886
Seq. No.
                  wty700168592.hl
Seq. ID
Method
                  BLASTX
NCBI GI
                   q3914468
BLAST score
                   226
E value
                   4.0e-19
Match length
                   61
% identity
                   75
NCBI Description
                  26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)
                   >qi 478411 pir JQ2257 nuclear antiqen 21D7 - carrot
                   >gi 217911 dbj BAA02696 (D13434) 21D7 antigen [Daucus
                   carota]
                   311887
Seq. No.
Seq. ID
                   wty700168603.h1
Method
                  BLASTX
NCBI GI
                   g1708462
```

Method BLASTX
NCBI GI g1708462
BLAST score 214
E value 1.0e-17
Match length 80
% identity 53

NCBI Description IAA-AMINO ACID HYDROLASE HOMOLOG 2 PRECURSOR >gi 902791

(U23796) ILL2 [Arabidopsis thaliana]

Seq. No. 311888

Seq. ID wty700168608.h1

Method BLASTX

```
g2414601
NCBI GI
BLAST score
                   139
E value
                   7.0e-09
Match length
                   64
                   44
% identity
NCBI Description (Z99295) phosphatidyl synthase [Schizosaccharomyces pombe]
Seq. No.
                   311889
                   wty700168638.hl
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2980768
                   214
BLAST score
E value
                   6.0e-24
Match length
                   69
                   87
% identity
NCBI Description (AL022198) putative protein [Arabidopsis thaliana]
                   311890
Seq. No.
                   wty700168653.h1
Seq. ID
                   BLASTN
Method
                   g4218534
NCBI GI
                   38
BLAST score
                   3.0e-12
E value
Match length
                   50
% identity
                   94
NCBI Description Triticum sp. mRNA for GRAB1 protein
                   311891
Seq. No.
                   wty700168657.h1
Seq. ID
                   BLASTN
Method
                   q747914
NCBI GI
                   53
BLAST score
                   4.0e-21
E value
Match length
                   77
                   92
 % identity
 NCBI Description Z.mays CaM1 mRNA for calmodulin
                   311892
 Seq. No.
                   wty700168714.hl
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   q2388561
 BLAST score
                   261
                   3.0e-23
 E value
                   74
 Match length
 % identity
                   66
                   (ACO00098) Similar to Arabidopsis hypothetical protein
 NCBI Description
                   PID:e326839 (gb_Z97337). [Arabidopsis thaliana]
 Seq. No.
                   311893
                   wty700168745.hl
 Seq. ID
 Method
                   BLASTN
 NCBI GI
                   q609287
 BLAST score
                   83
                   4.0e-39
 E value
 Match length
                   154
```

.

NCBI Description Z.diploperennis Grandel gene

89

% identity

```
Seq. No.
                  311894
                  wty700168754.h1
Seq. ID
                  BLASTX
Method
                  q2213594
NCBI GI
                  213
BLAST score
                  2.0e-17
E value
Match length
                  57
% identity
                  (AC000348) T7N9.14 [Arabidopsis thaliana]
NCBI Description
                  311895
Seq. No.
                  wty700168775.hl
Seq. ID
                  BLASTX
Method
                  g3157910
NCBI GI
BLAST score
                   300
                   1.0e-27
E value
                   58
Match length
                   100
% identity
                   (AF003551) lysine-ketoglutarate reductase/saccharopine
NCBI Description
                   dehydrogenase bifunctional enzyme [Zea mays]
                   311896
Seq. No.
Seq. ID
                   wty700168852.hl
                   BLASTX
Method
                   q4467147
NCBI GI
BLAST score
                   162
                   1.0e-11
E value
                   39
Match length
                   72
% identity
                  (AL035540) putative protein [Arabidopsis thaliana]
NCBI Description
                   311897
Seq. No.
                   wty700168855.h1
Seq. ID
Method
                   BLASTN
NCBI GI
                   q4416300
BLAST score
                   39
                   8.0e-13
E value
                   136
Match length
% identity
                   Zea mays chromosome 4 22 kDa zein-associated intercluster
NCBI Description
                   region, complete sequence
                   311898
Seq. No.
                   wty700168880.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1206013
BLAST score
                   322
E value
                   3.0e-30
                   78
Match length
% identity
                   (U44087) beta-D-glucosidase precursor [Zea mays]
NCBI Description
Seq. No.
                   311899
                   wty700168882.h1
Seq. ID
```

BLASTN

g22118

Method NCBI GI

Match length

NCBI Description

% identity

53

81

```
BLAST score
                  1.0e-14
E value
Match length
                   42
                  100
% identity
NCBI Description Z.mays DNA for Adh1-Cm allele
                   311900
Seq. No.
                   wty700168917.h1
Seq. ID
                   BLASTN
Method
                   g2306980
NCBI GI
BLAST score
                   45
                   2.0e-16
E value
Match length
                   83
% identity
                   89
                  Oryza sativa photosystem I antenna protein (Lhca) mRNA,
NCBI Description
                   complete cds
                   311901
Seq. No.
                   wty700168963.hl
Seq. ID
                   BLASTX
Method
                   g2282473
NCBI GI
                   202
BLAST score
                   2.0e-16
E value
Match length
                   64
% identity
                   59
                   (AB005911) xanthine dehydrogenase [Bombyx mori]
NCBI Description
                   311902
Seq. No.
                   wty700169005.h1
Seq. ID
Method
                   BLASTN
                   g3821780
NCBI GI
BLAST score
                   36
E value
                   5.0e-11
Match length
                   36
                   100
% identity
NCBI Description
                  Xenopus laevis cDNA clone 27A6-1
                   311903
Seq. No.
                   wty700169036.hl
Seq. ID
Method
                   BLASTX
                   q2618696
NCBI GI
                   148
BLAST score
                   5.0e-10
E value
                   56
Match length
% identity
                   50
                   (AC002510) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   311904
Seq. No.
                   wty700169037.hl
Seq. ID
Method
                   BLASTX
                   g2440033
NCBI GI
BLAST score
                   233
E value
                   5.0e-20
```

(X98543) endo-1,4-beta-glucanase [Arabidopsis thaliana]

```
Seq. No.
                  311905
Seq. ID
                  wty700169061.hl
                  BLASTX
Method
                  q4539404
NCBI GI
                  203
BLAST score
E value
                  2.0e-16
Match length
                  45
                  76
% identity
                  (AL049524) putative protein [Arabidopsis thaliana]
NCBI Description
                  311906
Seq. No.
                  wty700169063.hl
Seq. ID
Method
                  BLASTX
                  q4263790
NCBI GI
                   171
BLAST score
                   1.0e-12
E value
                   64
Match length
                   62
% identity
                  (ACO06068) putative ch-TOG protein [Arabidopsis thaliana]
NCBI Description
                   311907
Seq. No.
                   wty700169146.h1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g644492
                   160
BLAST score
                   5.0e-85
E value
                   233
Match length
                   97
% identity
                  Corn elongation factor lalpha gene, complete cds
NCBI Description
                   311908
Seq. No.
                   wty700169151.hl
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2760324
                   200
BLAST score
E value
                   4.0e-16
Match length
                   68
                   60
% identity
                   (AC002130) F1N21.9 [Arabidopsis thaliana]
NCBI Description
                   311909
Seq. No.
                   wty700169189.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3036805
BLAST score
                   155
                   7.0e-11
E value
Match length
                   55
                   62
% identity
                   (AL022373) thaumatin-like protein [Arabidopsis thaliana]
NCBI Description
                   311910
Seq. No.
                   wty700169210.hl
Seq. ID
Method
                   BLASTX
```

g3980413

166 5.0e-12

52

NCBI GI BLAST score

E value Match length

```
% identity
NCBI Description (AC004561) pumilio-like protein [Arabidopsis thaliana]
                  311911
Seq. No.
                  wty700169220.h1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4587533
                  145
BLAST score
                  1.0e-09
Evalue
                  54
Match length
                  56
% identity
                   (AC007060) EST gb_AA721821 comes from this gene.
NCBI Description
                   [Arabidopsis thaliana]
                  311912
Seq. No.
                  wty700169261.hl
Seq. ID
                  BLASTX
Method
                  g3386611
NCBI GI
                  194
BLAST score
                   3.0e-15
E value
                  77
Match length
                   48
% identity
                  (AC004665) unknown protein [Arabidopsis thaliana]
NCBI Description
                   311913
Seq. No.
                   wty700169273.h1
Seq. ID
                   BLASTN
Method
                   q3449334
NCBI GI
BLAST score
                   48
                   4.0e-18
E value
                   104
Match length
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MYH9, complete sequence [Arabidopsis thaliana]
                   311914
Seq. No.
Seq. ID
                   wty700169284.h1
                   BLASTX
Method
                   q4539676
NCBI GI
BLAST score
                   194
                   2.0e-15
E value
                   50
Match length
                   78
% identity
                  (AF061282) patatin-like protein [Sorghum bicolor]
NCBI Description
                   311915
Seq. No.
                   wty700169307.hl
Seq. ID
                   BLASTX
Method
NCBI GI
                   g549063
                   146
BLAST score
E value
                   1.0e-09
                   30
Match length
                   83
 % identity
                   TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)
NCBI Description
                   >gi 1072464 pir __A38958 IgE-dependent histamine-releasing
```

21kd polypeptide [Oryza sativa]

factor homolog - rice >gi_303835_dbj_BAA02151_ (D12626)

```
Seq. No.
                  311916
                  wty700169338.hl
Seq. ID
Method
                  BLASTX
                  q4454012
NCBI GI
                   173
BLAST score
E value
                   3.0e-14
                   75
Match length
                   50
% identity
                   (AL035396) Pollen-specific protein precursor like
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   311917
                   wty700169377.hl
Seq. ID
                   BLASTX
Method
                   q4490331
NCBI GI
                   332
BLAST score
E value
                   2.0e-31
                   78
Match length
                   83
% identity
                  (AL035656) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   311918
Seq. No.
Seq. ID
                   wty700169406.hl
                   BLASTX
Method
                   q4204793
NCBI GI
                   237
BLAST score
                   3.0e-20
E value
Match length
                   86
                   28
% identity
                  (U52079) P-glycoprotein [Solanum tuberosum]
NCBI Description
                   311919
Seq. No.
                   wty700169410.hl
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2982463
BLAST score
                   203
                   3.0e-20
E value
Match length
                   64
% identity
                   84
                  (AL022223) putative protein [Arabidopsis thaliana]
NCBI Description
                   311920
Seq. No.
Seq. ID
                   wty700169427.h1
Method
                   BLASTX
```

Method BLASTX
NCBI GI g3915826
BLAST score 251
E value 6.0e-22
Match length 68
% identity 74

NCBI Description 60S RIBOSOMAL PROTEIN L5

Seq. No. 311921

Seq. ID wty700169435.h1

Method BLASTN
NCBI GI g475252
BLAST score 128

```
7.0e-66
E value
Match length
                    227
                    89
% identity
NCBI Description Z.mays MPI gene
                     311922
Seq. No.
                    wty700169445.hl
Seq. ID
Method
                    BLASTX
                  7 q100665
NCBI GI
                     341
BLAST score
E value
                     2.0e-32
Match length
                     66
% identity
                     50
                     calmodulin 2 (clone lambda DASH) - rice
NCBI Description
                     >gi_20190_emb_CAA78288_ (Z12828) calmodulin [Oryza sativa]
                     >gi 310313 (L18914) calmodulin [Oryza sativa]
Seq. No.
                     311923
                     wty700169476.h1
Seq. ID
Method
                     BLASTX
                     g3746598
NCBI GI
                     148
BLAST score
E value
                     5.0e-10
Match length
                     47
                     57
% identity
                    (AF064613) RNA polymerase II subunit 2 [Kopsia fruticosa]
NCBI Description
                     311924
Seq. No.
                     wty700169481.hl
Seq. ID
                     BLASTX
Method
                     g2499819
NCBI GI
                     204
BLAST score
E value
                     1.0e-16
Match length
                     45
                     89
% identity
                     ASPARTIC PROTEINASE ORYZASIN 1 PRECURSOR
NCBI Description
                     >gi_2130068_pir__S66516 aspartic proteinase 1 precursor - rice >gi_1030715_dbj_BAA06876_ (D32165) aspartic protease [Oryza sativa] >gi_1711289_dbj_BAA06875_ (D32144) aspartic
                     protease [Oryza sativa]
                     311925
Seq. No.
                     wty700169485.h1
Seq. ID
Method
                     BLASTN
NCBI GI
                     g1816585
BLAST score
                     51
                     5.0e-20
E value
Match length
                     51
 % identity
                     100
NCBI Description Zea mays LON1 protease (LON1) mRNA, complete cds
                     311926
 Seq. No.
                     wty700169532.h1
 Seq. ID
                     BLASTX
Method
```

g3287679

8.0e-23

258

NCBI GI

E value

BLAST score

```
Match length
% identity
                  81
                  (AC003979) T22J18.6 [Arabidopsis thaliana]
NCBI Description
                  311927
Seq. No.
                  wty700169556.h1
Seq. ID
Method
                  BLASTX
                  g1839188
NCBI GI
BLAST score ~
                  174
                   6.0e-13
E value
Match length
                  57
% identity
                   63
                  (U86081) root hair defective 3 [Arabidopsis thaliana]
NCBI Description
                   311928
Seq. No.
                  wty700169564.hl
Seq. ID
                  BLASTX
Method
NCBI GI
                   q1710546
                   223
BLAST score
                   1.0e-18
E value
                   67
Match length
                   67
% identity
                   60S RIBOSOMAL PROTEIN L36 >gi_1276967 (U47095) putative
NCBI Description
                   ribosomal protein [Daucus carota]
                   311929
Seq. No.
                   wty700169616.hl
Seq. ID
                   BLASTN
Method
NCBI GI
                   g3004949
                   165
BLAST score
                   6.0e-88
E value
                   173
Match length
                   99
% identity
                   Zea mays tonoplast intrinsic protein (ZmTIP1) mRNA,
NCBI Description
                   complete cds
                   311930
                                    - 1
Seq. No.
                   wty700169619.hl
Seq. ID
Method
                   BLASTX
                   q417154
NCBI GI
BLAST score
                   386
E value
                   1.0e-37
                   77
Match length
                   99
% identity
                   HEAT SHOCK PROTEIN 82 >gi_100685_pir__S25541 heat shock
NCBI Description
                   protein 82 - rice (strain Taichung Native One)
                   >gi 20256_emb_CAA77978_ (Z11920) heat shock protein 82
                   (HSP82) [Oryza sativa]
                   311931
Seq. No.
                   wty700169776.h1
Seq. ID
                   BLASTN
Method
                   g1531540
NCBI GI
                   47
BLAST score
```

1.0e-17

82

89

E value

Match length

% identity



Zea mays mRNA for uroporphyrinogen III methyltransferase, complete cds

Seq. No. 311932

NCBI Description

Seq. ID wty700169787.h1

Method BLASTX
NCBI GI g3033386
BLAST score 145
E value 1.0e-09
Match length 52

Match length 52 % identity 54

NCBI Description (AC004238) RING3-like protein [Arabidopsis thaliana]

Seq. No. 311933

Seq. ID wty700169852.h1

Method BLASTX
NCBI GI g4467153
BLAST score 314
E value 2.0e-29
Match length 78
% identity 72

NCBI Description (AL035540) putative thaumatin-like protein [Arabidopsis

thaliana]

Seq. No. 311934

Seq. ID wty700169937.h1

Method BLASTN
NCBI GI g167107
BLAST score 36
E value 2.0e-11
Match length 36
% identity 100

NCBI Description Hordeum vulgare vacuolar ATPase B subunit isoform mRNA,

complete cds

Seq. No. 311935

Seq. ID wty700169975.h1

Method BLASTX
NCBI GI g2829911
BLAST score 255
E value 1.0e-22
Match length 68
% identity 74

NCBI Description (AC002291) Unknown protein [Arabidopsis thaliana]

Seq. No. 311936

Seq. ID wty700170020.h1

Method BLASTX
NCBI GI g4581207
BLAST score 234
E value 4.0e-20
Match length 71
% identity 65

NCBI Description (Y17914) cyclic nucleotide and calmodulin-regulated ion

channel [Arabidopsis thaliana]

Seq. No. 311937

44517

```
wty700170029.h1
Seq. ID
                  BLASTX
Method
                  q4105798
NCBI GI
                  192
BLAST score
                  5.0e-15
E value
                  45
Match length
                  69
% identity
                  (AF049930) PGP237-11 [Petunia x hybrida]
NCBI Description
                  311938
Seq. No.
                  wty700170059.h1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3421384
                  199
BLAST score
                   6.0e-16
E value
                   57
Match length
                   65
% identity
                   (AF081067) IAA-Ala hydrolase; IAA-amino acid hydrolase
NCBI Description
                   [Arabidopsis thaliana]
                   311939
Seq. No.
                   wty700170128.h1
Seq. ID
                   BLASTX
Method
                   g2047324
NCBI GI
BLAST score
                   155
                   8.0e-11
E value
                   33
Match length
                   85
% identity
NCBI Description (U80192) HAL3 homolog [Arabidopsis thaliana]
                   311940
Seq. No.
                   wty700170137.h1
Seq. ID
                   BLASTN
Method
                   g4416300
NCBI GI
BLAST score
                   70
                   1.0e-31
E value
                   82
Match length
                   96
% identity
                   Zea mays chromosome 4 22 kDa zein-associated intercluster
NCBI Description
                   region, complete sequence
                   311941
Seq. No.
                   wty700170141.hl
Seq. ID
                   BLASTX
Method
                   q228412
```

NCBI GI 172 BLAST score

8.0e-13 E value 34 Match length 94 % identity

NCBI Description malic enzyme [Populus trichocarpa x Populus deltoides]

311942 Seq. No.

wty700170205.h1 Seq. ID

BLASTN Method g3821780 NCBI GI BLAST score 36 E value 5.0e-11

```
36
```

Match length 36 % identity 100

NCBI Description Xenopus laevis cDNA clone 27A6-1

-...

Seq. No. 311943

Seq. ID wty700170215.h1

Method BLASTN
NCBI GI g22507
BLAST score 70
E value 1.0e-31
Match length 102
% identity 25

NCBI Description Maize (strain W64A) mRNA for cell wall glycoprotein

قد. .

Seq. No. 311944

Seq. ID wty700170239.h1

Method BLASTN
NCBI GI g2645165
BLAST score 65
E value 3.0e-28
Match length 85
% identity 94

NCBI Description Oryza sativa mRNA, similar to ribosomal protein

Seq. No. 311945

Seq. ID wty700170266.h1

Method BLASTX
NCBI GI g2288988
BLAST score 192
E value 3.0e-15
Match length 42
% identity 81

NCBI Description (AC002335) hypothetical protein [Arabidopsis thaliana]

Seq. No. 311946

Seq. ID wty700170275.h1

Method BLASTX
NCBI GI g548770
BLAST score 270
E value 3.0e-24
Match length 61
% identity 85

NCBI Description 60S RIBOSOMAL PROTEIN L3 >gi_481228_pir__S38359 ribosomal

protein L3 - rice >gi_303853_dbj_BAA02155_ (D12630)

ribosomal protein L3 [Oryza sativa]

Seq. No. 311947

Seq. ID wty700170277.h1

Method BLASTX
NCBI GI g4586055
BLAST score 169
E value 2.0e-12
Match length 76
% identity 46

NCBI Description (AC007020) hypothetical protein [Arabidopsis thaliana]

Seq. No. 311948

```
wty700170291.h1
Seq. ID
                  BLASTX
Method
                  g2388565
NCBI GI
                  214
BLAST score
                  1.0e-17
E value
                  59
Match length
% identity
                   (AC000098) Similar to Prunus pectinesterase (gb_X95991).
NCBI Description
                   [Arabidopsis thaliana]
                   311949
Seq. No.
                  wty700170302.h1
Seq. ID
                  BLASTX
Method
                   g2809237
NCBI GI
BLAST score
                   162
                   7.0e-19
E value
Match length
                   79
                   65
% identity
                   (AC002560) F21B7.6 [Arabidopsis thaliana]
NCBI Description
                   311950
Seq. No.
                   wty700170303.hl
Seq. ID
                   BLASTN
Method
                   g3821780
NCBI GI
BLAST score
                   36
                   5.0e-11
E value
                   48
Match length
                   67
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                   311951
Seq. No.
                   wty700170306.h1
Seq. ID
                   BLASTN
Method
                   g3153236
NCBI GI
                   203
BLAST score
                   1.0e-110
E value
                   219
Match length
                   98
% identity
NCBI Description Zea mays terminal ear1 mRNA, complete cds
                   311952
 Seq. No.
                   wty700170354.hl
 Seq. ID
                   BLASTX
Method
                   g2865424
 NCBI GI
 BLAST score
                   168
                   3.0e-12
 E value
                   57
 Match length
                   54
 % identity
                   (AF039371) polyprotein [Arabidopsis thaliana]
 NCBI Description
 Seq. No.
                    311953
                   wty700170380.hl
 Seq. ID
                   BLASTN
 Method
                    g643596
 NCBI GI
```

157

3.0e-40

BLAST score E value

Match length

```
% identity
NCBI Description Corn mRNA for cysteine proteinase, clone CCP, complete cds
                  311954
Seq. No.
                  wty700170408.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4204263
                  188-
BLAST score
                   1.0è-14
E value
                   64
Match length
% identity
                  (AC005223) 40409 [Arabidopsis thaliana]
NCBI Description
                   311955
Seq. No.
                   wty700170424.h1
Seq. ID
```

Method BLASTX g2827143 NCBI GI BLAST score 282 9.0e-26 E value 60 Match length

83

% identity (AF027174) cellulose synthase catalytic subunit NCBI Description

[Arabidopsis thaliana]

Seq. No. 311956 wty700170443.h1 Seq. ID BLASTX Method q1708110 NCBI GI BLAST score 153 1.0e-10 E value

32 Match length 97 % identity

HISTONE H4 >gi 2119025 pir S59586 histone H4 (clone NCBI Description

CH-III) - Chlamydomonas reinhardtii >gi_2119027_pir_ histone H4 - Chlamydomonas reinhardtii >gi_571471 (U16724) histone H4 [Chlamydomonas reinhardtii] >gi_571476 (U16725) histone H4 [Chlamydomonas reinhardtii] >gi_576634 (U16825) histone H4 [Chlamydomonas reinhardtii] >gi_790701 (L41841)

histone H4 [Chlamydomonas reinhardtii]

311957 Seq. No.

wty700170502.h1 Seq. ID

Method BLASTX g2160692 NCBI GI 188 BLAST score 1.0e-14 E value Match length 40 % identity 80

(U73527) B' regulatory subunit of PP2A [Arabidopsis NCBI Description

thaliana]

311958 Seq. No.

Seq. ID wty700170547.h1

BLASTX Method g3004565 NCBI GI 142 BLAST score 3.0e-09 E value

44521



Match length 45 % identity 58

NCBI Description (AC003673) putative protein kinase [Arabidopsis thaliana]

Seq. No. 311959

Seq. ID wty700170603.h1

Method BLASTX
NCBI GI g3641836
BLAST score 381
E value 3.0e-37
Match length 82
% identity 87

NCBI Description (AL023094) putative serine/threonine protein kinase

[Arabidopsis thaliana]

Seq. No. 311960

Seq. ID wty700170608.h1

Method BLASTN
NCBI GI g2832242
BLAST score 133
E value 7.0e-69
Match length 204
% identity 90

NCBI Description Zea mays 22-kDa alpha zein gene cluster, complete sequence

Seq. No. 311961

Seq. ID wty700170726.h1

Method BLASTX
NCBI GI g2541876
BLAST score 147
E value 9.0e-10
Match length 65
% identity 46

NCBI Description (D26015) CND41, chloroplast nucleoid DNA binding protein

[Nicotiana tabacum]

Seq. No. 311962

Seq. ID wty700170727.h1

Method BLASTX
NCBI GI g3874214
BLAST score 153
E value 1.0e-10
Match length 74
% identity 43

NCBI Description (Z83217) Similarity to Yeast E1-E2 ATPase YEL031W

(SW:YED1_YEAST); cDNA EST EMBL:D27574 comes from this gene;

cDNA EST EMBL:D33757 comes from this gene; cDNA EST EMBL:D34256 comes from this gene; cDNA EST EMBL:D37288

comes from

Seq. No. 311963

Seq. ID wty700170923.h1

Method BLASTX
NCBI GI g2326343
BLAST score 213
E value 1.0e-17
Match length 77



```
% identity
                   (Y11187) G14587-5 [Arabidopsis thaliana]
NCBI Description
                  >gi 2326350_emb_CAA72042_ (Y11155) hypothetical protein
                   [Arabidopsis thaliana]
                   311964
Seq. No.
                  wty700170983.h1
Seq. ID
                  BLASTN
Method
                   g3821780
                                              ٠٠٠.
NCBI GI
                   36
BLAST score
                   5.0e-11
E value
                   36
Match length
% identity
                   100
NCBI Description Xenopus laevis cDNA clone 27A6-1
                   311965
Seq. No.
                   wty700170984.h1
Seq. ID
                   BLASTN
Method
                   g459267
NCBI GI
                   120
BLAST score
                   4.0e-61
E value
                   136
Match length
                   98
% identity
NCBI Description
                  Z.mays gene for HMG protein
                   311966
Seq. No.
                   wty700170990.h1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4512653
                   155
BLAST score
E value
                   1.0e-10
                   53
Match length
                   58
% identity
                   (AC007048) unknown protein [Arabidopsis thaliana]
NCBI Description
                   311967
Seq. No.
                   wty700170993.h1
Seq. ID
                   BLASTX
Method
                   q1136122
NCBI GI
BLAST score
                   396
                   5.0e-39
E value
                   74
Match length
                   100
% identity
                   (X91807) alfa-tubulin [Oryza sativa]
NCBI Description
                   311968
Seq. No.
Seq. ID
                   wty700171013.h1
Method
                   BLASTX
                   g4538993
NCBI GI
BLAST score
                   202
E value
                   3.0e-16
Match length
                   71
```

thaliana]

311969

NCBI Description

% identity

Seq. No.

44523

(AL049481) putative host response protein [Arabidopsis

```
wty700171018.hl
Seq. ID
Method
                  BLASTX
                  a3719211
NCBI GI
BLAST score
                  199
                  7.0e-16
E value
                   58
Match length
                   67
% identity
NCBI Description (U97021) UIP2 [Arabidopsis thaliana]
                   311970
Seq. No.
                  wty700171046.h1
Seq. ID
Method
                  BLASTX
                   g3925277
NCBI GI
BLAST score
                   170
                   2.0e-12
E value
                   69
Match length
                   54
% identity
                   (AL032643) similar to Uncharacterized protein family
NCBI Description
                   UPF0034, Double-stranded RNA binding motif; cDNA EST
                   yk489b3.5 comes from this gene; cDNA EST yk439g7.5 comes
                   from this gene [Caenorhabditis elegans]
                   311971
Seq. No.
                   wty700171061.hl
Seq. ID
Method
                   BLASTX
                   q4337044
NCBI GI
                   271
BLAST score
                   2.0e-24
E value
                   76
Match length
                   75
% identity
                   (AF124161) molybdopterin synthase sulphurylase [Nicotiana
NCBI Description
                   plumbaginifolia]
                   311972
Seq. No.
                   wty700171068.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q400758
                   179
BLAST score
                   1.0e-13
E value
Match length
                   56
                   59
% identity
                   POLYGALACTURONASE PRECURSOR (PG) (PECTINASE)
NCBI Description
                   >qi 22631 emb CAA47055 (X66426) polygalacturonase [Persea
                   americana]
                   311973
Seq. No.
                   wty700171075.hl
Seq. ID
Method
                   BLASTX
                   q4090935
NCBI GI
BLAST score
                   159
                   3.0e-11
E value
Match length
                   75
 % identity
                   45
                   (AF028719) DNA polymerase type I [Rhodothermus sp. 'ITI
NCBI Description
```

518']

311974

Seq. No.



```
wty700171184.h1
  Seq. ID
                    BLASTN
  Method
                    g2062705
  NCBI GI
                    36
  BLAST score
                    5.0e-11
  E value
  Match length
                    48
                    67
  % identity
NCBI Description
                    Human butyrophilin (BTF5) mRNA, complete cds
                    311975
  Seq. No.
                    wty700171252.h1
  Seq. ID
  Method
                    BLASTX
                    g2673906
  NCBI GI
                    259
  BLAST score
                    8.0e-23
  E value
  Match length
                    85
  % identity
                     59
                     (ACO02561) putative DNA polymerase delta small subunit
  NCBI Description
                     [Arabidopsis thaliana]
  Seq. No.
                     311976
  Seq. ID
                     wty700171264.h1
  Method
                     BLASTN
                     g3821780
  NCBI GI
  BLAST score
                     36
  E value
                     6.0e-11
  Match length
                     36
                     100
  % identity
  NCBI Description Xenopus laevis cDNA clone 27A6-1
                     311977
  Seq. No.
                     wty700171314.h1
  Seq. ID
  Method
                     BLASTN
                     g432367
  NCBI GI
                     72
  BLAST score
                     2.0e-32
  E value
                     220
  Match length
                     83
  % identity
  NCBI Description Rice mRNA for elongation factor 1 beta, complete cds
                     311978
  Seq. No.
  Seq. ID
                     wty700171386.hl
                     BLASTN
  Method
                     g3821780
  NCBI GI
  BLAST score
                     36
                     6.0e-11
  E value
                     48
  Match length
                     67
  % identity
  NCBI Description Xenopus laevis cDNA clone 27A6-1
                     311979
  Seq. No.
  Seq. ID
                     wty700171392.hl
  Method
                     BLASTX
  NCBI GI
                     g4218011
  BLAST score
                     207
```

8.0e-17

46

E value Match length



% identity

(AC006135) putative protein kinase [Arabidopsis thaliana] NCBI Description

>gi_4309721_gb_AAD15491_ (AC006439) putative
serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No. 311980

wty700171393.h1 Seq. ID

Method BLASTX NCBI GI g1709129 BLAST score 255 E value 2.0e-22 Match length 52 % identity

NCBI Description GLYCOGEN SYNTHASE KINASE-3 HOMOLOG MSK-3

> >qi 481018 pir S37642 protein kinase MSK-3 (EC 2.7.1.-) alfalfa >gi 313148_emb_CAA48472_ (X68409) protein kinase

[Medicago sativa]

311981 Seq. No.

Seq. ID wty700171413.h1

Method BLASTX NCBI GI g2497964 BLAST score 165 E value 5.0e-12 Match length 57 % identity ິ56∙

MOLYBDOPTERIN BIOŚYNTHESIS CNX3 PROTEIN (MOLYBDENUM NCBI Description

COFACTOR BIOSYNTHESIS ENZYME CNX3) >gi 662873 emb CAA88106

(Z48046) Cnx3 [Arabidopsis thaliana]

Seq. No. 311982

Seq. ID wty700171449.h1

Method BLASTX NCBI GI g1174853 BLAST score 174 4.0e-13 E value 37 Match length 84 % identity

UBIQUITIN-CONJUGATING ENZYME E2-18 KD (UBIQUITIN-PROTEIN NCBI Description

LIGASE) (UBIQUITIN CARRIER PROTEIN) (PM42)

>gi 481811 pir S39483 ubiquitin-conjugating enzyme UBC2-1 - Arabidopsis thaliana >gi_22658_emb_CAA48378_ (X68306) ubiquitin-conjugating enzyme [Arabidopsis thaliana]

Seq. No. 311983

Seq. ID wty700171501.h1

Method BLASTX NCBI GI q2827623 BLAST score 214 E value 9.0e-18 Match length 45 % identity 87

NCBI Description (AL021636) putative protein [Arabidopsis thaliana]

Seq. No. 311984

Seq. ID wty700171537.hl

Method BLASTN

```
g3821780
NCBI GI
BLAST score
                  36
                  4.0e-11
E value
Match length
                  36
                  100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                  311985
                  wty700171550.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2827143
BLAST score
                  137
E value
                  1.0e-08
Match length
                  47
                  57
% identity
                  (AF027174) cellulose synthase catalytic subunit
NCBI Description
                  [Arabidopsis thaliana]
                  311986
Seq. No.
Seq. ID
                  wty700171673.h1
Method
                  BLASTX
NCBI GI
                  q2501494
BLAST score
                  212
E value
                  2.0e-17
Match length
                  56
                  6.4
% identity
                  FLAVONOL 3-O-GLUCOSYLTRANSFERASE 5 (UDP-GLUCOSE FLAVONOID
NCBI Description
                  3-O-GLUCOSYLTRANSFERASE 5) >qi 542015 pir S41951
                  UTP-glucose glucosyltransferase - cassava
                  >gi 453249 emb CAA54612 (X77462) UTP-glucose
                  glucosyltransferase [Manihot esculenta]
Seq. No.
                  311987
                  wty700171703.h1
Seq. ID
Method
                  BLASTN
                  g4185305
NCBI GI
                  62
BLAST score
                  2.0e-26
E value
Match length
                  144
                  88
% identity
                  Zea mays cosmid IV.1E1 22-kDa alpha zein protein 21
NCBI Description
                   (sz22-21) gene, complete cds; retrotransposon Opie-2 gag
                  protein, polyprotein, and copia protein genes, complete
                  cds; and unknown genes
                  311988
Seq. No.
                  wty700171719.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3292817
```

BLAST score 186 E value 2.0e-14 64 Match length 56 % identity

(AL031018) hypothetical protein [Arabidopsis thaliana] NCBI Description

Seq. No.

311989

Seq. ID

wty700171730.h1

NCBI GI

E value

BLAST score

g3821780

36 5.0e-11

```
BLASTX
Method
NCBI GI
                  g1545871
                  317
BLAST score
                  1.0e-29
E value
Match length
                   61
                   98
% identity
                   (U66607) cyclin type B-like [Zea mays] >gi_1545873 (U66608)
NCBI Description
                  cyclin type B-like [Zea mays]...
                   311990
Seq. No.
Seq. ID
                  wty700171739.h1
                  BLASTX
Method
                   q3779024
NCBI GI
                   173
BLAST score
                   7.0e-13
E value
                   46
Match length
                   74
% identity
                   (AC005171) unknown protein [Arabidopsis thaliana]
NCBI Description
                   311991
Seq. No.
Seq. ID
                  wty700171749.h1
Method -
                   BLASTX
                   q2642640
NCBI GI
                   331
BLAST score
                   2.0e-31
E value
                   75
Match length
                   77
% identity
                   (AF032473) ADP-glucose pyrophosphorylase large subunit 2
NCBI Description
                   [Citrullus lanatus]
                   311992
Seq. No.
Seq. ID
                   wty700171752.h1
Method
                   BLASTX
NCBI GI
                   g2832408
BLAST score
                   253
                   4.0e-22
E value
                   56
Match length
                   77
% identity
                   (Y14209) R2R3-MYB transcription factor [Arabidopsis
NCBI Description
                   thaliana]
                   311993
Seq. No.
Seq. ID
                   wty700171786.hl
Method
                   BLASTN
NCBI GI
                   q532622
                   195
BLAST score
                   1.0e-106
E value
                   219
Match length
                   97
% identity
                  Zea mays lipase (LIP) mRNA, complete cds
NCBI Description
Seq. No.
                   311994
                   wty700171826.hl
Seq. ID
                   BLASTN
Method
```

44528

Method NCBI GI

E value

BLAST score

Match length

```
Match length
                  100
% identity
                  Xenopus laevis cDNA clone 27A6-1
NCBI Description
Seq. No.
                  311995
Seq. ID
                  wty700171844.h1
Method
                  BLASTX
NCBI GI
                  g1345587
BLAST score
                  150
                  7.0e-14
E value
Match length
                  47
                  98
% identity
                  14-3-3-LIKE PROTEIN GF14-6 >qi 998430 bbs 164522 (S77133)
NCBI Description
                  GF14-6=14-3-3 protein homolog [Zea mays, XL80, Peptide, 261
                  aa] [Zea mays]
Seq. No.
                  311996
Seq. ID
                  wty700171849.h1
Method
                  BLASTX
                  g4220479
NCBI GI
BLAST score
                  142
E value
                  3.0e-09
Match length
                   41
% identity
                   61
NCBI Description
                  (AC006069) unknown protein [Arabidopsis thaliana]
Seq. No.
                  311997
Seq. ID
                  wty700171882.h1
Method
                  BLASTX
NCBI GI
                  g3269290
BLAST score
                  262
E value
                  3.0e-23
Match length
                   68
                  71
% identity
NCBI Description
                   (AL030978) putative receptor like kinase [Arabidopsis
                  thaliana]
                  311998
Seq. No.
Seq. ID
                  wty700171888.h1
Method
                  BLASTX
NCBI GI
                  g3859944
BLAST score
                  257
E value
                  8.0e-23
Match length
                  66
% identity
                   (AF084570) FKBP12 interacting protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  311999
Seq. ID
                  wty700171978.h1
```

% identity 100
NCBI Description (X92428) HOX1B protein [Zea mays]

BLASTX

321

59

g1648931

3.0e-30

Method

NCBI GI

BLASTX

g1345132

0.5

```
312000
Seq. No.
                   wty700172016.hl
Seq. ID
Method
                   BLASTX
                   g4056437
NCBI GI
BLAST score
                   251
E value
                   5.0e-22
Match length
                   67
                   72
% identity
NCBI Description
                   (AC005990) Strong similarity to PFAM PF 00069 Eukaryotic
                  protein kinase domain. [Arabidopsis thaliana]
Seq. No.
                   312001
                   wty700172022.h1
Seq. ID
Method
                   BLASTN
NCBI GI
                   q4127347
BLAST score
                   41
E value
                   5.0e-14
Match length
                   65
                   91
% identity
NCBI Description Alopecurus myosuroides mRNA for glutathione transferase 1b
Seq. No.
                   312002
Seq. ID
                   wty700172062.h1
Method
                   BLASTX
NCBI GI
                   q1711205
BLAST score
                   284
E value
                   7.0e-26
Match length
                   62
                   84
% identity
                  (U79555) IAA23 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   312003
Seq. ID
                   wty700172081.h1
Method
                   BLASTN
                   g168502
NCBI GI
BLAST score
                   96
                   5.0e-47
E value
Match length
                   128
% identity
                   94
                  Maize (Zea mays) histone H4 gene (H4C7), complete cds
NCBI Description
                   312004
Seq. No.
Seq. ID
                   wty700172137.h1
Method
                   BLASTX
                   g4090884
NCBI GI
BLAST score
                   167
E value
                   3.0e-12
Match length
                   61
% identity
                   57
                   (AF025333) vesicle-associated membrane protein 7B;
NCBI Description
                   synaptobrevin 7B [Arabidopsis thaliana]
Seq. No.
                   312005
Seq. ID
                   wty700172182.h1
```

44530

BLAST score 175 E value 4.0e-13 Match length 68 % identity 55

NCBI Description (U47029) ERECTA [Arabidopsis thaliana]

>gi_1389566_dbj_BAA11869_ (D83257) receptor protein kinase

j. -

[Arabidopsis thaliana] >gi_3075386 (AC004484) receptor

protein kinase, ERECTA [Arabidopsis thaliana]

Seq. No. 312006

Seq. ID wty700172230.h1

Method BLASTX
NCBI GI g4263825
BLAST score 191
E value 4.0e-15
Match length 69
% identity 55

NCBI Description (AC006067) hypothetical protein [Arabidopsis thaliana]

Seq. No. 312007

Seq. ID wty700172325.h1

Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 5.0e-11
Match length 48

% identity 67

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 312008

Seq. ID wty700172328.h1

Method BLASTN
NCBI GI g3821780
BLAST score 35
E value 2.0e-10
Match length 35
% identity 100

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 312009

Seq. ID wty700172364.h1

Method BLASTN
NCBI GI g4104241
BLAST score 49
E value 3.0e-19
Match length 93
% identity 88

NCBI Description Gossypium hirsutum palmitoyl-acyl carrier protein

thioesterase (FatB1) mRNA, partial cds

Seq. No. 312010

Seq. ID wty700172385.h1

Method BLASTX
NCBI GI g3024122
BLAST score 225
E value 5.0e-19
Match length 48



% identity S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE NCBI Description ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2) >gi_1778821 (U82833) S-adenosyl-L-methionine synthetase [Oryza sativa] 312011 Seq. No. wty700172430.h1 Seq. ID

BLASTN Method g169818 NCBI GI 56 BLAST score 6.0e-23 E value 200 Match length 84 % identity

NCBI Description Rice 25S ribosomal RNA gene

312012 Seq. No.

wty700172439.h1 Seq. ID

BLASTX Method g4539298 NCBI GI 157 BLAST score 4.0e-11 E value 51 Match length 55

% identity (AL049480) putative calmodulin-binding protein [Arabidopsis NCBI Description

thaliana]

312013 Seq. No.

wty700172459.h1 Seq. ID

BLASTX Method q2244878 NCBI GI 295 BLAST score 4.0e-27 E value 71 Match length 85 % identity

(Z97338) hypothetical protein [Arabidopsis thaliana] NCBI Description

312014 Seq. No.

wty700172475.hl Seq. ID

BLASTX Method NCBI GI q2444271 215 BLAST score 1.0e-22 E value 69 Match length % identity 75

(AF019637) putative amino acid or GABA permease NCBI Description

[Arabidopsis thaliana]

312015 Seq. No.

wty700172520.hl Seq. ID

BLASTN Method q3695004 NCBI GI 78 BLAST score 4.0e-36 E value Match length 118 92 % identity

Zea mays pyruvate dehydrogenase kinase isoform 2 mRNA, NCBI Description nuclear gene encoding mitochondrial protein, complete cds

NCBI GI

BLAST score

g3355477

168



```
312016
Seq. No.
                  wty700172524.h1
Seq. ID
                  BLASTN
Method
                  g3821780
NCBI GI
                  37
BLAST score
                  1.0e-11
E value
                  37
Match length
                  100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                  312017
Seq. No.
                  wty700172619.h1
Seq. ID
                  BLASTN
Method
                  g2645165
NCBI GI
BLAST score
                   66
                  7.0e-29
E value
                  74
Match length
                   97
% identity
NCBI Description Oryza sativa mRNA, similar to ribosomal protein
                   312018
Seq. No.
                   wty700172629.h1
Seq. ID
                   BLASTN
Method
                   g431269
NCBI GI
BLAST score
                   35
                   2.0e-10
E value
Match length
                   67
                   88
% identity
                  Arabidopsis thaliana ubiquitin conjugating enzyme (UBC5)
NCBI Description
                   gene, complete cds
                   312019
Seq. No.
                   wty700172636.h1
Seq. ID
Method
                   BLASTX
                   g2245066
NCBI GI
                   245
BLAST score
                   3.0e-21
E value
                   62
Match length
                   66
% identity
                   (Z97342) Beta-Amylase [Arabidopsis thaliana]
NCBI Description
                   312020
Seq. No.
                   wty700172674.h1
Seq. ID
                   BLASTX
Method
                   g4455232
NCBI GI
                   180
BLAST score
                   1.0e-13
E value
                   48
Match length
                   69
% identity
                   (AL035523) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   312021
                   wty700172675.h1
Seq. ID
                   BLASTX
Method
```

BLAST score

E value

168

3.0e-12

```
3.0e-12
E value
Match length
                    66
 % identity
                    (AC004218) putative P-glycoprotein, pgpl [Arabidopsis
NCBI Description
                    thaliana]
                    312022
 Seq. No.
                    wty700172676.h1
 Seq. ID
 Method
                    BLASTX
                    g2500107
 NCBI GI
                    346
 BLAST score
                    4.0e-33
 E value
                    75
 Match length
                    95
 % identity
                    DNA REPAIR PROTEIN RAD51 HOMOLOG >gi_1143810 (U22441)
 NCBI Description
                    LeRAD51 [Solanum lycopersicum]
                     312023
 Seq. No.
                    wty700172740.h1
 Seq. ID
                    BLASTX
 Method
                     g3482917
 NCBI GI
 BLAST score
                     221
                     1.0e-18
 E value
                    52
 Match length
                     83
 % identity
                     (AC003970) Similar to Glucose-6-phosphate dehydrogenases,
NCBI Description
                     gi_2276344, gi_2829880, gi_2352919 and others. [Arabidopsis
                     thaliana]
                     312024
 Seq. No.
                     wty700172747.h1
 Seq. ID
                     BLASTX
 Method
                     g1313907
 NCBI GI
                     353
 BLAST score
                     6.0e-34
 E value
                     78
 Match length
                     85
 % identity
                     (D84507) CDPK-related protein kinase [Zea mays]
 NCBI Description
                     312025
 Seq. No.
                     wty700172758.h1
 Seq. ID
 Method
                     BLASTX
                     g1353193
 NCBI GI
                     153
 BLAST score
 E value
                     1.0e-10
 Match length
                     37
                     78
 % identity
                     O-METHYLTRANSFERASE ZRP4 (OMT) >gi_542186_pir__JQ2268
O-methyltransferase (EC 2.1.1.-) - maize >gi_404070
 NCBI Description
                     (L14063) O-methyltransferase [Zea mays]
                     312026
 Seq. No.
                     wty700172766.h1
 Seq. ID
 Method
                     BLASTX
 NCBI GI
                     g4587533
```

44534



```
Match length
% identity
                   48
NCBI Description
                   (AC007060) EST gb AA721821 comes from this gene.
                   [Arabidopsis thaliana]
                   312027
Seq. No.
Seq. ID
                  wty700172805.hl
Method :
                  BLASTX
                  q120670
```

NCBI GI BLAST score 180 8.0e-14 E value Match length 38 97 % identity

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi 100879_pir_ S06879 glyceraldehyde-3-phosphate

dehydrogenase (EC 1.2.1.12) C - maize

>gi 295853_emb_CAA33620_ (X15596) GAPDH [Zea mays]

312028 Seq. No. Seq. ID wty700172823.h1 Method BLASTX NCBI GI q1091678 BLAST score 144 E value 2.0e-09

Match length 68 38 % identity

NCBI Description activator-like transposable element [Pennisetum glaucum]

Seq. No. 312029

Seq. ID wty700172865.hl

Method BLASTX NCBI GI g2253278 BLAST score 166 2.0e-25 E value 76 Match length % identity 82

NCBI Description (AF005492) RF2a [Oryza sativa]

312030 Seq. No.

Seq. ID wty700172912.h1

Method BLASTX NCBI GI q1706958 . BLAST score 311 5.0e-29 E value Match length 63 % identity 84

NCBI Description (U58284) cellulose synthase [Gossypium hirsutum]

Seq. No. 312031

wty700172919.h1 Seq. ID

Method BLASTN g3821780 NCBI GI BLAST score 36 E value 5.0e-11 Match length 36 100 % identity

NCBI Description Xenopus laevis cDNA clone 27A6-1

```
312032
Seq. No.
                   wty700172939.h1
Seq. ID
                   BLASTX
Method
                   g537319
NCBI GI
BLAST score
                   223
                   1.0e-18
E value
Match length
                   73
                   56
% identity ~
                   (L36158) peroxidase [Medicago sativa]
NCBI Description
                   312033
Seq. No.
                   wty700172944.hl
Seq. ID
Method
                   BLASTN
                   q1890574
NCBI GI
BLAST score
                   47
                   1.0e-17
E value
                   107
Match length
% identity
                   86
                   H.vulgare mRNA for xyloglucan endotransglycosylase-like
NCBI Description
                   protein (XEA)
                   312034
Seq. No.
Seq. ID
                   wty700172945.h1
Method
                   BLASTX
NCBI GI
                   g548770
                   320
BLAST score
                   3.0e-30
E value
Match length
                   67
                   88
% identity
                   60S RIBOSOMAL PROTEIN L3 >gi_481228_pir__S38359 ribosomal
NCBI Description
                   protein L3 - rice >gi_303853_dbj_BAA02155_ (D12630)
                   ribosomal protein L3 [Oryza sativa]
                   312035
Seq. No.
Seq. ID
                   wty700172979.h1
Method
                   BLASTX
                   q2462822
NCBI GI
                    263
BLAST score
E value
                    2.0e-23
                   83
Match length
% identity
                    65
                   (AF000657) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                    312036
                    wty700173009.h1
Seq. ID
Method
                    BLASTX
NCBI GI
                    q464707
BLAST score
                    171
E value
                    1.0e-12
Match length
                    38
                    84
% identity
                   40S RIBOSOMAL PROTEIN S18 >gi 480908 pir S37496 ribosomal
NCBI Description
                   protein S18.A - Arabidopsis thaliana >gi_405613_emb_CAA80684_ (Z23165) ribosomal protein S18A
                    [Arabidopsis thaliana] >gi_434343_emb_CAA82273_ (Z28701)
```

S18 ribosomal protein [Arabidopsis thaliana]



>gi_434345_emb_CAA82274_ (Z28702) S18 ribosomal protein [Arabidopsis thaliana] >gi_434906_emb_CAA82275_ (Z28962) S18 ribosomal protein [Arabidopsis thaliana] >gi_2505871_emb_CAA72909_ (Y12227) ribosomal protein S18A [Arabidopsis thaliana] >gi_3287678 (AC003979) Match to ribosomal S18 gene mRNA gb_Z28701, DNA gb_Z23165 from A. thaliana. ESTs gb_T21121, gb_Z17755, gb_R64776 and gb_R30430 come from this gene. [Arabidopsis thaliana] >gi_4538910_emb_CAB39647.1_ (AL049482) S18.A ribosomal protein [Arabidopsis thaliana]

Seq. No. 312037 Seq. ID wty700173034.h1 Method BLASTX NCBI GI g1619297 BLAST score 375 1.0e-36 E value Match length 73 100 % identity NCBI Description (Y08490) alpha-tubulin 2 [Hordeum vulgare] Seq. No. 312038 wuj700282008.hl Seq. ID Method BLASTX g2130121 NCBI GI BLAST score 509 5.0e-52 E value 100 Match length % identity 98 NCBI Description cyclin II - maize >gi 516550 (U10077) cyclin IIZm [Zea mays] Seq. No. 312039 Seq. ID wuj700282050.h1 Method BLASTN NCBI GI g1864000 BLAST score 77 E value 2.0e-35 Match length 117 91 % identity

 Seq. No.
 312040

 Seq. ID
 wuj700282052.h1

 Method
 BLASTN

 NCBI GI
 g1617470

NCBI Description Maize DNA for Fd III, complete cds

NCBI GI g1617470
BLAST score 112
E value 2.0e-56
Match length 230
% identity 88

NCBI Description Z.diploperennis DNA for Grandel-4 retrotransposon

 Seq. No.
 312041

 Seq. ID
 wuj700282074.hl

 Method
 BLASTX

Method BLASTX NCBI GI g1663724 BLAST score 318



```
1.0e-29
E value
Match length
% identity
                  63
NCBI Description (U50846) 4-coumarate:coenzyme A ligase [Nicotiana tabacum]
                  312042
Seq. No.
                  wuj700282114.h1
Seq. ID
Method
                  BLASTX
                  g4406775
NCBI GI
                  147
BLAST score
                  1.0e-09
E value
                   64
Match length
% identity
                   48
                  (AC006836) unknown protein [Arabidopsis thaliana]
NCBI Description
                  312043
Seq. No.
                  wuj700282171.hl
Seq. ID
Method
                  BLASTX
                   g4006872
NCBI GI
BLAST score
                   186
                   4.0e-14
E value
                   72
Match length
                   56
% identity
                   (Z99707) methionyl aminopeptidase-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   312044
Seq. No.
                   wyr700235112.h1
Seq. ID
Method
                   BLASTN
                   q3063690
NCBI GI
                   38
BLAST score
                   4.0e-12
E value
Match length
                   82
                   87
% identity
                   Arabidopsis thaliana DNA chromosome 4, BAC clone F4D11
NCBI Description
                   (ESSAII project)
                   312045
Seq. No.
                   wyr700235118.h1
Seq. ID
Method
                   BLASTN
NCBI GI
                   q22144
BLAST score
                   148
                   9.0e-78
E value
Match length
                   258
% identity
                   91
                   Maize anaerobically regulated gene for fructose
NCBI Description
                   bisphosphate aldolase (EC 4.1.2.13)
                   312046
Seq. No.
                   wyr700235138.h1
Seq. ID
                   BLASTX
Method
                   q3337356
NCBI GI
                   201
BLAST score
                   4.0e-16
E value
Match length
                   42
                   90
% identity
```

NCBI Description (AC004481) putative protein transport protein SEC61 alpha



· E',

subunit [Arabidopsis thaliana]

```
312047
Seq. No.
Seq. ID
                   wyr700235162.hl
Method
                   BLASTX
NCBI GI
                   g1345977
BLAST score
                   303
                   6.0e-28
E value
Match length
                   88
% identity
                   64
                   OMEGA-6 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM
NCBI Description
                   ISOZYME 2 >gi 904154 (L43921) microsomal omega-6 desaturase
                   [Glycine max]
Seq. No.
                   312048
Seq. ID
                   wyr700235185.h1
                   BLASTN
Method
NCBI GI
                   g732806
BLAST score
                   35
                   2.0e-10
E value
Match length
                   59
                   90
% identity
NCBI Description H.vulgare Bpr1-1 gene for type-1 pathogenesis-related
                   protein
                   312049
Seq. No.
Seq. ID
                   wyr700235186.h1
Method
                   BLASTX
NCBI GI
                   g3522943
BLAST score
                   305
                   3.0e-28
E value
                   84
Match length
% identity
                   67
NCBI Description (AC004411) putative p-glycoprotein [Arabidopsis thaliana]
                   312050
Seq. No.
Seq. ID
                   wyr700235203.h1
                   BLASTX
Method
NCBI GI
                   g2832680
BLAST score
                   197
E value
                   1.0e-15
Match length
                   63
% identity
                   38
NCBI Description (AL021712) putative protein [Arabidopsis thaliana]
Seq. No.
                   312051
                   wyr700235206.h1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3024018
BLAST score
                   387
E value
                   7.0e-38
                   73
Match length
                   100
% identity
NCBI Description
                   INITIATION FACTOR 5A (EIF-5A) (EIF-4D)
                   >gi_1546919_emb_CAA69225_ (Y07920) translation initiation factor 5A [Zea mays] >gi_2668738 (AF034943) translation
```

initiation factor 5A [Zea mays]



```
312052
Seq. No.
Seq. ID
                  wyr700235234.hl
Method
                  BLASTX
NCBI GI
                  q3047096
BLAST score
                  215
E value
                  1.0e-17
Match length
                  80
% identity
NCBI Description
                   (AF058826) similar to eukaryotic protein kinase domains
                   (Pfam: pkinase.hmm, score: 189.74) [Arabidopsis thaliana]
Seq. No.
                  312053
Seq. ID
                  wyr700235235.h1
Method
                  BLASTX
                  g4587533
NCBI GI
                  162
BLAST, score
E value
                  1.0e-11
                   74
Match length
                   47
% identity
                   (AC007060) EST gb AA721821 comes from this gene.
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   312054
                  wyr700235236.h1
Seq. ID
Method
                  BLASTX
                  q4512624
NCBI GI
                   253
BLAST score
E value
                   4.0e-22
Match length
                   71
% identity
                   (AC004793) Strong similarity to gi 3033401 F19I3.29
NCBI Description
                   putative potassium transporter from Arabidopsis thaliana
                   BAC gb_AC004238
Seq. No.
                   312055
                   wyr700235253.h1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2062705
BLAST score
                   37
                   1.0e-11
E value
                   37
Match length
                   100
% identity
                  Human butyrophilin (BTF5) mRNA, complete cds
NCBI Description
Seq. No.
                   312056
                   wyr700235273.h1
Seq. ID
Method
                   BLASTN
NCBI GI
                   q168496
BLAST score
                   113
E value
                   4.0e-57
                   121
Match length
```

Seq. No. 312057

% identity

NCBI Description

Seq. ID wyr700235293.h1

98

Maize (Zea mays) histone H3 gene (H3C4), complete cds



```
BLASTX
 Method
                    q131772
 NCBI GI
 BLAST score
                    228
                    2.0e-19
 E value
                    48
 Match length
                    94
 % identity
                    40S RIBOSOMAL PROTEIN S14 (CLONE MCH1)
 NCBI Description
                    >gi_82723_pir__A30097 ribosomal protein S14 (clone MCH1) -
                    maize
                    312058
 Seq. No.
                    wyr700235389.h1
 Seq. ID
                    BLASTX
 Method
                    g1352468
 NCBI GI
 BLAST score
                    411
                    1.0e-40
 E value
                    86 -
 Match length
                    94
 % identity
                    BETA-FRUCTOFURANOSIDASE 1 PRECURSOR (SUCROSE-6-PHOSPHATE
 NCBI Description
                    HYDROLASE 1) (INVERTASE 1) >gi_1122439 (U16123) invertase
                    [Zea mays]
                    312059
 Seq. No.
                    wyr700235427.h1
 Seq. ID
                    BLASTX
 Method
                    g3219273
🔊 NCBI GI
                     339
 BLAST score
                     4.0e-32
  E value
                    95
 Match length
                     67
  % identity
                     (AB015316) MAP kinase kinase 5 [Arabidopsis thaliana]
  NCBI Description
                     312060
  Seq. No.
                     wyr700235430.h1
  Seq. ID `
                     BLASTX
  Method
                     g2137812
  NCBI GI
  BLAST score
                     211
                                                 , in
                     4.0e-17
  E value
                     77
  Match length
                     52
  % identity
                     tetrahydrofolylpolyglutamate synthase (EC 6.3.2.17)
  NCBI Description
                     precursor - mouse >gi_1199594 (U32197) folylpolyglutamate
                     synthetase [Mus musculus] >gi_1587164_prf_2206297A
                     folylpoly-gamma-Glu synthetase [Mus musculus]
                     312061
  Seq. No.
                     wyr700235434.h1
  Seq. ID
                     BLASTX
  Method
                     g2497539
  NCBI GI
  BLAST score
                     411
                     1.0e-40
```

E value 92 Match length % identity 84

PYRUVATE KINASE, CHLOROPLAST ISOZYME A PRECURSOR >gi 169703 NCBI Description (M64736) ATP:pyruvate phosphotransferase [Ricinus communis]

312062 Seq. No.



```
wyr700235446.hl
Seq. ID
                  BLASTX
Method
                  q3176661
NCBI GI
                  384
BLAST score
                  2.0e-37
E value
                  93
Match length
                  81
% identity
                  (AC004393) Similar to putative DNA polymerase gb_M29683
NCBI Description
                  from S. cerevisiae. [Arabidopsis thaliana]
                  312063
Seq. No.
                  wyr700235447.h1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2780192
                  193
BLAST score
                  5.0e-15
E value
                   43
Match length
                   79
% identity
                  (AJ222713) unnamed protein product [Arabidopsis thaliana]
NCBI Description
                   312064
Seq. No.
                  wyr700235488.h1
Seq. ID
                   BLASTX
Method
                   g4467124
NCBI GI
BLAST score
                   166
                   6.0e-12
E value
                   65
Match length
                   45
% identity
                  (AL035538) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   312065
Seq. No.
                   wyr700235533.h1
Seq. ID
                   BLASTN
Method
NCBI GI
                   q4468793
                   84
BLAST score
E value
                   9.0e-40
Match length
                   121
                   93
% identity
                   Zea mays mRNA for glutathione transferase III(b)
NCBI Description
                   312066
Seq. No.
Seq. ID
                   wyr700235557.h1
                   BLASTX
Method
                   g3386565
NCBI GI
BLAST score
                   163
                   2.0e-11
E value
                   51
Match length
                   73
% identity
                   (AF079588) 1-aminocyclopropane-1-carboxylate oxidase
NCBI Description
                   [Sorghum bicolor]
```

312067 Seq. No. wyr700235561.h1

Seq. ID

Method BLASTN g3452291 NCBI GI 108 BLAST score 7.0e-54E value



```
Match length
                   85
 % identity
 NCBI Description Zea mays retrotransposon Huck-2 3' LTR, partial sequence
                   312068
 Seq. No.
                   wyr700235645.h1
 Seq. ID
                   BLASTX
 Method
                   g478740
 NCBI GI
                    193
*BLAST score
                    5.0e-15
 E value
                    49
 Match length
                    78
 % identity
 NCBI Description phenylalanine ammonia-lyase (EC 4.1.3.5) - rice
                    312069
 Seq. No.
                    wyr700235655.h1
 Seq. ID
                    BLASTX
 Method
                    q4371280
 NCBI GI
                    196
 BLAST score
                    2.0e-15
 E value
                    54
 Match length
                    65
 % identity
 NCBI Description (AC006260) hypothetical protein [Arabidopsis thaliana]
 Seq. No.
                    312070
                    wyr700235659.h1
 Seq. ID
                    BLASTX
 Method
                    g3913804
 NCBI GI
                    185
 BLAST score
                    2.0e-14
 E value
                    51
 Match length
                    89
 % identity
                    HISTONE H2B.3 >gi_577825_emb_CAA49584_ (X69960) H2B histone
 NCBI Description
                    [Zea mays]
                    312071
  Seq. No.
                    wyr700235660.h1
  Seq. ID
                    BLASTN
 Method
                    g3821792
 NCBI GI
 BLAST score
                    79
                    1.0e-36
 E value
                    83
 Match length
                    99
  % identity
  NCBI Description Z.mays mRNA for casein kinase II alpha subunit
                    312072
  Seq. No.
                    wyr700235682.h1
  Seq. ID
                    BLASTN
  Method
  NCBI GI
                    q22272
                    98
  BLAST score
  E value
                    2.0e-48
                    98
  Match length
                    100
  % identity
  NCBI Description Maize mRNA for enolase (2-phospho-D-glycerate hydrolase)
```

312073

wyr700235704.h1

Seq. No.

Seq. ID

```
Method
NCBI GI
                   q3540201
                   247
BLAST score
                   1.0e-21
E value
                   66
Match length
                   73
% identity
                   (AC004260) Putative nuclear protein [Arabidopsis thaliana]
NCBI Description
                   312074
Seq. No.
                   wyr700235706.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2499488
BLAST score
                   181
                   7.0e-14
E value
                   56
Match length
% identity
                   61
                   PYROPHOSPHATE--FRUCTOSE 6-PHOSPHATE 1-PHOSPHOTRANSFERASE
NCBI Description
                   ALPHA SUBUNIT (PFP) (6-PHOSPHOFRUCTOKINASE (PYROPHOSPHATE))
                   (PYROPHOSPHATE-DEPENDENT 6-PHOSPHOFRUCTOSE-1-KINASE)
                   (PPI-PFK) >gi_483547_emb_CAA83682_ (Z32849)
                   pyrophosphate-dependent phosphofructokinase alpha subunit
           40.0
                   [Ricinus communis]
Seq. No.
                   312075
                   wyr700235765.h1
Seq. ID
                                                                              ٠,٠
                   BLASTX
Method
                   g2921304
NCBI GI
                   151
BLAST score
E value
                   3.0e-10
                   43
Match length
% identity
                   (AF033496) herbicide safener binding protein [Zea mays]
NCBI Description
Seq. No.
                   312076
                   wyr700235791.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2695933
BLAST score
                   197
E value
                   1.0e-15
Match length
                   43
% identity
                   (AJ222780) hypothetical protein [Hordeum vulgare]
NCBI Description
Seq. No.
                   312077
                   wyr700235801.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1469369
                   187
BLAST score
                   2.0e-14
E value
Match length
                   91
                   41
% identity
                   (U35731) trehalose phosphate synthase/phosphatase
NCBI Description
```

Seq. No. 312078

Seq. ID wyr700235883.h1

Method BLASTN

[Emericella nidulans]

NCBI GI g4185305 BLAST score 41 E value 5.0e-14 Match length 53 % identity 94

NCBI Description Zea mays cosmid IV.1E1 22-kDa alpha zein protein 21

(sz22-21) gene, complete cds; retrotransposon Opie-2 gag protein, polyprotein, and copia protein genes, complete

cds; and unknown genes

Seq. No. 312079

Seq. ID wyr700235902.h1

Method BLASTX
NCBI GI g168489
BLAST score 309
E value 1.0e-28
Match length 60
% identity 98

NCBI Description (M16902) glutathione S-transferase I [Zea mays] >gi_168491

(M16901) glutathione S-transferase I [Zea mays]

>gi_225458_prf__1303351A transferase,glutathione S [Zea

mays]

Seq. No. 312080

Seq. ID wyr700235928.h1

Method BLASTN
NCBI GI g4206305
BLAST score 35
E value 2.0e-10
Match length 55
% identity 91

NCBI Description Zea mays retrotransposon Cinful-1, complete sequence

Seq. No. 312081

Seq. ID wyr700235952.h1

Method BLASTN
NCBI GI g1420923
BLAST score 34
E value 1.0e-09
Match length 54
% identity 91

NCBI Description Zea mays repressor-like protein (in1) gene, complete cds

Seq. No. 312082

Seq. ID wyr700235983.h1

Method BLASTX
NCBI GI g4099148
BLAST score 230
E value 2.0e-19
Match length 68
% identity 75

NCBI Description (U84268) YLP [Hordeum vulgare]

Seq. No. 312083

Seq. ID wyr700236021.h1

Method BLASTX NCBI GI g2281705

```
BLAST score
                  5.0e-24
E value
                  67
Match length
                  77
% identity
                  (AF013979) ethylene responsive factor [Oryza sativa]
NCBI Description
                  312084
Seq. No.
                  wyr700236071.h1
Seq. ID
                  BLASTX
Method
                  g3386565
NCBI GI
BLAST score
                  321
                  4.0e-30
E value
                  64
Match length
                  98
% identity
                  (AF079588) 1-aminocyclopropane-1-carboxylate oxidase
NCBI Description
                   [Sorghum bicolor]
                  312085
Seq. No.
                  wyr700236114.h1
Seq. ID
                  BLASTX
Method
                   g4314401
NCBI GI
                   363
BLAST score
                   6.0e-35
E value
                   95
Match length
% identity
                   (AC006232) putative beta-1,3-glucanase [Arabidopsis
NCBI Description
                   thaliana]
                   312086
Seq. No.
                   wyr700236145.hl
Seq. ID
                   BLASTX
Method
                   g115871
NCBI GI
                   229
BLAST score
                   3.0e-19
E value
                   87
Match length
                   54
% identity
                   [Segment 2 of 2] SERINE CARBOXYPEPTIDASE II CHAINS A AND B
NCBI Description
                   (CARBOXYPEPTIDASE D) (CPDW-II) (CP-WII)
                   >gi_82623_pir__B29639 serine-type carboxypeptidase (EC
                   3.4.16.1) II B chain - wheat >gi_1421108_pdb_1BCR_B Chain
                   B, Complex Of The Wheat Serine Carboxypeptidase, Cpdw-Ii,
                   With The Microbial Peptide Aldehyde Inhibitor, Antipain,
                   And Arginine At Room Temperature >gi_1421113_pdb_1BCS_B
                   Chain B, Complex Of The Wheat Serine Carboxypeptidase,
                   Cpdw-Ii, With The Microbial Peptide Aldehyde Inhibitor,
                   Chymostatin, And Arginine At 100 Degrees Kelvin
                   >gi_226041_prf__1408164B CPase II B [Triticum aestivum]
                   312087
Seq. No.
                   wyr700236183.hl
```

 Seq. No.
 312087

 Seq. ID
 wyr700236183.h1

 Method
 BLASTX

 NCBI GI
 g3688180

 BLAST score
 161

 E value
 2.0e-11

Match length 85 % identity 39

NCBI Description (AL031804) putative protein [Arabidopsis thaliana]



```
312088
Seq. No.
Seq. ID
                   wyr700236227.h1
Method
                   BLASTX
                   q3256035
NCBI GI
BLAST score
                   192
                   8.0e-16
E value
Match length
                   68
% identity
                   63
                   (Y14274) putative serine/threonine protein kinase [Sorghum
NCBI Description
                   bicolor]
                   312089
Seq. No.
Seq. ID
                   wyr700236230.h1
                   BLASTX
Method
                   g3123270
NCBI GI
BLAST score
                   268
E value
                   2.0e-24
                   62
Match length
                   95
% identity
                   40S RIBOSOMAL PROTEIN S4 (SCAR PROTEIN SS620)
NCBI Description
                   >gi_2463335_emb_CAA75242_ (Y150Q9) ribosomal protein S4
                   [Oryza sativa]
                   312090
Seq. No.
Seq. ID
                   wyr700236334.hl
Method
                   BLASTN
NCBI GI
                   q433041
BLAST score
                   55
                   3.0e-22
E value
Match length
                   108
                   89
% identity
NCBI Description
                   Zea mays W-22 clone PREM-1B retroelement PREM-1, partial
                   sequence
                   312091
Seq. No.
Seq. ID
                   wyr700236421.h1
                   BLASTX
Method
NCBI GI
                   g4587550
BLAST score
                   191
E value
                   8.0e-15
Match length
                   57
% identity
NCBI Description
                   (AC006577) EST gb R64848 comes from this gene. [Arabidopsis
                   thaliana]
                   312092
Seq. No.
                   wyr700236423.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4063747
BLAST score
                   163
E value
                   1.0e-11
Match length
                   67
                   48
% identity
                  (AC005851) hypothetical protein [Arabidopsis thaliana]
NCBI Description
```

Seq. No.

NCBI GI

E value

BLAST score

g4539001 202

2.0e-21



```
wyr700236435.h1
Seq. ID
Method
                  BLASTN
                  q3821780
NCBI GI
                   36
BLAST score
                   6.0e-11
E value
Match length
                   36
                  100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                   312094
Seq. No.
                  wyr700236455.h1
Seq. ID
                  BLASTX
Method
NCBI GI
                   g2252830
                   139
BLAST score
                   9.0e-09
E value
                   76
Match length
                   36
% identity
                   (AF013293) weak similarity to receptor protein kinase
NCBI Description
                   [Arabidopsis thaliana]
                   312095
Seq. No.
                   wyr700236507.h1
Seq. ID
                   BLASTX
Method
                   g3702351
NCBI GI
BLAST score
                   165
                   1.0e-11
E value
                   66
Match length
                   52
% identity
                   (AC005397) putative desiccation protectant protein
NCBI Description
                   [Arabidopsis thaliana]
                   312096
Seq. No.
                   wyr700236566.h1
Seq. ID
                   BLASTX
Method
                   g4455356
NCBI GI
BLAST score
                   194
E value
                   2.0e-15
                   47
Match length
                   74
% identity
                   (AL035524) putative protein [Arabidopsis thaliana]
NCBI Description
                   312097
Seq. No.
                   wyr700236603.hl
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3643594
                   189
BLAST score
                   1.0e-14
E value
                   39
Match length
% identity
                   90
                   (AC005395) unknown protein [Arabidopsis thaliana]
NCBI Description
                   312098
Seq. No.
                   wyr700236743.h1
Seq. ID
Method
                   BLASTX
```



Match length 84 % identity 68

NCBI Description (AL049481) putative protein [Arabidopsis thaliana]

Seq. No. 312099

Seq. ID wyr700236787.h1

Method BLASTX
NCBI GI g3367638
BLAST score 375
E value 2.0e-36
Match length 87
% identity 76

NCBI Description (AJ000331) monogalactosyldiacylglycerol synthase

[Arabidopsis thaliana]

Seq. No. 312100

Seq. ID wyr700236804.h1

Method BLASTX
NCBI GI 94510377
BLAST score 252
E value 6.0e-22
Match length 91
% identity 55

NCBI Description (AC007017) putative RNA helicase A [Arabidopsis thaliana]

Seq. No. 312101

Seq. ID wyr700236814.h1

Method BLASTX
NCBI GI g3024018
BLAST score 360
E value 1.0e-34
Match length 69
% identity 99

o Identity

NCBI Description INITIATION FACTOR 5A (EIF-5A) (EIF-4D)

>gi_1546919_emb_CAA69225_ (Y07920) translation initiation factor 5A [Zea mays] >gi_2668738 (AF034943) translation

initiation factor 5A [Zea mays]

Seq. No. 312102

Seq. ID wyr700236816.h1

Method BLASTN
NCBI GI 9474390
BLAST score 76
E value 9.0e-35
Match length 136
% identity 89

NCBI Description H.vulgare L. (Alexis) Serine carboxypeptidase II-2 mRNA

Seq. No. 312103

Seq. ID wyr700236868.h1

Method BLASTX
NCBI GI g4539327
BLAST score 334
E value 1.0e-31
Match length 74
% identity 84

NCBI Description (AL035679) putative proton pump [Arabidopsis thaliana]



```
312104
Seq. No.
Seq. ID
                   wyr700236989.h1
Method
                   BLASTX
                   q1518540
NCBI GI
                   328
BLAST score
E value
                   6.0e-31
                   73
Match length
% identity
                   (U53418) UDP-glucose dehydrogenase [Glycine max]
NCBI Description
                   312105
Seq. No.
Seq. ID
                   wyr700237041.h1
                   BLASTX
Method
                   q112994
NCBI GI
                   284
BLAST score
                   1.0e-25
E value
Match length
                   62
% identity
                   GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN
NCBI Description
                   >gi_82685_pir__S04536 embryonic abundant protein,
                   glycine-rich - maize >gi_22313_emb_CAA31077_ (X12564)
                   ABA-inducible gene protein [Zea mays]
                   >gi_226091_prf__1410284A abscisic acid inducible gene [Zea
                   mays]
                   312106
Seq. No.
                   wyr700237077.hl
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4038055
BLAST score
                   187
E value
                   1.0e-14
Match length
                   54
% identity
                   65
                   (AC005897) putative cytochrome P450 [Arabidopsis thaliana]
NCBI Description
                   >gi 4557077 gb AAD22516.1 AC007045_16 (AC007045) putative
                   cytochrome p450 [Arabidopsis thaliana]
Seq. No.
                   312107
Seq. ID
                   wyr700237078.h1
Method
                   BLASTN
                   g1370602
NCBI GI
BLAST score
                   127
E value
                   2.0e-65
Match length
                   131
                   99
 % identity
NCBI Description
                   Z.mays mRNA for annexin p35
                   312108
Seq. No.
Seq. ID
                   wyr700237087.hl
                   BLASTX
Method
NCBI GI
                   g2851508
BLAST score
                   196
E value
                   1.0e-15
Match length
                   39
                   87
 % identity
                  60S RIBOSOMAL PROTEIN L21 >gi_2160162 (AC000132) Similar to
NCBI Description
```

```
ibacomal protoin 121 (ch 120026) F
```

ribosomal protein L21 (gb_L38826). ESTs gb_AA395597,gb_ATTS5197 come from this gene. [Arabidopsis thaliana] >gi_3482935 (AC003970) Putative ribosomal protein L21 [Arabidopsis thaliana]

Seq. No. 312109 Seq. ID wyr700237104.h1 Method . BLASTX NCBI GI q3522943 BLAST score 140 E value 7.0e-09 Match length 70 % identity 51 (AC004411) putative p-glycoprotein [Arabidopsis thaliana] NCBI Description Seq. No. 312110 wyr700237106.h1 Seq. ID Method BLASTN NCBI GI g3264595 109 BLAST score 2.0e-54 E value Match length 177 92 % identity

NCBI Description Zea mays putative tonoplast aquaporin mRNA, complete cds

Seq. No. 312111

Seq. ID wyr700237111.h1

Method BLASTX
NCBI GI g2190992
BLAST score 201
E value 5.0e-16
Match length 88

Match length 88 % identity 47

NCBI Description (AF004358) glutathione S-transferase TSI-1 [Aegilops

tauschii]

Seq. No. 312112

Seq. ID wyr700237129.h1

Method BLASTX
NCBI GI g3080532
BLAST score 143
E value 3.0e-09
Match length 66
% identity 38

NCBI Description (AL022600) hypothetical protein [Schizosaccharomyces pombe]

Seq. No. 312113

Seq. ID wyr700237152.h1

Method BLASTX
NCBI GI 94557817
BLAST score 299
E value 2.0e-27
Match length 86
% identity 69

NCBI Description 3-oxoacid CoA transferase precursor;

succinyl-CoA:3-ketoacid-CoA transferase precursor

>gi_2492998_sp_P55809_SCOT_HUMAN



SUCCINYL-COA: 3-KETOACID-COENZYME A TRANSFERASE PRECURSOR (SUCCINYL COA:3-OXOACID COA-TRANSFERASE) (OXCT) >gi 1519052 (U62961) succinyl CoA:3-oxoacid CoA transferase precursor [Homo sapiens]

312114 Seq. No. wyr700237155.h1 Seq. ID Method BLASTX NCBI GI g4508068 BLAST score 209 7.0e-17 E value Match length 51 % identity 82

312115

NCBI Description (AC005882) 3063 [Arabidopsis thaliana]

Seq. No. wyr700237166.h1 Seq. ID Method BLASTX g2197050 NCBI GI 155 BLAST score 1.0e-10 E value Match length 57 % identity 58

NCBI Description (AF001033) putative 20kDa subunit of the V-ATPase

[Neurospora crassa]

Seq. No. 312116 Seq. ID

wyr700237256.h1 Method BLASTX

NCBI GI g2511546 BLAST score 159 E value 5.0e-11 Match length 85 % identity 45

NCBI Description (AF022658) putative c2h2 zinc finger transcription factor

[Arabidopsis thaliana]

Seq. No. 312117

wyr700237265.h1 Seq. ID

BLASTX Method NCBI GI q1321661 BLAST score 296 E value 3.0e-27 Match length 61 % identity 93

(D45423) ascorbate peroxidase [Oryza sativa] NCBI Description

Seq. No. 312118

wyr700237287.h1 Seq. ID

Method BLASTX NCBI GI g1172836 BLAST score 405 E value 6.0e-40Match length 76

% identity 97

NCBI Description GTP-BINDING NUCLEAR PROTEIN RAN-B1 >gi 496272 (L16787)

small ras-related protein [Nicotiana tabacum]

```
312119
Seq. No.
                  wyr700237335.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1491929
BLAST score
                   231
                   2.0e-19
E value
Match length
                   91
% identity
NCBI Description
                   (U51272) 1,3-beta-D-glucan synthase catalytic subunit
                   [Emericella nidulans]
Seq. No.
                   312120
Seq. ID
                   wyr700237339.hl
Method
                   BLASTX
NCBI GI
                   q3757521
BLAST score
                   315
E value
                   2.0e-29
Match length
                   91
                   64
% identity
                   (ACOÖ5167) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   312121
                   wyr700237347.hl
Seq. ID
Method
                   BLASTX
NCBI GI
                   q510907
BLAST score
                   269
E value
                   6.0e-24
Match length
                   55
                   84
% identity
```

(Z35108) calnexin [Helianthus tuberosus] NCBI Description

Seq. No. 312122 Seq. ID

wyr700237368.h1

Method BLASTX g1706958 NCBI GI 254 BLAST score 2.0e-22 E value Match length 53 87 % identity

(U58284) cellulose synthase [Gossypium hirsutum] NCBI Description

Seq. No.

Seq. ID wyr700237429.h1

312123

BLASTX Method NCBI GI g2191136 156 BLAST score 2.0e-13 E value Match length 68 57 % identity

(AF007269) Similar to UTP-Glucose Glucosyltransferase; NCBI Description

coded for by A. thaliana cDNA T46230; coded for by A. thaliana cDNA H76538; coded for by A. thaliana cDNA H76290

[Arabidopsis thaliana]

312124 Seq. No.

wyr700237435.h1 Seq. ID

```
BLASTN
Method
NCBI GI
                  g2696018
                  34
BLAST score
                  9.0e-10
E value
                  70
Match length
% identity
                  87
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MXC9, complete sequence [Arabidopsis thaliana]
                 312125
Seq. No.
                  wyr700237473.h1
Seq. ID
Method
                  BLASTX
                  g3292821
NCBI GI
                   142
BLAST score
                   5.0e-09
E value
                   91
Match length
% identity
                   38
                  (AL031018) putative protein [Arabidopsis thaliana]
NCBI Description
                   312126
Seq. No.
                  wyr700237480.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                   q507844
BLAST score
                   130
                   5.0e-67
E value
                   230
Match length
% identity
                   89
NCBI Description Zea mays A188 retrotransposon gag gene, complete cds
                   312127
Seq. No.
                   wyr700237526.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4008156
                   425
BLAST score
E value
                   3.0e-42
Match length
                   86
% identity
                   97
                  (AB008845) NADH dependent Glutamate Synthase [Oryza sativa]
NCBI Description
                   312128
Seq. No.
                   wyr700237544.h1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3461836
                   321
BLAST score
                   4.0e-30
E value
                   83
Match length
% identity
                   71
                   (AC005315) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                   >gi 3927841 (AC005727) putative protein kinase [Arabidopsis
                   thaliana]
```

Seq. No. 312129

Seq. ID wyr700237549.h1 Method BLASTX

NCBI GI g4249388 BLAST score 149 E value 7.0e-10

```
Match length
                   56
% identity
                   (AC005966) Similar to gb_AF025438 Opa-interacting protein
NCBI Description
                   (OIP2) from Homo sapiens. [Arabidopsis thaliana]
                   312130
Seq. No.
                   wyr700237552.h1
Seq. ID
                   BLASTN
Method
                   q3821780
NCBI GI
                   36
BLAST score
                   6.0e-11
E value
                   48
Match length
                   67
 % identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                   312131
 Seq. No.
                   wyr700237582.h1
 Seq. ID
                   BLASTX
Method
NCBI GI
                   q1944573
                   293
BLAST score
                   8.0e-27
E value
                   72
Match length
                   82
 % identity
                   (Z49146) phenylalanine ammonia-lyase [Hordeum vulgare]
 NCBI Description
                   312132
 Seq. No.
                   wyr700237592.h1
 Seq. ID
                   BLASTX
 Method
                   g3355477
 NCBI GI
                   293
 BLAST score
                   6.0e-27
 E value
                   84
 Match length
                   65
 % identity
                   (AC004218) putative P-glycoprotein, pgp1 [Arabidopsis
 NCBI Description
                   thaliana]
                   312133
Seq. No.
 Seq. ID
                   wyr700237603.hl
                   BLASTX
 Method
 NCBI GI
                   q3063469
 BLAST score
                    181
                    1.0e-13
 E value
                   73
 Match length
                    47
 % identity
                   (AC003981) F22013.31 [Arabidopsis thaliana]
 NCBI Description
```

Seq. No. 312134

Seq. ID wyr700237605.hl

Method BLASTX
NCBI GI g2494174
BLAST score 264
E value 2.0e-23
Match length 59
% identity 88

, ; ,

NCBI Description GLUTAMATE DECARBOXYLASE 1 (GAD 1) >gi_497979 (U10034)

glutamate decarboxylase [Arabidopsis Thaliana]

```
312135
Seq. No.
                  wyr700237658.hl
Seq. ID
                  BLASTX
Method
                   g2809246
NCBI GI
                   234
BLAST score
                   7.0e-20
E value
                   69
Match length
                   62
% identity
                   (AC002560) F2401.15 [Arabidopsis thaliana]
NCBI Description
                   312136
Seq. No.
                   wyr700237675.hl
Seq. ID
                   BLASTN
Method
                   g559535
NCBI GI
BLAST score
                   206
                   1.0e-112
E value
                   234
Match length
                   97
% identity
                   Z.mays mRNA for metallothionein
NCBI Description
                   312137
Seq. No.
                   wyr700237712.h1
Seq. ID
                   BLASTX
Method
                   g3265058
NCBI GI
BLAST score
                   324
                   2.0e-30
E value
                   65
Match length
                   100
% identity
                   (AF060232) monoubiquitin/carboxy extension protein fusion
NCBI Description
                   [Botryotinia fuckeliana]
                   312138
Seq. No.
                   wyr700237713.h1
Seq. ID
                   BLASTX
Method
                   g4210330
NCBI GI
                   323
BLAST score
                   2.0e-30
E value
Match length
                   79
                   77
% identity
                   (AJ223802) 2-oxoglutarate dehydrogenase, El subunit
NCBI Description
                   [Arabidopsis thaliana]
                   312139
Seq. No.
Seq. ID
                   wyr700237715.hl
Method
                   BLASTX
                   q3986291
NCBI GI
```

NCBI GI g3986291
BLAST score 303
E value 6.0e-28
Match length 91
% identity 60

NCBI Description (AB018078) oligo-1,4 - 1,4-glucantransferase / amylo-1,6-glucosidase [Saccharomyces cerevisiae]

 Seq. No.
 312140

 Seq. ID
 wyr700237734.h1

 Method
 BLASTN

Method BLASTN NCBI GI g19064

```
BLAST score
E value
                  6.0e-11
                  60
Match length
                  90
% identity
                  Hordeum vulgare nar7 gene for NAD(P)H-bispecific nitrate
NCBI Description
                  reductase
                  312141
Seq. No.
                  wyr700237745.h1
Seq. ID
                  BLASTN
Method
                  g3399678
NCBI GI
                  51
BLAST score
                   6.0e-20
E value
Match length
                  135
% identity
                   84
                  Arabidopsis thaliana chromosome 1 BAC F13M7 sequence,
NCBI Description
                   complete sequence [Arabidopsis thaliana]
                   312142
Seq. No.
                   wyr700237774.hl
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3549626
                   267
BLAST score
                   1.0e-23
E value
Match length
                   85
                   67
% identity
                  (AJ009696) wall-associated kinase 1 [Arabidopsis thaliana]
NCBI Description
                   312143
Seq. No.
                   wyr700237827.h1
Seq. ID
                   BLASTX
Method
                   g1764100
NCBI GI
                   385
BLAST score
E value
                   1.0e-37
                   88
Match length
                   80
% identity
                   (U81805) GDP-D-mannose-4,6-dehydratase [Arabidopsis
NCBI Description
                   thaliana]
                   312144
Seq. No.
                   wyr700237829.h1
Seq. ID
Method
                   BLASTX
                   g1076809
NCBI GI
BLAST score
                   284
                   8.0e-26
E value
Match length
                   66
                   85
% identity
                   H+-transporting ATPase (EC 3.6.1.35) - maize
NCBI Description
                   >gi_758355_emb_CAA59800_ (X85805) H(+)-transporting ATPase
                   [Zea mays]
                   312145
 Seq. No.
                   wyr700237893.hl
 Seq. ID
                   BLASTX
Method
```

44557

g2865394

2.0e-44

443

NCBI GI

E value

BLAST score



```
Match length
                  99
% identity
                  (AF036949) basic leucine zipper protein [Zea mays]
NCBI Description
                  312146
Seq. No.
                  wyr700237896.h1
Seq. ID
                  BLASTX
Method
                  g4239879
NCBI GI
                   254
BLAST score
                   3.0e-22
E value
                  71
Match length
                   65
% identity
                   (AB016780) Glutamine:fructose-6-phosphate amidotransferase
NCBI Description
                   2 [Mus musculus]
                   312147
Seq. No.
                  wyr700237918.hl
Şeq. ID
                   BLASTX
Method
                   g2832408
NCBI GI
BLAST score
                   251
                   8.0e-22
E value
                   57
Match length
                   81
% identity
                   (Y14209) R2R3-MYB transcription factor [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   312148
                   wyr700237921.h1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2982247
BLAST score
                   216
                   1.0e-17
E value
                   62
Match length
                   63
% identity
                  (AF051206) probable thioredoxin H [Picea mariana]
NCBI Description
                   312149
Seq. No.
                   wyr700237939.h1 -
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2129651
                   324
BLAST score
E value
                   2.0e-30
                   81
Match length
                   73
% identity
                   myosin heavy chain ATM2 - Arabidopsis thaliana (fragment)
NCBI Description
```

>gi_499045_emb_CAA84065_ (Z34292) myosin [Arabidopsis

thaliana]

Seq. No. 312150

wyr700237962.hl Seq. ID

Method BLASTX NCBI GI q4510339 BLAST score 278 5.0e-25 E value Match length 87 % identity 53

NCBI Description (AC006921) putative ABC transporter protein [Arabidopsis



thaliana]

```
312151
Seq. No.
Seq. ID
                  wyr700238022.h1
Method
                  BLASTX
NCBI GI
                  g2924247
BLAST score
                  188
                  2.0e-14
E value
                  66
Match length
                  53
% identity
NCBI Description (Y07782) expansin [Oryza sativa]
Seq. No.
                  312152
                  wyr700238030.h1
Seq. ID
Method
                  BLASTX
                  g4490304
NCBI GI
BLAST score
                   147
E value
                  2.0e-10
Match length
                  43
% identity
                  88
NCBI Description (AL035678) putative protein [Arabidopsis thaliana]
Seq. No.
                  312153
Seq. ID
                  wyr700238031.h1
Method
                  BLASTN
                   g2062705
NCBI GI
                   35
BLAST score
                   1.0e-10
E value
Match length
                   35
                   100
% identity
NCBI Description Human butyrophilin (BTF5) mRNA, complete cds
Seq. No.
                   312154
                   wyr700238044.h1
Seq. ID
Method
                  BLASTN
                  - g3821780
NCBI GI
BLAST score
                   36
E value
                   6.0e-11
Match length
                   48
% identity
                   67
NCBI Description Xenopus laevis cDNA clone 27A6-1
                   312155
Seq. No.
Seq. ID
                   wyr700238046.h1
Method
                   BLASTN
NCBI GI
                   g602252
BLAST score
                   112
E value
                   1.0e-56
                   112
Match length
% identity
                   100
NCBI Description Zea mays enolase (eno2) mRNA, complete cds
                   312156
Seq. No.
Seq. ID
                   wyr700238066.h1
```

44559

BLASTX

209

g3169012

Method NCBI GI

BLAST score

4.0e-17 E value 47 Match length % identity 83

(AJ002610) putative calmodulin binding transporter protein NCBI Description

[Hordeum vulgare]

312157. Seq. No.

wyr700238067.h1 Seq. ID

BLASTX Method g2384669 NCBI GI 151 BLAST score 2.0e-10 E value 69 Match length 38 % identity

(AF012656) putative potassium transporter AtKT1p NCBI Description

[Arabidopsis thaliana]

312158 Seq. No.

wyr700238076.hl Seq. ID

BLASTN Method g22469 NCBI GI 97 BLAST score 2.0e-47 E value 130 Match length 92 % identity

Maize mRNA for cytoplasmic ribosomal protein S11 NCBI Description

312159 Seq. No.

wyr700238077.hl Seq. ID

BLASTX Method q2244933 NCBI GI 149 BLAST score 4.0e-10 E value 48 Match length 62

% identity

(Z97339) similar to hypothetical protein YPL211w - yeast NCBI Description

[Arabidopsis thaliana]

312160 Seq. No.

wyr700238085.h1 Seq. ID

Method BLASTX q3024018 NCBI GI 280 BLAST score 4.0e-26 E value Match length 78 88 % identity

INITIATION FACTOR 5A (EIF-5A) (EIF-4D) NCBI Description

>gi_1546919_emb_CAA69225_ (Y07920) translation initiation factor 5A [Zea mays] >gi_2668738 (AF034943) translation

initiation factor 5A [Zea mays]

312161 Seq. No.

wyr700238121.h1 Seq. ID

BLASTX Method NCBI GI g3831440 254 BLAST score E value 4.0e-22



Match length 55 % identity

NCBI Description

(AC005819) putative cytochrome P450 [Arabidopsis thaliana] >gi 4415946 gb AAD20176 (AC006418) putative cytochrome

P450 [Arabidopsis thaliana]

Seq. No. 312162

Seq. ID wyr700238122.hl

Method BLASTX NCBI GI q3641838 BLAST score 150 E value 6.0e-10 Match length 34 76 % identity

(AL023094) putative protein (fragment) [Arabidopsis NCBI Description

312163 Seq. No.

wyr700238140.h1 Seq. ID

Method BLASTN q499011 NCBI GI 91 BLAST score E value 9.0e-44 Match length 184 % identity

S.vulgare SoAc1 mRNA NCBI Description

312164 Seq. No.

Seq. ID wyr700238173.h1

Method BLASTX NCBI GI g2190551 BLAST score 232 1.0e-19 E value Match length 48 92 % identity

(AC001229) Similar to C. elegans hypothetical protein NCBI Description

K07C5.6 (gb_Z71181). ESTs gb_H36844,gb_AA394956 come from

this gene. [Arabidopsis thaliana]

312165 Seq. No.

Seq. ID wyr700238190.hl

Method BLASTX g4539460 NCBI GI BLAST score 157 7.0e-11 E value Match length 85 % identity

(AL049500) putative protein [Arabidopsis thaliana] NCBI Description

Seq. No. 312166

wyr700238231.h1 Seq. ID

BLASTN Method g1491773 NCBI GI 98 BLAST score 3.0e-48 E value 102 Match length % identity 99





```
NCBI Description Z.mays mRNA for cysteine proteinase, See1
                   312167
Seq. No.
Seq. ID
                   wyr700238237.h1
                  BLASTX
Method
NCBI GI
                   q3786008
BLAST score
                   185
                   4.0e-14
E value
                   87
Match length
                   48
% identity
                  (AC005499) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   312168
                   wyr700238253.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2494643
                   380
BLAST score
E value
                   6.0e-37
                   76
Match length
                   96
% identity
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE (GAPDH)
NCBI Description
                   >gi_2143409_emb_CAA73141_ (Y12542)
                   glyceraldehyde-3-phosphate dehydrogenase [Trichoderma
                   harzianum]
                   312169
Seq. No.
                   wyr700238254.h1
Seq. ID
Method
                   BLASTX
                   g4376203
NCBI GI
                   211
BLAST score
                   4.0e-17
E value
                   88
Match length
                   47
% identity
NCBI Description
                   (U35226) putative cytochrome P-450 [Nicotiana
                   plumbaginifolia]
Seq. No.
                   312170
Seq. ID
                   wyr700238273.hl
Method
                   BLASTX
NCBI GI
                   q2618699
BLAST score
                   174
                   8.0e-13
E value
Match length
                   66
                   48
% identity
                   (AC002510) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   312171
Seq. ID
                   wyr700238296.h1
Method
                   BLASTX
NCBI GI
                   q4587572
BLAST score
                   282
                   2.0e-25
E value
```

Match length 76 % identity 67 NCBI Description (ACC

on (AC006550) Similar to gb_U70015 lysosomal trafficking regulator from Mus musculus and contains 2 PF_00400 WD40,



this gene. [Arabidopsis thaliana]

```
312172
Seq. No.
                  wyr700238302.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4406820
BLAST score
                  287
E value
                  4.0e-26
Match length
                  87
% identity
                  64
                  (AC006201) putative ras superfamily member [Arabidopsis
NCBI Description
                  312173
Seq. No.
                  wyr700238303.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1070358
BLAST score
                  322
E value
                  3.0e-30
Match length
                  88
                  76
% identity
NCBI Description
                   (X93171) oxalate oxidase-like protein or germin-like
                  protein [Hordeum vulgare]
Seq. No.
                  312174
Seq. ID
                  wyr700238310.h1
Method
                  BLASTX
NCBI GI
                  g3287683
BLAST score
                  276
E value
                  8.0e-25
Match length
                  89
% identity
                  30
                   (AC003979) Similar to apoptosis protein MA-3 gb D50465 from
NCBI Description
                  Mus musculus. [Arabidopsis thaliana]
                   312175
Seq. No.
                  wyr700238322.h1
Seq. ID
Method
                  BLASTN
                  g432606
NCBI GI
                   40
BLAST score
                   2.0e-13
E value
Match length
                   68
                   90
% identity
                  ricl=ras-related GTP binding protein possessing GTPase
NCBI Description
                  activity [Oryza sativa=rice, Yamahoushi, callus, mRNA, 955
                   312176
Seq. No.
Seq. ID
                  wyr700238329.h1
                  BLASTX
Method
                  g3970803
NCBI GI
BLAST score
                  183
E value
                  7.0e-14
                   51
Match length
                   63
% identity
                   (AJ130841) caffeoyl-CoA 3-O-methyltransferase [Populus
NCBI Description
                  balsamifera subsp. trichocarpa]
```

% identity

NCBI Description

59



```
Seq. No.
                   312177
                   wyr700238337.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g4263715
BLAST score
                   172
E value
                   1.0e-12
                   66
Match length
% identity
                   (AC006223) putative alanine acetyl transferase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   312178
Seq. ID
                   wyr700238348.h1
Method
                   BLASTX
NCBI GI
                   a4587512
                   148
BLAST score
E value
                   8.0e-10
                   70
Match length
                   49
% identity
                   (AC007060) Strong similarity to gi_2245113
NCBI Description
                   glycerol-3-phosphate permease homolog from Arabidopsis
                   thaliana BAC gb_Z97343 and a member of the PF_00083 Sugar
                   transporter family
Seq. No.
                   312179
                   wyr700238355.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2827555
BLAST score
                   276
                   9.0e-25
E value
                   91
Match length
% identity
                   58
NCBI Description
                   (AL021635) Translation factor EF-1 alpha - like protein
                   [Arabidopsis thaliana]
Seq. No.
                   312180
                   wyr700238357.hl
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4185515
BLAST score
                   149
E value
                   2.0e-13
Match length
                   72
                   54
% identity
                   (AF102824) actin depolymerizing factor 6 [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   312181
Seq. ID
                   wyr700238360.hl
Method
                   BLASTX
NCBI GI
                   g3915186
BLAST score
                   164
                   1.0e-11
E value
                   59
Match length
```

UBIQUITIN-CONJUGATING ENZYME E2-21 KD (UBIQUITIN-PROTEIN

LIGASE) (UBIQUITIN CARRIER PROTEIN) (PEROXIN-4) >gi_3128447

(AF061604) ubiquitin-conjugating enzyme homolog peroxin 4 [Pichia angusta]

Seq. No. 312182

Seq. ID wyr700238385.hl

Method BLASTX
NCBI GI g3122386
BLAST score 174
E value 8.0e-13
Match length 40
% identity 80

NCBI Description WD-40 REPEAT PROTEIN MSI1 >gi_2394227 (AF016845) WD-40

repeat protein [Lycopersicon esculentum]

Seq. No. 312183

Seq. ID wyr700238493.h1

Method BLASTX
NCBI GI g1172811
BLAST score 354
E value 6.0e-34
Match length 68
% identity 96

NCBI Description 60S RIBOSOMAL PROTEIN L10-1 (PUTATIVE TUMOR SUPRESSOR SC34)

>gi_1076751_pir__S49575 ribosomal protein L10.e, cytosolic
- rice >gi_575355_emb_CAA57339_ (X81691) putative tumor

suppresser [Oryza sativa]

Seq. No. 312184

Seq. ID wyr700238510.hl

Method BLASTX
NCBI GI g2244855
BLAST score 193
E value 5.0e-15
Match length 66
% identity 59

NCBI Description (Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No. 312185

Seq. ID wyr700238529.h1

Method BLASTX
NCBI GI g4539453
BLAST score 271
E value 3.0e-24
Match length 86
% identity 62

NCBI Description (AL049500) putative protein [Arabidopsis thaliana]

Seq. No. 312186

Seq. ID wyr700238539.h1

Method BLASTX
NCBI GI g3236247
BLAST score 268
E value 7.0e-24
Match length 83
% identity 66

NCBI Description (AC004684) SCARECROW-like protein [Arabidopsis thaliana]



```
312187
Seq. No.
                  wyr700238543.h1
Seq. ID
                  BLASTX
Method
                  g2435522
NCBI GI
BLAST score
                  239
E value
                  2.0e-20
Match length
                  80
% identity
                  59
                   (AF024504) contains similarity to other AMP-binding enzymes
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  312188
                  wyr700238544.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3402703
BLAST score
                  292
E value
                  1.0e-26
Match length
                  88
                  66
% identity
NCBI Description
                  (AC004261) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  312189
Seq. ID
                  wyr700238568.h1
Method
                  BLASTX
NCBI GI
                  g131770
BLAST score
                  224
E value
                  1.0e-18
Match length
                  59
% identity
                  71
                  40S RIBOSOMAL PROTEIN S9 (40S RIBOSOMAL PROTEIN 1024)
NCBI Description
                   (VEGETATIVE SPECIFIC PROTEIN V12) >gi_70880_pir__R3D024
                  ribosomal protein S9.e - slime mold (Dictyostelium
                   discoideum) >gi_7353_emb_CAA29844_ (X06636) rp1024 protein
                   [Dictyostelium discoideum]
Seq. No.
                  312190
Seq. ID
                  wyr700238572.h1
                  BLASTN
Method
                  q287834
NCBI GI
BLAST score
                   48
                   4.0e-18
E value
Match length
                   48
                  100
% identity
NCBI Description
                  Z.mays yptm2 cDNA
Seq. No.
                  312191
Seq. ID
                  wyr700238582.h1
Method
                  BLASTX
NCBI GI
                  q2651310
BLAST score
                  139
```

9.0e-09 E value 60 Match length % identity 48

NCBI Description (AC002336) putative PTR2-B peptide transporter [Arabidopsis

thaliana]

Seq. No. 312192

```
wyr700238593.h1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g3821780
BLAST score
                  36
                   6.0e-11
E value
Match length
                  36
% identity
                  100
MCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                  312193
                  wyr700238613.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q236729
BLAST score
                  95
                  5.0e-46
E value
Match length
                  143
% identity
                  93
NCBI Description metallothionein homologue [Zea mays, Genomic/mRNA, 1859 nt]
                  312194
Seq. No.
                  wyr700238656.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q629800
BLAST score
                  230
E value
                   1.0e-19
Match length
                   60
% identity
                   67
NCBI Description
                  pir7b protein - rice >gi 498747 emb CAA84024 (Z34270)
                  Pir7b [Oryza sativa]
                   312195
Seq. No.
Seq. ID
                  wyr700238660.h1
Method
                  BLASTX
NCBI GI
                  g218511
BLAST score
                   201
E value
                   6.0e-16
Match length
                   62
% identity
                   66
```

NCBI Description (D10226) ribosomal protein YL16 [Saccharomyces cerevisiae]

Seq. No. 312196

Seq. ID wyr700238662.h1

Method BLASTX
NCBI GI g1667389
BLAST score 405
E value 7.0e-40
Match length 80
% identity 97

NCBI Description (Y09238) 3-hydroxy-3-methylglutaryl coenzyme A reductase

[Zea mays]

Seq. No. 312197

Seq. ID wyr700238665.h1

Method BLASTX
NCBI GI g1174850
BLAST score 318
E value 1.0e-29



Match length 77 % identity 79

NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-21 KD 2 (UBIQUITIN-PROTEIN

LIGASE 5) (UBIQUITIN CARRIER PROTEIN 5)

Seq. No. 312198

Seq. ID wyr700238683.h1

Method BLASTX
NCBI GI g1352468
BLAST score 283
E value 9.0e-26
Match length 57
% identity 88

NCBI Description BETA-FRUCTOFURANOSIDASE 1 PRECURSOR (SUCROSE-6-PHOSPHATE

HYDROLASE 1) (INVERTASE 1) >gi 1122439 (U16123) invertase

[Zea mays]

Seq. No. 312199

Seq. ID wyr700238728.h1

Method BLASTX
NCBI GI g4417304
BLAST score 157
E value 9.0e-11
Match length 94
% identity 43

NCBI Description (AC006446) putative beta-1,4-mannosyl-glycoprotein

beta-1,4-N-acetylglucosaminyltransferase [Arabidopsis

thaliana]

Seq. No. 312200

Seq. ID wyr700238739.h1

Method BLASTX
NCBI GI g2842481
BLAST score 251
E value 7.0e-22
Match length 88
% identity 55

NCBI Description (AL021749) extensin-like protein [Arabidopsis thaliana]

Seq. No. 312201

Seq. ID wyr700238750.h1

Method BLASTX
NCBI GI g4539010
BLAST score 156
E value 9.0e-12
Match length 74
% identity 54

NCBI Description (AL049481) putative DNA-directed RNA polymerase

[Arabidopsis thaliana]

Seq. No. 312202

Seq. ID wyr700238753.h1

MethodBLASTNNCBI GIg4115614BLAST score160E value6.0e-85Match length266

```
% identity
                  Zea mays mRNA for root cap-specific glycine-rich protein,
NCBI Description
                  complete cds
                  312203
Seq. No.
Seq. ID
                  wyr700238758.h1
Method
                  BLASTX
NCBI GI
                  g3399676
BLAST score
                  252
E value
                  8.0e-32
Match length
                  90
% identity
                  79
NCBI Description (AC005390) R31180 1 [Homo sapiens]
Seq. No.
                  312204
                  wyr700238847.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3821780
BLAST score
                  36
E value
                   6.0e-11
Match length
                  36
                  100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                  312205
Seq. No.
Seq. ID
                  wyr700238957.hl
Method
                  BLASTX
```

Method BLASTX
NCBI GI g4106673
BLAST score 329
E value 5.0e-31
Match length 89
% identity 72

NCBI Description (AL035064) queuine trna-ribosyltransferase

[Schizosaccharomyces pombe]

Seq. No. 312206

Seq. ID wyr700238962.h1

Method BLASTX
NCBI GI g699621
BLAST score 311
E value 7.0e-29
Match length 59
% identity 100

NCBI Description (D14578) glutamine synthetase [Zea mays]

Seq. No. 312207

Seq. ID wyr700239008.h1

Method BLASTN
NCBI GI g22483
BLAST score 131
E value 1.0e-67
Match length 183
% identity 94

NCBI Description Z.mays RNA for superoxide dismutase Sod4

Seq. No. 312208

Seq. ID wyr700239029.h1



```
Method
NCBI GI
                   q464849
BLAST score
                   257
                   8.0e-23
E value
                   52
Match length
                   96
% identity
                   TUBULIN ALPHA CHAIN >gi_486847_pir__S36232 tubulin alpha
NCBI Description
                   chain - almond >gi 2041\overline{3} emb \overline{CAA47635} (X67162)
                   alpha-tubulin [Prunus dulcis]
                   312209
Seq. No.
                   wyr700239061.hl
Seq. ID
Method
                   BLASTX
                   g2641619
NCBI GI
                   256
BLAST score
                   2.0e-22
E value
Match length
                   51
                   94
% identity
                   (AF032468) ubiquitin-conjugating enzyme protein E2 [Zea
NCBI Description
                   mays]
                   312210
Seq. No.
                   wyr700239147.hl
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2460251
BLAST score
                   388
                   6.0e-38
E value
Match length
                   82
                   93
% identity
                   (AF020791) ferrochelatase [Hordeum vulgare]
NCBI Description
                   312211
Seq. No.
                   wyr700239183.hl
Seq. ID
Method
                   BLASTN
                   g644492
NCBI GI
BLAST score
                   71
                   4.0e-32
E value
Match length
                   96
                   92
% identity
NCBI Description
                   Corn elongation factor lalpha gene, complete cds
                   312212
Seq. No.
                   wyr700239212.h1
Seq. ID
Method
                   BLASTX
                   g4375833
NCBI GI
                   278
BLAST score
                   6.0e-25
E value
                   88
Match length
% identity
                   61
                    (AL021713) receptor serine/threonine kinase-like protein
NCBI Description
                    [Arabidopsis thaliana]
```

Seq. No. 312213

Seq. ID wyr700239252.h1

Method BLASTX NCBI GI g1684855 BLAST score 303



7.0e-28 E value Match length 90 % identity 22

(U77939) ubiquitin-like protein [Phaseolus vulgaris] NCBI Description

Seq. No. 312214

wyr700239265.h1 Seq. ID

Method BLASTX NCBI GI g135417 BLAST score 500 E value 5.0e-51 Match length 93 % identity 100

NCBI Description

TUBULIN ALPHA-3 CHAIN >gi_100946_pir__JN0105 tubulin alpha-3 chain - maize >gi_22150 emb_CAA44861_ (X6317) (X63176) Alpha-tubulin #3 [Zea mays] >gi 485377 (M60171) alpha-3

tubulin [Zea mays]

312215 Seq. No.

wyr700239267.h1 Seq. ID

Method BLASTX q4314378 NCBI GI BLAST score 144 E value 3.0e-09 85 Match length 38 % identity

(AC006232) putative lipase [Arabidopsis thaliana] NCBI Description

Seq. No. 312216

Seq. ID wyr700239278.h1

Method BLASTN NCBI GI q408384 BLAST score 37 E value 2.0e-11 Match length 37 % identity 100

Rattus norvegicus clone ndf20 neu differentiation factor NCBI Description

mRNA, complete cds

312217 Seq. No.

wyr700239309.h1 Seq. ID

Method BLASTX g4514637 NCBI GI BLAST score 391 3.0e-38 E value Match length 82 % identity 95

(AB021176) root cap protein 2 [Zea mays] NCBI Description

312218 Seq. No.

Seq. ID wyr700239329.h1

Method BLASTN NCBI GI g4204375 BLAST score 170 6.0e-91 E value 193 Match length % identity 97



NCBI Description Zea mays acidic ribosomal protein P2a-4 (rpp2a-4) mRNA, partial cds

Seq. No. 312219

Seq. ID wyr700239376.h1

Method BLASTX
NCBI GI g3549639
BLAST score 230
E value 2.0e-19
Match length 89
% identity 62

NCBI Description (AJ005194) receiver-like protein 3 [Arabidopsis thaliana]

Seq. No. 312220

Seq. ID wyr700239383.h1

Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 6.0e-11
Match length 36
% identity 100

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 312221

Seq. ID wyr700239390.h1

Method BLASTX
NCBI GI g1778093
BLAST score 271
E value 3.0e-24
Match length 89
% identity 61

NCBI Description (U64902) putative sugar transporter; member of major

facilitative superfamily; integral membrane protein [Beta

vulgaris]

Seq. No. 312222

Seq. ID wyr700239461.h1

Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 6.0e-11
Match length 36
% identity 100

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 312223

Seq. ID wyr700239490.h1

Method BLASTX
NCBI GI g2760837
BLAST score 171
E value 2.0e-12
Match length 69
% identity 49

NCBI Description (AC003105) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No. 312224

Seq. ID wyr700239558.h1

```
BLASTX
Method
NCBI GI
                  q3858939
BLAST score
                  377
                  1.0e-36
E value
Match length
                  89
% identity
                  84
                   (AL021636) serine/threonine protein kinase like protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   312225
Seq. ID
                  wyr700239562.h1
Method
                  BLASTX
NCBI GI
                  q4101568
BLAST score
                   358
E value
                   2.0e-34
Match length
                   81
% identity
NCBI Description
                  (AF004816) unknown [Triticum aestivum]
Seq. No.
                   312226
Seq. ID
                  wyr700239568.h1
Method
                  BLASTX
NCBI GI
                  q1168654
BLAST score
                   263
E value
                   3.0e-23
Match length
                   69
% identity
                  62
NCBI Description
                  BETA-GALACTOSIDASE PRECURSOR (LACTASE)
                  >gi_542198_pir__S41889 beta-galactosidase (EC 3.2.1.23) -
                   garden asparagus >gi 452712 emb CAA54525
                                                              (X77319)
                  beta-galactosidase [Asparagus officinalis]
Seq. No.
                   312227
Seq. ID
                  wyr700239573.h1
Method
                  BLASTX
NCBI GI
                   g100602
BLAST score
                   228
E value
                   3.0e-19
                   49
Match length
                   80
% identity
NCBI Description infection-related protein - barley
Seq. No.
                   312228
Seq. ID
                  wyr700239587.h1
Method
                  BLASTX
NCBI GI
                   g399414
BLAST score
                   327
                   8.0e-31
E value
Match length
                   64
                   98
% identity
```

ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) NCBI Description

>gi_322865_pir__JC1454 translation elongation factor eEF-1 alpha chain - wheat >gi_170776 (M90077) translation elongation factor 1 alpha-subunit [Triticum aestivum]

>gi_949878_emb_CAA90651_ (Z50789) elongation factor 1-alpha

[Hordeum vulgare]



```
312229
Seq. No.
                  wyr700239595.h1
Seq. ID
Method
                  BLASTX
                  g4582448
NCBI GI
                   290
BLAST score
                  2.0e-26
E value
                   63
Match length
                  81
% identity
                  (AC007071) putative preprotein translocase SecY subunit
NCBI Description
                   [Arabidopsis thaliana]
                   312230
Seq. No.
                   wyr700239608.hl
Seq. ID
Method
                   BLASTX
                   g3021357
NCBI GI
                   209
BLAST score
                   3.0e-17
E value
                   62
Match length
                   68
% identity
                   (AJ005082) UDP-galactose 4-epimerase [Cyamopsis
NCBI Description
                   tetragonoloba]
                   312231
Seq. No.
                   wyr700239621.h1
Seq. ID
                   BLASTN
Method
                   g559533
NCBI GI
                   59
BLAST score
E value
                   1.0e-24
                   122
Match length
                   98
% identity
NCBI Description Z.mays mRNA for defense-related protein
Seq. No.
                   312232
Seq. ID
                   wyr700239675.h1
                   BLASTX
Method
NCBI GI
                   q1351772
BLAST score
                   362
                   7.0e-35
E value
                   88
Match length
% identity
                   78
                   HYPOTHETICAL 51.9 KD PROTEIN YCF45 (ORF455)
NCBI Description
                   >gi 1185186 emb CAA91669 (Z67753) ORF455, homologous to
                   Porphyra ORF565 [Odontella sinensis]
Seq. No.
                   312233
                   wyr700239718.hl
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1806140
BLAST score
                   150
E value
                   3.0e-10
```

39 Match length 79 % identity

(X97314) cdc2MsC [Medicago sativa] NCBI Description

312234 Seq. No.

wyr700239764.hl Seq. ID

BLASTX Method

```
g2921304
NCBI GI
BLAST score
                   363
                   6.0e-35
E value
Match length
                   88
                   85
% identity
                  (AF033496) herbicide safener binding protein [Zea mays]
NCBI Description
                   312235
Seq. No.
                   wyr700239768.h1
Seq. ID
Method
                   BLASTX
                   g3241943
NCBI GI
                   176
BLAST score
                   1.0e-16
E value
Match length
                   64
% identity
                   72
                   (AC004625) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   312236
Seq. No.
                   wyr700239780.h1
Seq. ID
                   BLASTX
Method
                   g4079800
NCBI GI
                   177
BLAST score
                   2.0e-13
E value
Match length
                   49
% identity
                   67
                   (AF052503) S-phase-specific ribosomal protein [Oryza
NCBI Description
                   sativa]
                   312237
Seq. No.
                   wyr700239811.h1
Seq. ID
Method
                   BLASTN
                   g4218534
NCBI GI
BLAST score
                   56
                   6.0e-23
E value
                   84
Match length
                   92
% identity
                  Triticum sp. mRNA for GRAB1 protein
NCBI Description
                   312238
Seq. No.
Seq. ID
                   wyr700239838.h1
Method
                   BLASTX
                   g4106515
NCBI GI
BLAST score
                   353
E value
                   8.0e-34
Match length
                   90
                   70
% identity
                   (AF092743) CAK associated cyclinH homolog [Populus tremula
NCBI Description
                   x Populus tremuloides]
```

Seq. No. 312239

Seq. ID wyr700239855.h1

Method BLASTX
NCBI GI g4586040
BLAST score 301
E value 1.0e-27
Match length 94
% identity 60



NCBI Description (AC007109) unknown protein [Arabidopsis thaliana]

Seq. No. 312240

Seq. ID wyr700239909.h1

Method BLASTX
NCBI GI g2335108
BLAST score 159
E value 5.0e-11
Match length 72
% identity 39

NCBI Description (AC002339) putative isulinase [Arabidopsis thaliana]

Seq. No. 312241

Seq. ID wyr700239912.h1

Method BLASTX
NCBI GI g2462748
BLAST score 357
E value 3.0e-34
Match length 75
% identity 93

NCBI Description (AC002292) putative Clathrin Coat Assembly protein

[Arabidopsis thaliana]

Seq. No. 312242

Seq. ID wyr700239913.h1

Method BLASTX
NCBI GI g3023817
BLAST score 279
E value 4.0e-25
Match length 69
% identity 80

NCBI Description GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE, CHOLOROPLAST ISOFORM

PRECURSOR (G6PD) >gi_1480344_emb_CAA67782_ (X99405) glucose-6-phosphate dehydrogenase [Nicotiana tabacum]

Seq. No. 312243

Seq. ID wyr700240002.h1

Method BLASTN
NCBI GI g4206305
BLAST score 54
E value 1.0e-21
Match length 194
% identity 82

NCBI Description Zea mays retrotransposon Cinful-1, complete sequence

Seq. No. 312244

Seq. ID wyr700240004.h1

Method BLASTX
NCBI GI g3549667
BLAST score 395
E value 1.0e-38
Match length 92
% identity 84

NCBI Description (AL031394) Arabidopsis dynamin-like protein ADL2

[Arabidopsis thaliana]

Seq. No. 312245

```
wyr700240041.h1
Seq. ID
Method
                  BLASTX
                  g510190
NCBI GI
                  275
BLAST score
                  1.0e-24
E value
                  66
Match length
                  83
% identity
                   (Z28341) chloroplast outer envelope protein 34 [Pisum
NCBI Description
                  sativum] >gi_3293201 (L36856) GTP-binding protein [Pisum
                  sativum]
Seq. No.
                   312246
Seq. ID
                  wyr700240062.h1
                  BLASTX
Method
                   q2648837
NCBI GI
                   178
BLAST score
                   3.0e-13
E value
Match length
                   70
% identity
                   49
                   (AE000985) carboxylesterase (estA) [Archaeoglobus fulgidus]
NCBI Description
                   312247
Seq. No.
                   wyr700240071.hl
Seq. ID
Method
                   BLASTN
                   q3341647
NCBI GI
                   101
BLAST score
                   1.0e-49
E value
                   287
Match length
% identity
                   85
                  Zea mays Ama gene encoding single-subunit RNA polymerase
NCBI Description
                   312248
Seq. No.
                   wyr700240073.h1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2232016
BLAST score
                   287
E value
                   1.0e-160
Match length
                   295
% identity
                   99
                   Zea mays viviparous-14 (vp14) mRNA, complete cds
NCBI Description
                   312249
Seq. No.
                   wyr700240108.h1
Seq. ID
Method
                   BLASTX
                   g345731
NCBI GI
BLAST score
                   161
E value
                   1.0e-11
Match length
                   56
% identity
                   45
                  trithorax homolog HTX, version 1 - human (fragment)
NCBI Description
                   312250
Seq. No.
                   wyr700240132.h1
Seq. ID
```

Method BLASTX g4105125 NCBI GI BLAST score 188 1.0e-14 E value



```
Match length
  % identity
                     94
                     (AF043347) cell wall invertase; beta-fructosidase; Incw4
  NCBI Description
                     [Zea mays]
                     312251
  Seq. No.
  Seq. ID
                     wyr700240133.h1
. Method
                     BLASTX
  NCBI GI
                     q1076809
  BLAST score
                     266
  E value
                     7.0e-24
  Match length
                     58
  % identity
                     90
                     H+-transporting ATPase (EC 3.6.1.35) - maize
  NCBI Description
                     >gi_758355_emb_CAA59800_ (X85805) H(+)-transporting ATPase
                     [Zea mays]
  Seq. No.
                     312252
                     wyr700240160.hl
  Seq. ID
  Method
                     BLASTX
                     g1778093
  NCBI GI
                     333
  BLAST score
  E value
                     2.0e-31
  Match length
                     83
  % identity
                     76
                     (U64902) putative sugar transporter; member of major
  NCBI Description
                     facilitative superfamily; integral membrane protein [Beta
                     vulgaris]
                     312253
  Seq. No.
                     wyr700240165.h1
  Seq. ID
  Method
                     BLASTN
  NCBI GI
                     q559535
  BLAST score
                     70
  E value
                     3.0e-31
  Match length
                     90
  % identity
                     94
  NCBI Description Z.mays mRNA for metallothionein
  Seq. No. (
                     312254
                     wyr700240170.h1
  Seq. ID
  Method
                     BLASTX
  NCBI GI
                     g3850113
  BLAST score
                     211
                     4.0e-17
  E value
  Match length
                     69
  % identity
                     61
                     (AL033388) hypothetical integral membrane protein
  NCBI Description
                     [Schizosaccharomyces pombe]
                     312255
```

Seq. No. 312255 Seq. ID wyr700240174.h1

Method BLASTN
NCBI GI g3819487
BLAST score 86

E value 8.0e-41 Match length 170



% identity 88
NCBI Description Hordeum vulgare genomic DNA fragment; clone MWG2013.uni

Seq. No. 312256

Seq. ID wyr700240188.h1

Method BLASTX
NCBI GI g2500036
BLAST score 153
E value 2.0e-10
Match length 50
% identity 54

NCBI Description DIHYDROOROTASE PRECURSOR (DHOASE) >gi 2121273 (AF000146)

dihydroorotase [Arabidopsis thaliana]

>gi_3292818_emb_CAA19808_ (AL031018) dihydroorotase

[Arabidopsis thaliana]

Seq. No. 312257

Seq. ID wyr700240212.h1

Method BLASTX
NCBI GI g2388561
BLAST score 189
E value 1.0e-14
Match length 80
% identity 50

NCBI Description (AC000098) Similar to Arabidopsis hypothetical protein

PID:e326839 (gb_Z97337). [Arabidopsis thaliana]

Seq. No. 312258

Seq. ID wyr700240237.h1

Method BLASTX
NCBI GI g2062169
BLAST score 199
E value 9.0e-16
Match length 86
% identity 41

NCBI Description (AC001645) ABC transporter (PDR5-like) isolog [Arabidopsis

thaliana]

Seq. No. 312259

Seq. ID wyr700240269.h1

Method BLASTX
NCBI GI g3451066
BLAST score 172
E value 2.0e-12
Match length 64
% identity 45

NCBI Description (AL031326) hypothetical protein [Arabidopsis thaliana]

Seq. No. 312260

Seq. ID wyr700240291.h1

Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 7.0e-11
Match length 48
% identity 67

NCBI Description Xenopus laevis cDNA clone 27A6-1



```
Seq. No.
                   312261
Seq. ID
                   wyr700240293.h1
Method
                   BLASTX
NCBI GI
                   g116923
                   159
BLAST score
E value
                   5.0e-11
                   60
Match length
                   57
% identity
                   COATOMER BETA SUBUNIT (BETA-COAT PROTEIN) (BETA-COP)
NCBI Description
                   >gi_111414_pir__S13520 beta-COP protein - rat
                   >gi_55819_emb_CAA40505_ (X57228) beta COP [Rattus
                   norvegicus]
                   312262
Seq. No.
                   wyr700240308.h1
Seq. ID
Method
                   BLASTN
NCBI GI
                   q397395
                   125
BLAST score
                   5.0e-64
E value
                   125
Match length
                   100
% identity
                  Z.mays MNB1b mRNA for DNA-binding protein
NCBI Description
Seq. No.
                   312263
Seq. ID
                   wyr700240322.h1
                   BLASTX
Method
                   g2244965
NCBI GI
BLAST score
                   279
                   3.0e-25
E value
                   70
Match length
                   74
% identity
                   (Z97340) unnamed protein product [Arabidopsis thaliana]
NCBI Description
                   312264
Seq. No.
Seq. ID
                   wyr700240352.hl
Method
                   BLASTX
                   g2306977
NCBI GI
BLAST score
                   271
                   4.0e-24
E value
                   97
Match length
% identity
                   51
                   (AF010145) hexose transporter [Aspergillus parasiticus]
NCBI Description
                   312265
Seq. No.
Seq. ID
                   wyr700240365.h1
Method
                   BLASTX
NCBI GI
                   g4038642
BLAST score
                   362
                   9.0e-35
E value
                   98
Match length
                   68
% identity
                   (D87063) chitinase [Emericella nidulans]
NCBI Description
```

Seq. No. 312266

Seq. ID wyr700240379.h1 Method BLASTX

```
NCBI GI
                  q4587528
BLAST score
                  148
                  1.0e-09
E value
Match length
                  66
% identity
                  (AC007060) Strong similarity to F19I3.2 gi_3033375 putative
NCBI Description
                  berberine bridge enzyme from Arabidopsis thataliana BAC
                  gb AC004238. EST gb_R90518 comes from this gene
                  312267
Seq. No.
                  wyr700240403.hl
Seq. ID
Method
                  BLASTN
NCBI GI
                  g532622
BLAST score
                  94
E value
                  2.0e-45
Match length
                  252
                  92
% identity
NCBI Description Zea mays lipase (LIP) mRNA, complete cds
                  312268
Seq. No.
                  wyr700240425.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3075397
BLAST score
                  207
                  1.0e-16
E value
Match length
                   61
                   69
% identity
                  (AC004484) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   312269
Seq. ID
                  wyr700240437.h1
Method
                  BLASTX
NCBI GI
                   g1420873
BLAST score
                   337
E value
                   6.0e-32
Match length
                   78
                  76
% identity
                   (X98891) inorganic phosphate transporter 2 [Solanum
NCBI Description
                   tuberosum]
                   312270
Seq. No.
                   wyr700240467.h1
Seq. ID
                  BLASTN
Method
                   g3821780
NCBI GI
BLAST score
                   36
E value
                   6.0e-11
```

Match length 36 100 % identity

NCBI Description Xenopus laevis cDNA clone 27A6-1

312271 Seq. No.

Seq. ID wyr700240472.hl

Method BLASTX NCBI GI g4586038 BLAST score 347 4.0e-33 E value Match length 93



% identity 67
NCBI Description (AC007109) putative heat shock protein [Arabidopsis thaliana]

Seq. No. 312272

Seq. ID wyr700240547.h1

Method BLASTN
NCBI GI g1657766
BLAST score 67
E value 2.0e-29
Match length 159

% identity 43
NCBI Description Zea mays retrotransposon Opie-2 5' LTR, primer binding

and 3' LTR

Seq. No. 312273

Seq. ID wyr700240549.h1

Method BLASTX
NCBI GI g2213629
BLAST score 357
E value 3.0e-34
Match length 93
% identity 80

NCBI Description (AC000103) F21J9.21 [Arabidopsis thaliana]

Seq. No. 312274

Seq. ID wyr700240564.h1

Method BLASTX
NCBI GI g1345977
BLAST score 314
E value 4.0e-29
Match length 80
% identity 69

NCBI Description OMEGA-6 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM

ISOZYME 2 >gi_904154 (L43921) microsomal omega-6 desaturase

site, gag gene, pol gene, complete cds, polypurine tract

[Glycine max]

Seq. No. 312275

Seq. ID wyr700240576.h1

Method BLASTX
NCBI GI g134597
BLAST score 297
E value 3.0e-27
Match length 57
% identity 98

NCBI Description SUPEROXIDE DISMUTASE-4A (CU-ZN) >gi 100926 pir S07007

superoxide dismutase (EC 1.15.1.1) (Cu-Zn) 4, cytosolic -

maize

Seq. No. 312276

Seq. ID wyr700240649.h1

Method BLASTX
NCBI GI g4324597
BLAST score 386
E value 1.0e-37
Match length 94



% identity 82

NCBI Description (AF106324) sodium proton exchanger Nhx1 [Arabidopsis

thaliana]

Seq. No. 312277

Seq. ID wyr700240674.h1

Method BLASTX
NCBI GI g3334200
BLAST score 192
E value 4.0e-15
Match length 43
% identity 86

NCBI Description GLYCINE DEHYDROGENASE (DECARBOXYLATING) PRECURSOR (GLYCINE

DECARBOXYLASE) (GLYCINE CLEAVAGE SYSTEM P-PROTEIN)
>gi_2894362_emb_CAB16918_ (Z99770) P-Protein precursor

[Solanum tuberosum]

Seq. No. 312278

Seq. ID wyr700240708.h1

Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 6.0e-11
Match length 36
% identity 100

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 312279

Seq. ID wyr700240722.h1

Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 6.0e-11
Match length 36
% identity 100

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 312280

Seq. ID wyr700240731.h1

Method BLASTX
NCBI GI g3152620
BLAST score 197
E value 2.0e-15
Match length 60
% identity 53

NCBI Description (AC004482) putative C2H2 zinc finger protein [Arabidopsis

thaliana]

Seq. No. 312281

Seq. ID wyr700240739.h1

Method BLASTX
NCBI GI g113621
BLAST score 395
E value 9.0e-39
Match length 79
% identity 99

NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME





>qi 68196 pir ADZM fructose-bisphosphate aldolase (EC 4.1.2.13), cytosolic - maize >gi_168420 (M16220) aldolase [Zea mays] >gi_295850_emb_CAA31366_ (X12872) fructose bisphosphate aldolase [Zea mays] >gi 225624_prf__1307278A cytoplasmic aldolase [Zea mays]

Seq. No. 312282 wyr700240776.h1 Seq. ID Method BLASTN q559535 NCBI GI BLAST score 69 E value 1.0e-30 Match length 169 % identity 91

Z.mays mRNA for metallothionein NCBI Description

312283 Seq. No.

Seq. ID wyr700240806.h1

Method BLASTN g470670 NCBI GI BLAST score 108 E value 7.0e-54Match length 173 % identity 91

Zea mays transposable element ILS-1 NCBI Description

312284 Seq. No.

wyr700240838.h1 Seq. ID

Method BLASTX q3738294 NCBI GI 204 BLAST score 2.0e-16 E value 87 Match length

% identity 49

(AC005309) hypothetical protein [Arabidopsis thaliana] NCBI Description

Seq. No. 312285

Seq. ID wyr700240889.h1

Method BLASTX NCBI GI q3885882 BLAST score 256 2.0e-22 E value Match length 56 89 % identity

(AF093629) inorganic pyrophosphatase [Oryza sativa] NCBI Description

Seq. No. 312286

Seq. ID wyr700240895.hl

61

Method BLASTX NCBI GI g4006827 BLAST score 306 3.0e-28 E value 97 Match length

% identity (AC005970) subtilisin-like protease [Arabidopsis thaliana] NCBI Description

312287 Seq. No.

```
wyr700240909.h1
 Seq. ID
 Method
                    BLASTX
                    q4204793
 NCBI GI
                    165
 BLAST score
 E value
                    8.0e-12
 Match length
                    77
                    45
 % identity
                    (U52079) P-glycoprotein [Solanum tuberosum]
 NCBI Description
                    312288
 Seq. No.
                    wyr700240923.h1
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g3080433
 BLAST score
                    268
                    6.0e-24
 E value
                    69
 Match length
 % identity
                    71
                    (AL022605) putative gamma-glutamyltransferase [Arabidopsis
 NCBI Description
                    thaliana]
                    312289
 Seq. No.
                    wyr700241011.h1
 Seq. ID
 Method
                    BLASTN
 NCBI GI
                    g2062705
 BLAST score
                    37
E value
                    1.0e-11
                    37
 Match length
                    100
 % identity
 NCBI Description Human butyrophilin (BTF5) mRNA, complete cds
                    312290
 Seq. No.
                    wyr700241016.hl
 Seq. ID
 Method
                    BLASTN
 NCBI GI
                    g312180
 BLAST score
                    41
                    6.0e-14
 E value
 Match length
                    65
 % identity
                    91
 NCBI Description Z.mays GapC4 gene
                    312291
 Seq. No.
 Seq. ID
                    wyr700241018.h1
 Method
                    BLASTX
                    g112994
 NCBI GI
 BLAST score
                    232
                    1.0e-19
 E value
```

Match length 60 % identity

NCBI Description GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN

>gi_82685_pir__S04536 embryonic abundant protein,

glycine-rich - maize >gi_22313_emb_CAA31077_ (X12564)

ABA-inducible gene protein [Zea mays]

>gi 226091 prf 1410284A abscisic acid inducible gene [Zea

mays]

312292 Seq. No.

Seq. ID wyr700241043.hl

```
Method
 NCBI GI
                    g1209756
 BLAST score
                    230
                    2.0e-19
 E value
                    76
 Match length
 % identity
                    55
                   (U43629) integral membrane protein [Beta vulgaris]
 NCBI Description
 Seq. No.
                    312293
                   wyr700241047.h1
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                    g3292825
 BLAST score
                    363
                    5.0e-35
 E value
 Match length
                    84
                    77
 % identity
                   (AL031018) hypothetical protein [Arabidopsis thaliana]
 NCBI Description
 Seq. No.
                    312294
                    wyr700241058.h1
 Seq. ID
 Method
                    BLASTX
                    g3080397
 NCBI GI
 BLAST score
                    182
 E value
                    2.0e-15
Match length
                    76
% identity
                    50
                    (AL022603) hypothetical protein [Arabidopsis thaliana]
NCBI Description
 Seq. No.
                    312295
                    wyr700241067.h1
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    q2827714
 BLAST score
                    193
 E value
                    5.0e-15
 Match length
                    90
 % identity
                    51
 NCBI Description
                    (ALO21684) receptor protein kinase - like protein
                    [Arabidopsis thaliana]
 Seq. No.
                    312296
 Seq. ID
                    wyr700241076.h1
 Method
                    BLASTX
                    g3059131
 NCBI GI
 BLAST score
                    265
 E value
                    2.0e-24
 Match length
                    96
 % identity
 NCBI Description
                    (AJ000478) cytochrome P450 [Helianthus tuberosus]
```

Seq. No. 312297

Seq. ID wyr700241077.h1

Method BLASTX
NCBI GI g4510363
BLAST score 263
E value 4.0e-23
Match length 55
% identity 87



```
NCBI Description
                  (AC007017) putative DNA-binding protein [Arabidopsis
                  thaliana]
Seq. No.
                  312298
                  wyr700241081.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2244847
BLAST score
                  164
                  9.0e-21
E value
                  87
Match length
% identity
                  51
NCBI Description
                   (Z97337) hydroxyproline-rich glycoprotein homolog
                   [Arabidopsis thaliana]
Seq. No.
                  312299
                  wyr700241083.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g710626
BLAST score
                  177
                  4.0e-13
                                                                    À.
E value
Match length
                  39
                  72
% identity
NCBI Description
                  (D30719) ERD15 protein [Arabidopsis thaliana] >gi_3241941
                   (AC004625) dehydration-induced protein ERD15 [Arabidopsis
                  thaliana] >gi_3894181 (AC005662) ERD15 protein [Arabidopsis
                  thaliana]
                  312300
Seq. No.
Seq. ID
                  wyr700241085.h1
Method
                  BLASTN
NCBI GI
                  q2062705
BLAST score
                  37
E value
                  2.0e-11
Match length
                  41
% identity
                  Human butyrophilin (BTF5) mRNA, complete cds
NCBI Description
Seq. No.
                  312301
Seq. ID
                  wyr700241160.hl
Method
                  BLASTX
NCBI GI
                  q3548810
BLAST score
                  153
                  2.0e-10
E value
Match length
                  58
% identity
                  57
                  (AC005313) putative chloroplast nucleoid DNA binding
NCBI Description
                  protein [Arabidopsis thaliana]
```

312302 Seq. No.

Seq. ID wyr700241177.h1

Method BLASTX g2392025 NCBI GI BLAST score 250 E value 9.0e-22 53 Match length 87 % identity

NCBI Description (D88420) stromal ascorbate peroxidase [Cucurbita sp.]



```
Seq. No.
                  312303
Seq. ID
                  wyr700241186.h1
Method
                  BLASTX
                  q2132183
NCBI GI
                  221
BLAST score
E value
                  2.0e-18
Match length
                  65
% identity
                  62
                  hypothetical protein YPL088w - yeast (Saccharomyces
NCBI Description
                  cerevisiae) >gi 1151238 (U43281) Lpg20p [Saccharomyces
                  cerevisiae]
```

 Seq. No.
 312304

 Seq. ID
 wyr700241201.h1

 Method
 BLASTX

Method BLASTX
NCBI GI g4490330
BLAST score 260
E value 4.0e-23
Match length 53
% identity 94

NCBI Description (AL035656) splicing factor-like protein [Arabidopsis

thaliana]

Method BLASTX
NCBI GI g3024018
BLAST score 356
E value 4.0e-34
Match length 69

Match length 69 % identity 97

NCBI Description INITIATION FACTOR 5A (EIF-5A) (EIF-4D)

>gi_1546919_emb_CAA69225_ (Y07920) translation initiation factor 5A [Zea mays] >gi_2668738 (AF034943) translation

initiation factor 5A [Zea mays]

Seq. No. 312306

Seq. ID wyr700241303.h1

Method BLASTX
NCBI GI g2655295
BLAST score 286
E value 6.0e-26
Match length 57
% identity 95

NCBI Description (AF032976) germin-like protein 6 [Oryza sativa]

Seq. No. 312307

Seq. ID wyr700241308.h1

Method BLASTX
NCBI GI 94544389
BLAST score 212
E value 3.0e-17
Match length 48
% identity 75

NCBI Description (AC007047) putative homeodomain protein [Arabidopsis

thaliana]

NCBI Description



```
312308
Seq. No.
                  wyr700241323.h1
Seq. ID
Method
                  BLASTX
                  g3445209
NCBI GI
                  212
BLAST score
                  3.0e-17
E value
Match length
                  62
                  56
% identity
                  (AC004786) putative serine carboxypeptidase I [Arabidopsis
NCBI Description
                  thaliana]
                  312309
Seq. No.
Seq. ID
                  wyr700241344.hl
                  BLASTX
Method
                  g4468802
NCBI GI
                  283
BLAST score
                  1.0e-25
E value
                  75
Match length
% identity
                   63
                   (AL035601) cytochrome p450-like protein [Arabidopsis
NCBI Description
                  thaliana]
                   312310
Seq. No.
Seq. ID
                  wyr700241387.hl
                  BLASTX
Method
                   g3075400
NCBI GI
                   271
BLAST score
                   3.0e-24
E value
                   80
Match length
% identity
                   62
                   (AC004484) putative thromboxane-A synthase [Arabidopsis
NCBI Description
                   thaliana] >gi 3413720 (AC004747) putative thromboxin-A
                   synthase [Arabidopsis thaliana]
                   312311
Seq. No.
Seq. ID
                   wyr700241446.h1
Method
                   BLASTX
                   g4567303
NCBI GI
BLAST score
                   167
                   3.0e-12
E value
Match length
                   38
                   71
% identity
                   (AC005956) unknown protein [Arabidopsis thaliana]
NCBI Description
                   312312
Seq. No.
                   wyr700241511.hl
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1362152
                   443
BLAST score
E value
                   2.0e-44
Match length
                   92
                   90
% identity
```

44589

protein S6 kinase [Avena sativa]

ribosomal protein S6 kinase homolog (clone Aspk11) - oat

>qi 871986 emb CAA56313 (X79992) putative pp70 ribosomal



```
Seq. No.
Seq. ID
                  wyr700241512.h1
Method
                  BLASTX
                  g4204277
NCBI GI
                  209
BLAST score
                  6.0e-17
E value
Match length
                  44
                  82
% identity
                  (AC004146) Hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  312314
Seq. No.
                  wyr700241515.h1
Seq. ID
Method
                  BLASTX
                   q1402886
NCBI GI
BLAST score
                   356
E value
                   4.0e-34
                   93
Match length
                   71
% identity
                  (X98130) unknown [Arabidopsis thaliana]
NCBI Description
                                                                3
                   312315
Seq. No.
                  wyr700241518.hl
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2832661
BLAST score
                   252
                   6.0e-22
E value
                   92
Match length
                   51
% identity
                   (AL021710) pherophorin - like protein [Arabidopsis
NCBI Description
                   thaliana]
                   312316
Seq. No.
                   wyr700241537.h1
Seq. ID
Method
                   BLASTX
                   g3925229
NCBI GI
BLAST score
                   163
E value
                   1.0e-11
                   33
Match length
                   97
% identity
NCBI Description
                   (AF037032) peroxidase J [Zea mays]
                   312317
Seq. No.
                   wyr700241571.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3158372
BLAST score
                   150
E value
                   5.0e-10
Match length
                   32
% identity
                   (AF035383) polyubiquitin [Arabidopsis thaliana]
NCBI Description
```

312318 Seq. No.

Seq. ID wyr700241574.hl

Method BLASTN NCBI GI g1322276 BLAST score 63 E value 5.0e-27



Match length 102 % identity 91

NCBI Description Triticum aestivum histone H2A gene, complete cds.

>gi_1325967_emb_X94973_TAH2A274 T.aestivum histone H2A gene

(clone TH274)

Seq. No. 312319

Seq. ID wyr700241610.h1

Method BLASTN
NCBI GI g22330
BLAST score 99
E value 2.0e-48
Match length 119
% identity 97

NCBI Description Z.mays Zmhoxla mRNA for homeobox protein

Seq. No. 312320

Seq. ID wyr700241643.h1

Method BLASTN
NCBI GI g22292
BLAST score 68
E value 4.0e-30
Match length 112
% identity 90

NCBI Description Z.mays mRNA for glycine-rich protein

Seq. No. 312321

Seq. ID wyr700241687.h1

Method BLASTN
NCBI GI g551482
BLAST score 89
E value 1.0e-42
Match length 122
% identity 94

NCBI Description Zea mays ABA- and ripening-inducible-like protein mRNA,

complete cds

Seq. No. 312322

Seq. ID wyr700241707.h1

Method BLASTX
NCBI GI g2500522
BLAST score 367
E value 2.0e-35
Match length 78
% identity 95

NCBI Description EUKARYOTIC INITIATION FACTOR 4A (EIF-4A) >gi 603190

(U17979) translation initiation factor eIF-4A [Zea mays]

Seq. No. 312323

Seq. ID wyr700241718.h1

Method BLASTX
NCBI GI g122074
BLAST score 200
E value 5.0e-18
Match length 60
% identity 87

NCBI Description HISTONE H3.2

BLAST score

61



```
312324
Seq. No.
Seq. ID
                  wyr700241725.h1
Method
                  BLASTX
                  g1763277
NCBI GI
BLAST score
                  251
                  8.0e-22
E value
Match length
                  87
% identity
NCBI Description
                  (U73656) tryptophan decarboxylase [Camptotheca acuminata]
Seq. No.
                  312325
                  wyr700241751.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2062705
BLAST score
                  36
E value
                  7.0e-11
Match length
                  36
                  100
% identity
NCBI Description
                  Human butyrophilin (BTF5) mRNA, complete cds
Seq. No.
                  312326
Seq. ID
                  wyr700241753.h1
Method
                  BLASTX
NCBI GI
                  g4538968
BLAST score
                  176
E value
                  5.0e-13
Match length
                  70
% identity
NCBI Description
                  (AL049488) putative protein kinase [Arabidopsis thaliana]
Seq. No.
                  312327
Seq. ID
                  wyr700241761.h1
Method
                  BLASTX
NCBI GI
                  q678547
                  298
BLAST score
                  3.0e-27
E value
                  96
Match length
% identity
                  62
                  (L13654) peroxidase [Lycopersicon esculentum]
NCBI Description
                  312328
Seq. No.
Seq. ID
                  wyr700241763.h1
Method
                  BLASTX
                  g600872
NCBI GI
BLAST score
                  235
E value
                  6.0e-20
Match length
                  49
                  96
% identity
NCBI Description
                   (U17897) starch branching enzyme I [Zea mays] >gi 3309178
                   (AF072724) starch branching enzyme I [Zea mays]
                  312329
Seq. No.
                  wyr700241852.h1
Seq. ID
                  BLASTN
Method
                  g531030
NCBI GI
```



E value 6.0e-26 Match length 121 % identity 88

NCBI Description Pennisetum ciliare apomixis-associated mRNA

>gi_531483_emb_Z36546_PCAPOSPA3 P.ciliare (Higgins)

apospory associated mRNA, 876bp

>gi_549985_gb_U13149_PCU13149 Pennisetum ciliare possible apospory-associated mRNA clone pSUB 3-la, partial cds

Seq. No. 312330

Seq. ID wyr700241870.h1

Method BLASTN
NCBI GI g520567
BLAST score 72
E value 2.0e-32
Match length 156
% identity 87

NCBI Description Cenchrus ciliaris clone PX7 peroxidase mRNA, complete cds

Seq. No.

312331

Seq. ID

wyr700241916.h1

Method BLASTN
NCBI GI g532622
BLAST score 37
E value 1.0e-11
Match length 69
% identity 88

NCBI Description Zea mays lipase (LIP) mRNA, complete cds

Seq. No.

312332

Seq. ID

wyr700241931.h1

Method BLASTN
NCBI GI g3822035
BLAST score 96
E value 4.0e-47
Match length 116
% identity 96

NCBI Description Zea mays endo-1,3-1,4-beta-D-glucanase mRNA, complete cds

Seq. No.

312333

Seq. ID

wyr700241957.h1

Method BLASTN
NCBI GI g1045496
BLAST score 37
E value 2.0e-11
Match length 45
% identity 96

NCBI Description Spermophilus tridecemlineatus 26S Proteasome S.U. CADp44 -

a conserved ATPase domain protein of 44kDa (CADp44) gene,

complete cds

Seq. No.

312334

Seq. ID

wyr700242016.h1

Method BLASTX
NCBI GI g2425064
BLAST score 223
E value 1.0e-18



Match length 46 % identity 87

NCBI Description (AF019146) cysteine proteinase Mir2 [Zea mays]

Seq. No. 312335

Seq. ID wyr700242021.hl

Method BLASTX
NCBI GI g2388585
BLAST score 230
E value 2.0e-19
Match length 64
% identity 73

NCBI Description (AC000098) Similar to Caenorhabditis unknown protein

T03F1.1 (gb U88169). [Arabidopsis thaliana]

Seq. No. 312336

Seq. ID wyr700242041.h1

Method BLASTX
NCBI GI g2662341
BLAST score 213
E value 2.0e-17
Match length 42
% identity 98

NCBI Description (D63580) EF-1 alpha [Oryza sativa]

>gi_2662345_dbj_BAA23659_ (D63582) EF-1 alpha [Oryza
sativa] >gi_2662347_dbj_BAA23660_ (D63583) EF-1 alpha

[Oryza sativa]

Seq. No. 312337

Seq. ID wyr700242058.h1

Method BLASTX
NCBI GI g2665890
BLAST score 222
E value 1.0e-18
Match length 43
% identity 93

NCBI Description (AF035944) calcium-dependent protein kinase [Fragaria x

ananassa]

Seq. No. 312338

Seq. ID wyr700242073.h1

Method BLASTX
NCBI GI 93860263
BLAST score 204
E value 2.0e-16
Match length 91
% identity 48

NCBI Description (AC005824) putative cytochrome p450 protein [Arabidopsis

thaliana]

Seq. No. 312339

Seq. ID wyr700242128.h1

Method BLASTN
NCBI GI g1815659
BLAST score 107
E value 2.0e-53
Match length 142



% identity 94 NCBI Description Oryza sativa low molecular mass heat shock protein

Oshsp17.3 (OSHSP17.3) gene, complete cds

Seq. No. 312340

Seq. ID wyr700242131.h1

Method BLASTX
NCBI GI g1170937
BLAST score 215
E value 2.0e-19
Match length 60
% identity 87

NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE

ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)

>gi_450549_emb_CAA81481_ (Z26867) S-adenosyl methionine

synthetase [Oryza sativa]

Seq. No. 312341

Seq. ID wyr700242161.h1

Method BLASTN
NCBI GI g902585
BLAST score 46
E value 3.0e-17
Match length 95
% identity 93

NCBI Description Zea mays clone MubG9 ubiquitin gene, complete cds

Seq. No. 312342

Seq. ID wyr700242196.h1

Method BLASTX
NCBI GI g2911072
BLAST score 326
E value 1.0e-30
Match length 87
% identity 69

NCBI Description (AL021960) putative protein [Arabidopsis thaliana]

Seq. No. 312343

Seq. ID wyr700242203.h1

Method BLASTX
NCBI GI g2642158
BLAST score 176
E value 4.0e-13
Match length 88
% identity 45

NCBI Description (AC003000) hypothetical protein [Arabidopsis thaliana]

Seq. No. 312344

Seq. ID wyr700242216.h1

Method BLASTX
NCBI GI 94467134
BLAST score 310
E value 9.0e-29
Match length 90
% identity 70

NCBI Description (AL035540) protein kinase like protein [Arabidopsis

thaliana]



```
312345
Seq. No.
Seq. ID
                  wyr700242225.h1
Method
                  BLASTX
                  g1171965
NCBI GI
                  355
BLAST score
                  4.0e-34
E value
Match length
                  87
% identity
                  71
                  PHOSPHATIDYLINOSITOL 3-KINASE, ROOT ISOFORM (PI3-KINASE)
NCBI Description
                   (PTDINS-3-KINASE) (PI3K) (SPI3K-5) >gi_736339 (L27265)
                  phosphatidylinositol 3-kinase [Glycine max]
Seq. No.
                  312346
                  wyr700242258.h1
Seq. ID
Method
                  BLASTX
                  q2984709
NCBI GI
BLAST score
                  226
                  7.0e-19
E value
Match length
                  66
% identity
                  73
                   (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]
NCBI Description
                  312347
Seq. No.
                  wyr700242262.hl
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2330649
BLAST score
                  190
                   6.0e-15
E value
Match length
                  42
                  86
% identity
                  (Y14558) topoisomerase I [Pisum sativum]
NCBI Description
Seq. No.
                  312348
Seq. ID
                  wyr700242264.hl
Method
                  BLASTX
NCBI GI
                   g1769901
BLAST score
                   258
E value
                  1.0e-22
Match length
                  76
% identity
                   63
                   (X95737) proline transporter 1 [Arabidopsis thaliana]
NCBI Description
                  >gi 2088642 (AF002109) proline transporter 1 [Arabidopsis
                   thaliana]
                   312349
Seq. No.
                  wyr700242276.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q4263716
BLAST score
                   153
E value
                   2.0e-10
```

57 Match length % identity 47

NCBI Description

(AC006223) putative alanine acetyl transferase [Arabidopsis

thaliana]

Seq. No.

Method

NCBI GI

BLAST score

BLASTX

144

g1076331



```
Seq. ID
                   wyr700242289.h1
                  BLASTX
Method
NCBI GI
                   q2244906
BLAST score
                   160
E value
                   3.0e-11
Match length
                   77
% identity
                   39
                   (Z97339) indole-3-acetate beta-glucosyltransferase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   312351
Seq. ID
                  wyr700242309.h1
Method
                  BLASTX
NCBI GI
                   g3298474
BLAST score
                   181
E value
                   3.0e-25
Match length
                   78
% identity
                   83
                  (AB012765) ovpl [Oryza sativa]
NCBI Description
                   312352
Seq. No.
                  wyr700242310.h1
Seq. ID
Method
                   BLASTX
                   g639722
NCBI GI
BLAST score
                   231
                   1.0e-19
E value
Match length
                   45
% identity
                   91
NCBI Description
                  (L27484) calcium-dependent protein kinase [Zea mays]
                   312353
Seq. No.
Seq. ID
                  wyr700242352.h1
Method
                   BLASTX
NCBI GI
                   q4337187
BLAST score
                   202
E value
                   2.0e-16
Match length
                   54
% identity
                   69
NCBI Description
                   (AC006403) putative prolylcarboxypeptidase, 5' partial
                   [Arabidopsis thaliana]
                   312354
Seq. No.
Seq. ID
                   wyr700242353.h1
Method
                   BLASTX
                   g3510264
NCBI GI
BLAST score
                   201
E value
                   3.0e-16
Match length
                   55
% identity
NCBI Description
                   (AC005310) hypothetical protein, 5' partial [Arabidopsis
                   thaliana]
                   312355
Seq. No.
Seq. ID
                  wyr700242357.hl
```

```
E value 2.0e-09

Match length 64
% identity 48

NCBI Description histidine transport protein - Arabidopsis thaliana
>gi_510238_emb_CAA54634_ (X77503) oligopeptide transporter
1-1 [Arabidopsis thaliana] >gi_744157_prf__2014244A His
transporter [Arabidopsis thaliana]
```

 Seq. No.
 312356

 Seq. ID
 wyr700242361.h1

 Method
 BLASTX

 NCBI GI
 g167531

 BLAST score
 151

 E value
 2.0e-11

 Match length
 70

E value 2.0 Match length 70 % identity 53

NCBI Description (M91374) peroxidase [Cucumis sativus]

Seq. No. 312357

Seq. ID wyr700242376.h1

Method BLASTX
NCBI GI g571330
BLAST score 234
E value 6.0e-20
Match length 82
% identity 55

NCBI Description (U11034) ent-kaurene synthetase A [Arabidopsis thaliana] >gi_4263508 gb_AAD15334 (AC004044) ent-kaurene synthetase

A [Arabidopsis thaliana]

Seq. No. 312358

Seq. ID wyr700242436.h1

Method BLASTX
NCBI GI g3928543
BLAST score 176
E value 4.0e-13
Match length 76
% identity 41

NCBI Description (AB016819) UDP-glucose glucosyltransferase [Arabidopsis

thaliana]

Seq. No. 312359

Seq. ID wyr700242480.h1

Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 6.0e-11
Match length 36
% identity 100

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 312360

Seq. ID wyr700242489.h1

Method BLASTX
NCBI GI g118038
BLAST score 166
E value 4.0e-12

E value

Match length

% identity

83 69



```
Match length
                  78
% identity
                  CYTOCHROME C >gi 65493 pir CCUS cytochrome c - smut fungus
NCBI Description
                  (Ustilago sphaerogena)
Seq. No.
                  312361
                  wyr700242521.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3953479
BLAST score
                  402
E value
                  1.0e-39
Match length
                  90
% identity
                  84
                  (AC002328) F2202.24 [Arabidopsis thaliana]
NCBI Description
                  312362
Seq. No.
Seq. ID
                  wyr700242584.hl
Method
                  BLASTN
NCBI GI
                  q3819443
BLAST score
                  36
                  5.0e-11
E value
                  84
Match length
% identity
                  86
NCBI Description Hordeum vulgare genomic DNA fragment; clone MWG0943.uni
                  312363
Seq. No.
Seq. ID
                  wyr700242616.h1
Method
                  BLASTX
NCBI GI
                  g2911075
BLAST score
                  176
E value
                  3.0e-13
Match length
                  51
% identity
                  (AL021960) putative protein [Arabidopsis thaliana]
NCBI Description
                  312364
Seq. No.
                  wyr700242627.hl
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1706260
                  308
BLAST score
                  2.0e-28
E value
Match length
                  79
                  77
% identity
                  CYSTEINE PROTEINASE 1 PRECURSOR >gi 2118131_pir__$59597
NCBI Description
                  cysteine proteinase 1 precursor - maize
                  >gi_643597_dbj_BAA08244_ (D45402) cysteine proteinase [Zea
                  mays]
                  312365
Seq. No.
Seq. ID
                  wyr700242646.hl
                  BLASTX
Method
NCBI GI
                  q1935021
BLAST score
                   270
                   4.0e-24
```

NCBI Description (Z93775) monosaccharid transport protein [Vicia faba]



Seq. No.

```
Seq. ID
                  wyr700242696.hl
Method
                  BLASTX
                  g2129553
NCBI GI
BLAST score
                  238
E value
                  3.0e-20
Match length
                  60
                  72
% identity
NCBI Description
                  calcium-dependent protein kinase 6 - Arabidopsis thaliana
Seq. No.
                  312367
                  wyr700242701.hl
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1790483
BLAST score
                  163
                  8.0e-12
E value
Match length
                  63
                  51
% identity
                  (AE000478) orf, hypothetical protein [Escherichia coli]
NCBI Description
Seq. No.
                  312368
Seq. ID
                  wyr700242810.h1
Method
                  BLASTX
NCBI GI
                  q3249109
BLAST score
                  212
                  3.0e-17
E value
                  43
Match length
% identity
                  91
NCBI Description
                  (AC003114) Contains similarity to pre-mRNA splicing factor
                   (SF2), P33 subunit gb M72709 from Homo sapiens. ESTs
                  gb_T42588 and gb_R65514 come from this gene. [Arabidopsis
                  thaliana]
Seq. No.
                  312369
                  wyr700242813.hl
Seq. ID
Method
                  BLASTX
                  g1170303
NCBI GI
BLAST score
                  163
                  2.0e-11
E value
                  52
Match length
                  62
% identity
                  HEMOLYSIN SECRETION ATP-BINDING PROTEIN, CHROMOSOMAL
NCBI Description
                  >gi 146380 (M10133) chromosomal hemolysin B (hlyB)
                   [Escherichia coli]
Seq. No.
                  312370
Seq. ID
                  wyr700242839.hl
                  BLASTX
Method
                  q127579
NCBI GI
BLAST score
                  185
                  4.0e-14
E value
Match length
                  64
                  64
% identity
                  MYB-RELATED PROTEIN HV1 >gi 82423 pir S04896 transforming
NCBI Description
                  protein (myb) homolog (clone Hv1) - barley
                  >gi_2130044_pir__S61506 Myb1 protein - barley
```



>gi_19051_emb_CAA50222_ (X70877) MybHv1 [Hordeum vulgare]
>gi_19053_emb_CAA50224_ (X70879) MybHv1 [Hordeum vulgare]
>gi_227030_prf__1613412A myb-related gene Hv1 [Hordeum vulgare var. distichum]

Seq. No. 312371

Seq. ID wyr700242846.h1 Method BLASTN

 NCBI GI
 g6598523

 BLAST score
 45

 E value
 3.0e-16

 Match length
 88

 % identity
 89

NCBI Description Arabidopsis thaliana chromosome II BAC F10A8 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 312372

Seq. ID wyr700242885.h1

Method BLASTX
NCBI GI g1709000
BLAST score 371
E value 7.0e-36
Match length 76
% identity 91

NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE

ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)

>gi_960357_dbj_BAA09895_ (D63835) S-adenosylmethionine

synthetase [Hordeum vulgare]

Seq. No. 312373

Seq. ID wyr700242985.h1

Method BLASTX
NCBI GI g2829871
BLAST score 213
E value 2.0e-17
Match length 44
% identity 80

NCBI Description (AC002396) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 312374

Seq. ID wyr700242995.h1

Method BLASTN
NCBI GI g1491773
BLAST score 75
E value 3.0e-34
Match length 152
% identity 88

NCBI Description Z.mays mRNA for cysteine proteinase, Seel

Seq. No. 312375

Seq. ID wyr700243027.h1

Method BLASTX
NCBI GI g3360289
BLAST score 205
E value 2.0e-35
Match length 81
% identity 98



NCBI Description (AF023164) leucine-rich repeat transmembrane protein kinase 1 [Zea mays]

Seq. No. 312376

Seq. ID wyr700243054.h1

Method BLASTX
NCBI GI g3426062
BLAST score 179
E value 2.0e-13
Match length 56
% identity 64

NCBI Description (AJ007587) monooxygenase [Arabidopsis thaliana]

Seq. No. 312377

Seq. ID wyr700243085.h1

Method BLASTX
NCBI GI g3193290
BLAST score 176
E value 2.0e-13
Match length 66
% identity 58

NCBI Description (AF069298) contains similarity to a protein kinase domain

(Pfam: pkinase.hmm, score: 165.48), to legume lectins beta domain (Pfam: lectin_legB.hmm, score: 125.64) and legume lectins alpha domain (Pfam: lectin legA.hmm, score: 16.72)

[Arabido

Seq. No. 312378

Seq. ID wyr700243095.h1

Method BLASTX
NCBI GI g3874889
BLAST score 174
E value 8.0e-13
Match length 45
% identity 73

NCBI Description (Z48045) similarity to the transmembranous domains of yeast

ERS1 protein; cDNA EST EMBL:D69878 comes from this gene;

cDNA EST EMBL:D66181 comes from this gene; cDNA EST yk413c7.5 comes from this gene [Caenorhabditis elegans]

Seq. No. 312379

Seq. ID wyr700243138.h1

Method BLASTX
NCBI GI g3080432
BLAST score 199
E value 9.0e-16
Match length 58
% identity 71

NCBI Description (AL022605) hypothetical protein [Arabidopsis thaliana]

Seq. No. 312380

Seq. ID wyr700243159.h1

Method BLASTX
NCBI GI g1853968
BLAST score 171
E value 2.0e-12
Match length 52



```
% identity
                  (D88121) CPRD12 protein [Vigna unguiculata]
NCBI Description
Seq. No.
                  312381
                  wyr700243184.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3421109
BLAST score
                  204
                  2.0e-16
E value
Match length
                  41
% identity
                  100
NCBI Description
                  (AF043533) 20S proteasome beta subunit PBC2 [Arabidopsis
                  thaliana]
                  312382
Seq. No.
                  wyr700243186.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1617270
                  390
BLAST score
                  3.0e-38
E value
Match length
                  84
% identity
                  81
NCBI Description
                  (X94624) acyl-CoA synthetase [Brassica napus]
Seq. No.
                  312383
Seq. ID
                  wyr700243269.h1
Method
                  BLASTX
NCBI GI
                   g4406812
BLAST score
                   224
E value
                  1.0e-18
Match length
                   49
% identity
                   90
                   (AC006201) putative DNA binding protein (Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   312384
Seq. ID
                  wyr700243271.h1
Method
                  BLASTX
NCBI GI
                  g4544451
BLAST score
                   215
E value
                   1.0e-17
Match length
                   78
                   55
% identity
NCBI Description
                  (AC006592) unknown protein [Arabidopsis thaliana]
Seq. No.
                   312385
Seq. ID
                  wyr700243340.h1
Method
                  BLASTX
NCBI GI
                   q3450889
BLAST score
                   226
E value
                   6.0e-19
```

Match length 80 % identity

NCBI Description (AF083890) 19S proteosome subunit 9 [Arabidopsis thaliana]

Seq. No.

312386

wyr700243357.h1 Seq. ID

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Method NCBI GI q2654088 BLAST score 276 9.0e-25 E value 91 Match length % identity 51 NCBI Description

(AF033118) potassium transporter [Arabidopsis thaliana] >gi 2688979 (AF029876) high-affinity potassium transporter; AtKUP1p [Arabidopsis thaliana] >gi_3150413 (AC004165) high-affinity potassium transporter (AtKUP1) [Arabidopsis thaliana] >gi 3420045 (AC004680) high-affinity potassium

transporter (AtKUP1) [Arabidopsis thaliana]

Seq. No. 312387

wyr700243372.h1 Seq. ID

Method BLASTX g3024018 NCBI GI BLAST score 373 4.0e-36 E value Match length 73 % identity 97

INITIATION FACTOR 5A (EIF-5A) (EIF-4D) NCBI Description

>gi_1546919_emb_CAA69225_ (Y07920) translation initiation factor 5A [Zea mays] >gi_2668738 (AF034943) translation

initiation factor 5A [Zea mays]

Seq. No. 312388

wyr700243447.h1 Seq. ID

Method BLASTX g4164408 NCBI GI BLAST score 274 2.0e-24 E value Match length 75 60 % identity

NCBI Description (AJ132228) amino acid carrier [Ricinus communis]

312389 Seq. No.

Seq. ID wyr700243466.h1

Method BLASTX NCBI GI g4185131 BLAST score 246 E value 3.0e-21 Match length 48 83 % identity

(AC005724) putative zinc finger protein [Arabidopsis NCBI Description

thaliana]

312390 Seq. No.

Seq. ID wyr700243475.h1

Method BLASTX NCBI GI g1491774 BLAST score 267 E value 9.0e-24 Match length 79 % identity

NCBI Description (X99936) cysteine protease [Zea mays]



```
312391
Seq. No.
Seq. ID
                  wyr700243559.h1
Method
                  BLASTX
                  g3738319
NCBI GI
BLAST score
                  322
                  4.0e-30
E value
Match length
                  73
% identity
                  81
                  (AC005170) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  312392
Seq. No.
                  wyr700243578.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1546918
BLAST score
                  114
                  2.0e-57
E value
Match length
                  114
                  100
% identity
NCBI Description Z.mays mRNA for translation initiation factor 5A
                  312393
Seq. No.
                  wyr700243602.hl
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4558556
BLAST score
                  166
E value
                  6.0e-12
Match length
                  76
                  50
% identity
NCBI Description (AC007138) predicted protein of unknown function
                   [Arabidopsis thaliana]
                  312394
Seq. No.
                  wyr700243608.h1
Seq. ID
Methòd
                  BLASTN
NCBI GI
                  g551482
BLAST score
                  125
E value
                  5.0e-64
                  256
Match length
% identity
                  88
NCBI Description
                  Zea mays ABA- and ripening-inducible-like protein mRNA,
                  complete cds
                  312395
Seq. No.
                  wyr700243662.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q477819
BLAST score
                  280
E value
                  4.0e-25
Match length
                  96
                  59
% identity
NCBI Description
                  mitochondrial processing peptidase (EC 3.4.99.41) beta
```

chain precursor - potato >gi_410634_bbs_136741 cytochrome c reductase-processing peptidase subunit II, MPP subunit II, P53 [potatoes, var. Marfona, tuber, Peptide Mitochondrial,

530 aa]

Seq. No. 312396

Match length

% identity



```
wyr700243667.hl
  Seq. ID
  Method
                      BLASTX
  NCBI GI
                      q1654140
                      181
  BLAST score
                      1.0e-13
  E value
                      54
  Match length
  % identity
                      70
                      (U37840) lipoxygenase [Lycopersicon esculentum]
  NCBI Description
                      312397
  Seq. No.
                      wyr700243691.hl
  Seq. ID
  Method
                      BLASTX
  NCBI GI
                      q82696
  BLAST score
                      273
                      2.0e-24
  E value
  Match length
                      62
                      87
  % identity
NCBI Description
                      glycine-rich protein - maize >gi_22293_emb_CAA43431_
                      (X61121) glycine-rich protein [Zea mays]
                      312398
  Seq. No.
                      wyr700243721.h1
  Seq. ID
  Method
                      BLASTX
  NCBI GI
                      q1754999
                      273
  BLAST score
                      2.0e-24
  E value
                      54
  Match length
                      98
  % identity
                      (U48691) calmodulin TaCaM2-2 [Triticum aestivum]
  NCBI Description
                      >qi 1755001 (U48692) calmodulin TaCaM2-3 [Triticum
                      aestivum]
                      312399
  Seq. No.
  Seq. ID
                      wyr700243722.h1
                      BLASTX
  Method
  NCBI GI
                      q1709358
  BLAST score
                      273
                      2.0e-24
  E value
  Match length
                      87
  % identity
                      53
                      NUCLEOSIDE-TRIPHOSPHATASE (NUCLEOSIDE TRIPHOSPHATE
  NCBI Description
                      PHOSPHOHYDROLASE) (NTPASE) >gi 629638 pir S48859
                      nucleoside triphosphatase - garden pea
                      >gi 2129890 pir S65147 nucleoside triphosphatase
                      precursor, chromatin-associated - garden pea >gi_563612_emb_CAA83655_ (Z32743) nucleoside triphosphatase [Pisum_sativum] >gi_4519173_dbj_BAA75506.1_ (AB022319)
                      nucleoside triphosphatase (NTPase) [Pisum sativum]
  Seq. No.
                      312400
  Seq. ID
                      wyr700243744.hl
  Method
                      BLASTX
                      q4585873
  NCBI GI
  BLAST score
                      355
  E value
                      4.0e-34
```



```
NCBI Description
                  (AC005850) Putative protein kinase [Arabidopsis thaliana]
Seq. No.
                  312401
Seq. ID
                  wyr700243757.h1
Method
                  BLASTN
NCBI GI
                  q1935910
BLAST score
                  51
E value
                  7.0e-20
Match length
                  111
                  86
% identity
NCBI Description
                  Zea mays lethal leaf-spot 1 (lls1) gene, partial cds
Seq. No.
                  312402
Seq. ID
                  wyr700243760.h1
Method
                  BLASTX
NCBI GI
                  q3056725
BLAST score
                  236
E value
                  5.0e-20
Match length
                  94
                  49
% identity
                  (AF034774) ent-kaurene synthase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  312403
Seq. ID
                  wyr700243761.h1
Method
                  BLASTX
NCBI GI
                  q1181331
BLAST score
                  356
E value
                  4.0e-34
Match length
                  82
                  82
% identity
NCBI Description
                  (X77569) calnexin [Zea mays]
Seq. No.
                  312404
Seq. ID
                  wyr700243771.h1
Method
                  BLASTN
NCBI GI
                  g4140643
BLAST score
                  178
E value
                  1.0e-95
                  258
Match length
% identity
                  92
NCBI Description
                  Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster,
                  complete sequence
Seq. No.
                  312405
Seq. ID
                  wyr700243821.h1
Method
                  BLASTX
NCBI GI
                  g4585907
BLAST score
                  165
E value
                  8.0e-12
Match length
                  41
                  78
% identity
```

Seq. No. 312406

NCBI Description

Seq. ID wyr700243853.h1

Method BLASTX NCBI GI g1172836

(AC006298) unknown protein [Arabidopsis thaliana]



```
BLAST score
E value
                  8.0e-37
Match length
                  72
                  96
% identity
                  GTP-BINDING NUCLEAR PROTEIN RAN-B1 >gi 496272 (L16787)
NCBI Description
                  small ras-related protein [Nicotiana tabacum]
                  312407
Seq. No.
                  wyr700243864.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1946265
BLAST score
                  200
E value
                  8.0e-16
Match length
                  38
% identity
                  87
                  (Y11414) myb [Oryza sativa]
NCBI Description
                  312408
Seq. No.
                  wyr700243866.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g22263
BLAST score
                  77
                  2.0e-35
E value
Match length
                  211
% identity
                  85
NCBI Description Z.mays Ds insertion element
                  312409
Seq. No.
                  wyr700243882.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2499614
BLAST score
                  276
E value
                  9.0e-25
Match length
                  57
% identity
                  93
                  MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG NTF3 (P43)
NCBI Description
                  >gi_481830_pir__S39559 mitogen-activated protein kinase 3
                  homolog ntf3 - common tobacco >gi 406751 emb CAA49592
                  (X69971) NTF3 [Nicotiana tabacum]
Seq. No.
                  312410
Seq. ID
                  wyr700243886.h1
Method
                  BLASTX
NCBI GI
                  g2911052
BLAST score
                  205
                  1.0e-16
E value
Match length
                  54
                  69
% identity
NCBI Description (AL021961) putative protein [Arabidopsis thaliana]
```

Seq. No. 312411

Seq. ID wyr700243918.h1

Method BLASTX NCBI GI g129582 BLAST score 298 E value 1.0e-27 Match length 62

% identity PHENYLALANINE AMMONIA-LYASE 1 >gi_82063_pir__S04463 NCBI Description phenylalanine ammonia-lyase (EC 4.3.1.5) - parsley >gi 1524313 emb CAA68938_ (Y07654) PAL1 protein [Petroselinum crispum] 312412 Seq. No. wyr700243926.h1 Seq. ID, Method BLASTX g2578823 NCBI GI BLAST score 222 E value 2.0e-18 Match length 54 % identity 76 (AB000835) similar to YGR200c [Arabidopsis thaliana] NCBI Description 312413 Seq. No. Seq. ID wyr700243933.h1 Method BLASTX NCBI GI g4587525 BLAST score 173 1.0e-12 E value Match length 75 % identity 43 (AC007060) Contains the PF 00650 CRAL/TRIO NCBI Description phosphatidyl-inositol-transfer protein domain. ESTs gb_T76582, gb_N06574 and gb_Z25700 come from this gene. [Arabidopsis thaliana] Seq. No. 312414 wyr700243945.h1 Seq. ID Method BLASTN NCBI GI q2062705 BLAST score 36 E value 6.0e-11 Match length 36

% identity 100

NCBI Description Human butyrophilin (BTF5) mRNA, complete cds

312415 Seq. No.

wyr700243987.h1 Seq. ID

Method BLASTX NCBI GI g66615 BLAST score 418 2.0e-41 E value Match length 80 % identity 97

NCBI Description glutathione transferase (EC 2.5.1.18) I - maize

Seq. No. 312416

Seq. ID wyr700244044.h1

BLASTX Method g4206122 NCBI GI 156 BLAST score 4.0e-21 E value 69 Match length % identity 81



NCBI Description (AF097667) protein phosphatase 2C homolog [Mesembryanthemum crystallinum]

Seq. No. 312417

Seq. ID wyr700244055.h1

Method BLASTX
NCBI GI g3885341
BLAST score 210
E value 5.0e-17
Match length 91
% identity 44

NCBI Description (AC005623) unknown protein [Arabidopsis thaliana]

Seq. No. 312418

Seq. ID wyr700244057.h1

Method BLASTN
NCBI GI g22484
BLAST score 85
E value 2.0e-40
Match length 105
% identity 96

NCBI Description Z.mays RNA for superoxide dismutase Sod4A

Seq. No. 312419

Seq. ID wyr700244061.h1

Method BLASTN
NCBI GI g1805501
BLAST score 42
E value 2.0e-14
Match length 118
% identity 84

NCBI Description Oryza sativa mRNA for plastidic copper/zinc-superoxide

dismutase, complete cds

Seq. No. 312420

Seq. ID wyr700244072.h1

Method BLASTX
NCBI GI g3152568
BLAST score 184
E value 3.0e-14
Match length 52
% identity 63

NCBI Description (AC002986) Similar to hypothetical protein product

gb Z97337 from A. thaliana. EST gb H76597 comes from this

gene. [Arabidopsis thaliana]

Seq. No. 312421

Seq. ID wyr700244123.h1

Method BLASTX
NCBI GI g1703199
BLAST score 248
E value 9.0e-28
Match length 80
% identity 62

NCBI Description PROTEIN KINASE AFC1 >gi 601787 (U16176) protein kinase

[Arabidopsis thaliana]

```
312422
Seq. No.
Seq. ID
                   wyr700244129.h1
Method
                   BLASTN
                   g433042
NCBI GI
BLAST score
                   64
E value
                   1.0e-27
Match length
                   209
% identity
                   84
                  Zea mays W-22 clone PREM-1C retroelement PREM-1, partial
NCBI Description
                   sequence
Seq. No.
                   312423
Seq. ID
                   wyr700244183.hl
Method
                  BLASTN
                   g2062705
NCBI GI
                   36
BLAST score
                   6.0e-11
E value
Match length
                   36
% identity
                   100
NCBI Description Human butyrophilin (BTF5) mRNA, complete cds
Seq. No.
                   312424
Seq. ID
                   wyr700244252.h1
Method
                   BLASTX
                   g2232017
NCBI GI
                   391
BLAST score
                   3.0e-38
E value
Match length
                   93
% identity
                   73
NCBI Description
                  (U95953) viviparous-14 [Zea mays]
Seq. No.
                   312425
Seq. ID
                   wyr700244282.h1
Method
                   BLASTX
NCBI GI
                   g3450842
BLAST score
                   147
E value
                   1.0e-09
Match length
                   79
                   47
% identity
NCBI Description
                   (AF080436) mitogen activated protein kinase kinase [Oryza
                   sativa]
Seq. No.
                   312426
Seq. ID
                   wyr700244290.h1
Method
                   BLASTN
NCBI GI
                   g397395
BLAST score
                   209
E value
                   1.0e-114
                   209
Match length
% identity
                   100
NCBI Description
                  Z.mays MNB1b mRNA for DNA-binding protein
Seq. No.
                   312427
```

Seq. ID wyr700244316.h1

Method BLASTN NCBI GI g3821780 36

BLAST score

NCBI Description



```
E value
                   6.0e-11
Match length
                   36
                   100
% identity
NCBI Description
                  Xenopus laevis cDNA clone 27A6-1
                   312428
Seq. No.
Seq. ID
                  wyr700244323.hl
Method
                  BLASTX
NCBI GI
                  g4455171
BLAST score
                   212
                   3.0e-17
E value
Match length
                   89
% identity
                   53
                  (AL035521) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   312429
Seq. ID
                  wyr700244340.h1
Method
                  BLASTX
NCBI GI
                  q3068705
BLAST score
                  148
E value
                   8.0e-10
Match length
                   82
% identity
                   41
NCBI Description
                  (AF049236) unknown [Arabidopsis thaliana]
Seq. No.
                   312430
Seq. ID
                  wyr700244354.h1
Method
                  BLASTN
NCBI GI
                   g575730
BLAST score
                   65
                   3.0e-28
E value
Match length
                   155
% identity
                   95
NCBI Description
                  Z.mays mRNA for transmembrane protein
Seq. No.
                   312431
Seq. ID
                  xdb700337151.h1
Method
                  BLASTN
NCBI GI
                   q2668739
BLAST score
                   81
E value
                   3.0e-38
Match length
                   97
% identity
                   96
NCBI Description
                  Zea mays translation initiation factor GOS2 (TIF) mRNA,
                  complete cds
Seq. No.
                   312432
Seq. ID
                  xdb700337234.h1
Method
                  BLASTN
NCBI GI
                   q4503602
BLAST score
                   202
E value
                   1.0e-110
                   246
Match length
% identity
                   95
```

44612

receptor

Homo sapiens estrogen receptor 1 (ESR1) mRNA

>gi_31233_emb_X03635_HSERR Human mRNA for oestrogen

Seq. ID

Method

```
Seq. No.
                  312433
Seq. ID
                  xdb700337320.h1
Method
                  BLASTX
                  g3894214
NCBI GI
BLAST score
                  174
E value
                  4.0e-13
Match length
                  40
% identity
                  82
NCBI Description
                  (D83726) elongation factor 1 beta 2 [Oryza sativa]
                  >gi_3894216_dbj_BAA34599_ (D83727) elongation factor 1 beta
                  2 [Oryza sativa]
Seq. No.
                  312434
Seq. ID
                  xdb700337421.h1
Method
                  BLASTN
NCBI GI
                  g22192
BLAST score
                  52
                  2.0e-20
E value
Match length
                  108
                  88
% identity
NCBI Description
                  Z.mays B-I gene for B transcriptional activator
                  312435
Seq. No.
Seq. ID
                  xdb700337519.h1
Method
                  BLASTX
NCBI GI
                  g3402693
BLAST score
                  195
E value
                  3.0e-15
Match length
                  78
                  55
% identity
NCBI Description
                  (AC004697) unknown protein [Arabidopsis thaliana]
Seq. No.
                  312436
Seq. ID
                  xdb700337543.h1
Method
                  BLASTN
NCBI GI
                  q468055
BLAST score
                  69
E value
                  9.0e-31
Match length
                  175
                  93
% identity
NCBI Description
                  Zea mays B73 QM protein mRNA, complete cds
Seq. No.
                  312437
Seq. ID
                  xdb700337561.h1
Method
                  BLASTN
NCBI GI
                  q21634
BLAST score
                  40
E value
                  3.0e-13
Match length
                  96
% identity
                  85
NCBI Description
                  T.aestivum 1b-c38 gene for HBP-1b (leucine zipper type
                  transcription factor)
Seq. No.
                  312438
```

- ~ (

44613

xdb700337589.h1

BLASTN



```
NCBI GI g434329
BLAST score 147
E value 3.0e-77
Match length 147
% identity 100
```

NCBI Description Z.mays mRNA gs1-4 for glutamine synthetase

```
Seq. No. 312439
```

Seq. ID xdb700337595.h1

Method BLASTX
NCBI GI g2149640
BLAST score 289
E value 3.0e-26
Match length 65
% identity 85

NCBI Description (U91995) Argonaute protein [Arabidopsis thaliana]

```
Seq. No. 312440
```

Seq. ID xdb700337694.h1

Method BLASTX
NCBI GI g4559380
BLAST score 224
E value 1.0e-18
Match length 71
% identity 62

NCBI Description (AC006526) putative auxin-responsive GH3 protein

[Arabidopsis thaliana]

Seq. No. 312441

Seq. ID xdb700337712.h1

Method BLASTN
NCBI GI g1213276
BLAST score 41
E value 7.0e-14
Match length 45
% identity 98

NCBI Description Z.mays ZEMa gene

Seq. No. 312442

Seq. ID xdb700337981.h1

Method BLASTX
NCBI GI g3183405
BLAST score 181
E value 1.0e-13
Match length 63
% identity 52

NCBI Description HYPOTHETICAL 11.3 KD PROTEIN C2C6.07 IN CHROMOSOME I

>gi 3451305 emb CAA20442 (AL031324) very hypothetical

protein [Schizosaccharomyces pombe]

Seq. No. 312443

Seq. ID xdb700338046.h1

Method BLASTX
NCBI GI g461735
BLAST score 164
E value 1.0e-11
Match length 49



% identity

NCBI Description

MITOCHONDRIAL CHAPERONIN HSP60-1 PRECURSOR

>gi 478785_pir__S29315 chaperonin 60 - cucurbit

>gi_12544_emb_CAA50217_ (X70867) chaperonin 60 [Cucurbita

sp.]

Seq. No.

312444

Seq. ID

xdb700338238.h1

Method NCBI GI BLASTN g22292

BLAST score

75

E value Match length 1.0e-34 83

% identity

98

NCBI Description

Z.mays mRNA for glycine-rich protein

Seq. No.

312445

Seq. ID

xdb700338271.h1

Method NCBI GI BLASTN

g169819

BLAST score

49

E value Match length 1.0e-18 58

% identity

97 Rice gene encoding three ribosomal RNA's: the 17S, 3' end; NCBI Description

5.8S, complete; 25S, 5' end

Seq. No.

Seq. ID Method

xdb700338483.h1 BLASTX

NCBI GI

g2982451

BLAST score

167

312446

E value

6.0e-12

Match length % identity

41 80

NCBI Description

(AL022223) putative protein [Arabidopsis thaliana]

Seq. No.

312447

Seq. ID

xdb700338491.h1

Method NCBI GI BLASTN q2282583

BLAST score

155

E value

4.0e-82 167

Match length % identity

98

Zea mays elongation factor 1-alpha (EF1-A) mRNA, complete NCBI Description

cds

Seq. No.

312448

Seq. ID

xdb700338617.h1

Method NCBI GI BLASTN q984508

BLAST score

E value

200 1.0e-109

Match length

302

% identity

93

NCBI Description Human Tislld gene, complete cds



```
Seq. No.
                  312449
Seq. ID
                  xdb700338742.h1
Method
                  BLASTN
NCBI GI
                  g292328
BLAST score
                  202
E value
                  1.0e-110
Match length
                  274
% identity
NCBI Description
                  Human putative M phase phosphoprotein 1 (MPP1) mRNA,
                  partial cds
Seq. No.
                  312450
Seq. ID
                  xdb700338792.h1
Method
                  BLASTN
NCBI GI
                  q639721
BLAST score
                  229
E value
                  1.0e-126
                  237
Match length
                  99
% identity
                  Zea mays calcium-dependent protein kinase (CDPK) gene,
NCBI Description
                  exons 1-7 and partial cds
Seq. No.
                  312451
                  xdb700338957.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q929916
BLAST score
                  33
E value
                   4.0e-09
Match length
                   61
                  89
% identity
NCBI Description
                  Zea diploperennis retrotransposable-like element DNA
                   312452
Seq. No.
Seq. ID
                   xdb700339009.h1
Method
                  BLASTN
NCBI GI
                   g433415
BLAST score
                   103
E value
                   7.0e-51
Match length
                   178
% identity
                   91
NCBI Description Human mRNA for DNA-binding protein, TAXREB107, complete cds
Seq. No.
                   312453
Seq. ID
                   xdb700339030.h1
Method
                   BLASTX
                   g125157
NCBI GI
BLAST score
                   418
                   2.0e-41
E value
                   87
Match length
                   92
% identity
                  GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (AK3)
NCBI Description
                   >gi 1070480 pir KIHUA3 nucleoside-triphosphate--adenylate
```

sapiens]

kinase (EC 2.7.4.10) 3 - human >gi_28577_emb_CAA43088_ (X60673) nucleoside-triphosphate--adenylate kinase [Homo

Seq. No.

Seq. ID

312459

xdb700339496.h1



```
Seq. No.
                   312454
Seq. ID
                   xdb700339063:h1
Method
                  BLASTN
NCBI GI
                   g3342031
BLAST score
                   50
E value
                   3.0e-19
Match length
                   59
                   97
% identity
NCBI Description
                  Oryza sativa 18S small subunit ribosomal RNA gene, complete
Seq. No.
                   312455
Seq. ID
                  xdb700339079.h1
Method
                  BLASTX
NCBI GI
                   q629844
BLAST score
                  194
E value
                   4.0e-15
Match length
                   59
                   68
% identity
NCBI Description
                  heat shock protein hsp70-5 - maize (fragment)
                   >gi 498775 emb CAA55184 (X78415) heat shock protein 70 kDa
                   [Zea mays]
Seq. No.
                   312456
Seq. ID
                   xdb700339083.h1
Method
                  BLASTN
NCBI GI
                   a1778146
BLAST score
                   55
E value
                   2.0e-22
Match length
                   95
                   91
% identity
NCBI Description
                  Zea mays plastid phosphate/phosphoenolpyruvate translocator
                  precursor (MZPPT1) mRNA, complete cds
Seq. No.
                   312457
                  xdb700339185.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q3426046
BLAST score
                   176
E value
                   4.0e-13
Match length
                   82
% identity
                   40
NCBI Description
                   (AC005168) similar to salt-inducible protein [Arabidopsis
                   thaliana]
Seq. No.
                   312458
Seq. ID
                  xdb700339319.h1
Method
                  BLASTN
NCBI GI
                  g3057119
BLAST score
                   35
E value
                  2.0e-10
Match length
                  59
                   90
% identity
NCBI Description
                  Zea mays starch synthase DULL1 (dull1) mRNA, complete cds
```



```
Method
NCBI GI
                  q3264604
BLAST score
                  179
E value
                  3.0e-96
Match length
                  203
                  98
% identity
NCBI Description
                  Zea mays ribosomal protein L25 mRNA, partial cds
Seq. No.
                  312460
                  xdb700339515.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3894197
BLAST score
                  329
                  7.0e-31
E value
                  84
Match length
% identity
                  68
                  (AC005662) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  312461
                  xdb700339604.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2088647
BLAST score
                  163
E value
                  1.0e-11
Match length
                  42
% identity
                  76
                  (AF002109) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  >gi 3158394 (AF036340) LRR-containing F-box protein
                   [Arabidopsis thaliana]
Seq. No.
                  312462
Seq. ID
                  xdb700339814.h1
Method
                  BLASTN
NCBI GI
                  g36348
BLAST score
                  131
E value
                  1.0e-67
Match length
                  275
                  28
% identity
NCBI Description
                  Human alphoid satellite repeats from HeLa spc DNA (small
                  polydisperse circular DNA)
Seq. No.
                  312463
Seq. ID
                  xdb700339964.h1
Method
                  BLASTX
NCBI GI
                  g1620982
BLAST score
                  142
E value
                  3.0e-09
Match length
                  64
% identity
                  56
NCBI Description
                  (Y08860) 40S ribosomal protein S5 [Nicotiana
                  plumbaginifolia]
```

312464

Seq. ID xdb700340253.h1

Method BLASTX NCBI GI g4539660 BLAST score 404

Seq. No.

```
E value
                   1.0e-39
                   97
Match length
                   78
% identity
NCBI Description
                  (AF061282) polyprotein [Sorghum bicolor]
Seq. No.
                   312465
Seq. ID
                  xdb700340356.h1
Method
                  BLASTN
NCBI GI
                  g2599233
BLAST score
                  247
E value
                   1.0e-137
Match length
                   286
% identity
                   68
NCBI Description
                  Homo sapiens chromosome 17, clone HRPC987K16, complete
                   sequence [Homo sapiens]
```

Seq. No. 312466 Seq. ID xdb700340384.h1 Method BLASTX NCBI GI g123178

BLAST score 236 9.0e-41 E value Match length 93 % identity 90

NCBI Description HISTIDINOL DEHYDROGENASE, CHLOROPLAST PRECURSOR (HDH) >gi_99844_pir A39358 histidinol dehydrogenase (EC 1.1.1.23) precursor, chloroplast - cabbage >gi 167142

(M60466) histidinol dehydrogenase [Brassica oleracea]

Seq. No. 312467

Seq. ID xdb700340401.h1

Method BLASTN NCBI GI q3955064 BLAST score 52 E value 8.0e-21 Match length 129 % identity 86

NCBI Description Zea mays PHYT I gene for acidic phytase

Seq. No. 312468

Seq. ID xdb700340417.h1

Method BLASTX NCBI GI g2190543 BLAST score 151 E value 5.0e-10 Match length 46 % identity

NCBI Description (AC001229) EST gb N37484 comes from this gene. [Arabidopsis

thaliana]

Seq. No. 312469

Seq. ID xdb700340430.h1

Method BLASTN NCBI GI g2760545 BLAST score 247 E value 1.0e-137 Match length 289

```
% identity
                   Human DNA sequence from PAC 67M12 on chromosome 6p22.1-22.3. Contains ESTs, STSs and CA and TAA repeat
NCBI Description
                   polymorphisms
                   312470
Seq. No.
Seq. ID
                   xdb700340463.h1
Method
                   BLASTX
NCBI GI
                   g2641233
BLAST score
                   195
E value
                   1.0e-22
Match length
                   81
% identity
                   66
                   (AF031701) actin [Encephalitozoon hellem]
NCBI Description
                   312471
Seq. No.
                   xdb700340488.hl
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3089349
BLAST score
                   318
                   1.0e-29
E value
Match length
                   71
                   83
% identity
NCBI Description
                   (U64205) Cdc25C associated protein kinase C-TAK1 [Homo
                   sapiens]
Seq. No.
                   312472
                   xdb700340634.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2431767
BLAST score
                   224
                   1.0e-18
E value
Match length
                   56
                   77
% identity
NCBI Description (U62751) acidic ribosomal protein P3a [Zea mays]
                   312473
Seq. No.
                   xdb700340652.h1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2431768
BLAST score
                   71
                   6.0e-32
E value
Match length
                   183
% identity
                   85
NCBI Description
                   Zea mays acidic ribosomal protein Pla (rppla) mRNA,
                   complete cds
Seq. No.
                   312474
```

Seq. ID xdb700340670.h1

Method BLASTX
NCBI GI g3915826
BLAST score 161
E value 1.0e-11
Match length 65
% identity 52

NCBI Description 60S RIBOSOMAL PROTEIN L5

```
312475
Seq. No.
Seq. ID
                   xdb700340732.h1
Method
                   BLASTX
                   q4200249
NCBI GI
                   209
BLAST score
                   8.0e-17
E value
                   92
Match length
                   51
% identity
NCBI Description (AL035297) hypothetical protein [Homo sapiens]
                   312476
Seq. No.
                   xdb700340776.h1
Seq. ID
Method
                   BLASTX
                   g4206306
NCBI GI
BLAST score
                   373
                   4.0e-36
E value
                   98
Match length
                   80
% identity
                  (AF049110) prpol [Zea mays]
NCBI Description
                   312477
Seq. No.
                   xdb700340987.h1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3928097
BLAST score
                   147
E value
                   1.0e-09
Match length
                   84
                   45
% identity
                   (AC005770) unknown protein, 5' partial [Arabidopsis
NCBI Description
                   thalianal
Seq. No.
                   312478
                   xdb700341229.h1
Seq. ID
Method
                   BLASTX
                   g4506907
NCBI GI
BLAST score
                   194
E value
                   2.0e-15
Match length
                   36
% identity
NCBI Description
                   surfactant, pulmonary-associated protein C
                   >gi_131425_sp_P11686_PSPC_HUMAN_PULMONARY
SURFACTANT-ASSOCIATED_PROTEIN_C_PRECURSOR_(SP-C)_(SP5)
                   (PULMONARY SURFACTANT-ASSOCIATED PROTEOLIPID SPL(VAL))
                   >gi 71983 pir LNHUC pulmonary surfactant protein C
                   precursor - human >gi_338307 (J03553) pulmonary surfactant
                   protein (SP5) precursor [Homo sapiens] >gi_338413 (J03517)
                   pulmonary surfactant proteolipid precursor [Homo sapiens]
Seq. No.
                   312479
Seq. ID
                   xdb700341236.h1
Method
                   BLASTN
NCBI GI
                   q3256174
```

NCBI GI g3256174
BLAST score 150
E value 4.0e-79
Match length 158
% identity 99

NCBI Description Homo sapiens DNA sequence from PAC 168L15 on chromosome

NCBI Description

```
6q26-27. Contains RSK3 gene, ribosomal protein S6 kinase, EST, GSS, STS. CpG island, complete sequence [Homo sapiens]
```

```
Seq. No.
                   312480
Seq. ID
                   xdb700341240.hl
Method
                  BLASTN
NCBI GI
                  q4204375
                   64
BLAST score
                   6.0e-28
E value
Match length
                   145
% identity
NCBI Description
                  Zea mays acidic ribosomal protein P2a-4 (rpp2a-4) mRNA,
                  partial cds
                   312481
Seq. No.
                   xdb700341253.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4582434
                   190
BLAST score
                   1.0e-14
E value
Match length
                   48
                   77
% identity
NCBI Description
                   (AC007196) unknown protein [Arabidopsis thaliana]
Seq. No.
                   312482
Seq. ID
                   xdb700341416.hl
Method
                   BLASTN
NCBI GI
                   g747916
BLAST score
                   112
E value
                   1.0e-56
Match length
                   128
                   98
% identity
NCBI Description
                  Z.mays CaM2 mRNA for calmodulin
Seq. No.
                   312483
                   xdb700341431.h1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g4204375
BLAST score
                   103
E value
                   7.0e-51
Match length
                   261
% identity
                   94
                   Zea mays acidic ribosomal protein P2a-4 (rpp2a-4) mRNA,
NCBI Description
                   partial cds
                   312484
Seq. No.
Seq. ID
                   xdb700341502.h1
Method
                   BLASTX
NCBI GI
                   q2493852
BLAST score
                   326
                   2.0e-30
E value
Match length
                   63
                   97
% identity
```

>gi 1070356 emb CAA92107 (Z68091) cytochrome c oxidase, Vc

CYTOCHROME C OXIDASE POLYPEPTIDE VC

subunit [Hordeum vulgare]



```
Seq. No.
                  312485
Seq. ID
                  xdb700341622.hl
Method
                  BLASTN
NCBI GI
                  g1029494
BLAST score
                  110
E value
                  3.0e-55
Match length
                  162
                  92
% identity
NCBI Description . H.sapiens CpG island DNA genomic Msel fragment, clone 33f2,
                  forward read cpg33f2.ft1e
Seq. No.
                  312486
Seq. ID
                  xdb700341751.h1
Method
                  BLASTN
                  g1296663
NCBI GI
BLAST score
                  54
E value
                  1.0e-21
Match length
                  252
% identity
                  81
NCBI Description H.sapiens mRNA for Sec23A isoform, 2748bp
                  312487
Seq. No.
Seq. ID
                  xdb700341844.h1
Method
                  BLASTN
                  g533250
NCBI GI
BLAST score
                  45
                  2.0e-16
E value
                  85
Match length
% identity
                  88
                  Zea mays (clone Sh1-BMS) MISD1 insertion sequence from
NCBI Description
                  shrunken1 allele DNA
Seq. No.
                  312488
Seq. ID
                  xdb700341870.h1
Method
                  BLASTX
NCBI GI
                  q3242715
BLAST score
                  160
E value
                  3.0e-11
Match length
                  57
% identity
                  58
NCBI Description (AC003040) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  312489
Seq. ID
                  xdb700341893.h1
Method
                  BLASTX
NCBI GI
                  g2746079
BLAST score
                  253
E value
                  4.0e-22
Match length
                  65
% identity
                  75
                  (AF015310) BTH1 [Brassica napus]
NCBI Description
```

Seq. No. 312490

Seq. ID xdb700342052.h1

Method BLASTN NCBI GI g2431768

BLAST score 70



```
E value
                   3.0e-31
Match length
                   206
% identity
                   84
NCBI Description
                  Zea mays acidic ribosomal protein Pla (rppla) mRNA,
                   complete cds
Seq. No.
                  312491
Seq. ID
                  xdg700405119.h1
Method
                  BLASTX
NCBI GI
                  q3482914
BLAST score
                   150
E value
                   6.0e-10
Match length
                   92
                   39
% identity
                  (AC003970) Similar to nodulins and lipase [Arabidopsis
NCBI Description
                  thalianal
Seq. No.
                   312492
Seq. ID
                  xdg700405248.hl
Method
                  BLASTX
                   g4204849
NCBI GI
BLAST score
                   322
E value
                   3.0e-30
Match length
                   81
% identity
                   74
                  (U55875) protein kinase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   312493
Seq. ID
                  xjt700092020.h1
Method
                  BLASTX
NCBI GI
                   g1806140
BLAST score
                   205
E value
                   2.0e-16
Match length
                   87
% identity
                   51
NCBI Description
                  (X97314) cdc2MsC [Medicago sativa]
Seq. No.
                   312494
Seq. ID
                  xjt700092038.h1
Method
                  BLASTX
NCBI GI
                   q3927825
BLAST score
                   187
E value
                   1.0e-29
Match length
                   87
% identity
                   79
NCBI Description
                   (AC005727) putative dTDP-glucose 4-6-dehydratase
                   [Arabidopsis thaliana]
Seq. No.
                   312495
Seq. ID
                   xjt700092058.h1
Method
                   BLASTX
NCBI GI
                   g1514643
```

NCBI GI g151464
BLAST score 484
E value 5.0e-49
Match length 105
% identity 88

NCBI Description (270524) PDR5-like ABC transporter [Spirodela polyrrhiza]



Seq. No. 312496 Seq. ID xjt700092059.h1 Method BLASTX NCBI GI g2129830 BLAST score 224 E value 6.0e-19 47 Match length % identity heat shock transcription factor 31 - soybean (fragment) NCBI Description >gi_671867_emb_CAA87079_ (Z46955) heat shock transcription factor 31 [Glycine max] Seq. No. 312497

Seq. ID xjt700092060.h1 Method BLASTX g1084944 NCBI GI BLAST score 196 3.0e-15

E value Match length 103 42 % identity

NCBI Description hypothetical protein YPR021c - yeast (Saccharomyces cerevisiae) >gi_809586_emb_CAA89275_ (Z49274) unknown [Saccharomyces cerevisiae] >gi_1314095_emb_CAA95017_

(Z71255) unknown [Saccharomyces cerevisiae]

312498 Seq. No.

xjt700092079.h1 Seq. ID

Method BLASTX g3850585 NCBI GI BLAST score 224 1.0e-18 E value Match length 79 % identity 57

(AC005278) ESTs gb H36966, gb R65511, gb T42324 and NCBI Description gb T20569 come from this gene. [Arabidopsis thaliana]

Seq. No. 312499

Seq. ID xjt700092110.h1

Method BLASTX q3287270 NCBI GI BLAST score 255 E value 3.0e-22 Match length 103 % identity

NCBI Description (Y09533) involved in starch metabalism [Solanum tuberosum]

Seq. No. 312500

xjt700092127.h1 Seq. ID

Method BLASTN NCBI GI q550541 BLAST score 55 E value 3.0e-22 Match length 144 % identity 93

NCBI Description Z.mays CYP71C4 mRNA for cytochrome P-450

NCBI Description



```
312501
Seq. No.
                  xjt700092144.h1
Seq. ID
                  BLASTX
Method
                  g115771
NCBI GI
                  342
BLAST score
                  2.0e-32
E value
                  77
Match length
                  83
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                  (CAB-1) (LHCP) >gi_82682_pir__S04453 chlorophyll
                  a/b-binding protein precursor - maize
                  >gi 22224_emb_CAA32900_ (X14794) chlorophyll a/b-binding
                  preprotein (AA 1 - 262) [Zea mays]
Seq. No.
                  312502
                  xjt700092236.h1
Seq. ID
                  BLASTN
Method
                  q347843
NCBI GI
BLAST score
                  35
                  3.0e-10
E value
Match length
                  43
                  95
% identity
NCBI Description Zea mays globulin-1 gene, promoter region
Seq. No.
                  312503
Seq. ID
                  xjt700092324.h1
Method
                  BLASTX
NCBI GI
                  q4544402
BLAST score
                  142
                  6.0e-09
E value
                  71
Match length
% identity
                   42
                   (AC007047) putative leucine rich repeat protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  312504
                  xjt700092326.h1
Seq. ID
Method
                  BLASTX
                  g3892056
NCBI GI
                   406
BLAST score
E value
                   6.0e-40
                   88
Match length
                   86
% identity
                  (AC002330) putative vacuolar ATPase [Arabidopsis thaliana]
NCBI Description
                   312505
Seq. No.
                  xjt700092332.h1
Seq. ID
Method
                  BLASTX
                   g129916
NCBI GI
BLAST score
                   369
E value
                   1.0e-35
Match length
                   77
                   95
% identity
```

(AA 1 - 401) [Triticum aestivum]

PHOSPHOGLYCERATE KINASE, CYTOSOLIC >gi_66911_pir__TVWTGY

phosphoglycerate kinase (EC 2.7.2.3), cytosolic - wheat >gi_21835_emb_CAA33302_ (X15232) phosphoglycerate kinase

```
Seq. No.
                    312506
Seq. ID
                    xjt700092343.hl
Method
                    BLASTX
NCBI GI
                    q1362051
BLAST score
                    141
E value
                    7.0e-09
                    37
Match length
                    76
% identity
                    protein kinase 3 - soybean >gi_310582 (L19361) protein
NCBI Description
                    kinase 3 [Glycine max]
Seq. No.
                    312507
                    xjt700092409.h1
Seq. ID
Method
                    BLASTX
                    q3738306
NCBI GI
                    150
BLAST score
                    1.0e-13
E value
Match length
                    79
                    51
% identity
                   (AC005309) unknown protein [Arabidopsis thaliana]
NCBI Description
                    312508
Seq. No.
Seq. ID
                    xjt700092414.h1
Method
                    BLASTN
NCBI GI
                    g22354
BLAST score
                    61
                    7.0e-26
E value
Match length
                    172
% identity
                    88
                    Zea mays L. mRNA for light-harvesting chlorophyll a/b
NCBI Description
                    binding protein
Seq. No.
                    312509
Seq. ID
                    xjt700092428.h1
                    BLASTX
Method
NCBI GI
                    g115771
BLAST score
                    361
E value
                    1.0e-34
Match length
                    82
                    80
% identity
                    CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                    (CAB-1) (LHCP) >gi_82682_pir__S04453 chlorophyll a/b-binding protein precursor - maize
                    >gi_22224_emb_CAA32900_ (X14794) chlorophyll a/b-binding preprotein (AA 1 - 262) [Zea mays]
Seq. No.
                    312510
Seq. ID
                    xjt700092470.h1
Method
                    BLASTX
```

Method BLASTX
NCBI GI g115786
BLAST score 308
E value 2.0e-28
Match length 78
% identity 78

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB) (LHCP) >gi 82680 pir A29119 chlorophyll a/b-binding



```
protein - maize >gi_22357_emb_CAA68451_ (Y00379) LHCP [Zea
mays]
```

Seq. No. 312511

Seq. ID xjt700092520.h1

Method BLASTX
NCBI GI g115815
BLAST score 313
E value 6.0e-29
Match length 76
% identity 76

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-M9) (LHCP) >gi_100866_pir__S13098 chlorophyll

a/b-binding protein precursor - maize

>gi 22355_emb_CAA39376_ (X55892) light-harvesting

chlorophyll a/b binding protein [Zea mays]

Seq. No. 312512

Seq. ID xjt700092535.h1

Method BLASTX
NCBI GI g4091117
BLAST score 286
E value 7.0e-26
Match length 68
% identity 76

NCBI Description (AF047428) nucleic acid binding protein [Oryza sativa]

Seq. No. 312513

Seq. ID xjt700092596.h1

Method BLASTX
NCBI GI g3128231
BLAST score 185
E value 5.0e-14
Match length 100
% identity 42

NCBI Description (AC004077) hypothetical protein [Arabidopsis thaliana]

>gi 3337370 (AC004481) hypothetical protein [Arabidopsis

thaliana]

Seq. No. 312514

Seq. ID xjt700092676.h1

Method BLASTX
NCBI GI g4455338
BLAST score 414
E value 7.0e-41
Match length 101
% identity 70

NCBI Description (AL035525) putative protein [Arabidopsis thaliana]

Seq. No. 312515

Seq. ID xjt700092677.h1

Method BLASTX
NCBI GI g3779244
BLAST score 256
E value 2.0e-22
Match length 91
% identity 54





```
(AF061243) metalloprotease 1 [Homo sapiens]
NCBI Description
                   312516
Seq. No.
                   xjt700092702.h1
Seq. ID
Method
                   BLASTX
                   g4559333
NCBI GI
BLAST score
                   184
                   6.0e-14
E value
                   76
Match length
% identity
                   47
                   (AC007087) unknown protein [Arabidopsis thaliana]
NCBI Description
                   312517
Seq. No.
                   xjt700092716.h1
Seq. ID
Method
                   BLASTX
                   q3600039
NCBI GI
BLAST score
                   177
                   4.0e-13
E value
                   52
Match length
% identity
                   65
                   (AF080119) similar to Schizosaccharomyces pombe isp4
NCBI Description
                   protein (GB:D14061) [Arabidopsis thaliana]
                   312518
Seq. No.
                   xjt700092769.h1
Seq. ID
Method
                   BLASTX
                   g2760832
NCBI GI
BLAST score
                   309
E value
                   1.0e-28
                   100
Match length
                   53
% identity
                    (AC003105) similar to barley ids-4 gene product
NCBI Description
                    [Arabidopsis thaliana]
                   312519
Seq. No.
Seq. ID
                   xjt700092823.h1
Method
                   BLASTX
NCBI GI
                   g1346396
BLAST score
                   230
                   3.0e-19
E value
                   96
Match length
% identity
                   51
                   PUTATIVE RECEPTOR PROTEIN KINASE ZMPK1 PRECURSOR
NCBI Description
                   >gi 100913 pir S10930 probable receptor protein kinase (EC
                    2.7.1.-) precursor - maize >gi 22432 emb CAA36611 (X52384)
                   precursor protein (AA -26 to 791) [Zea mays]
                   >gi_22436_emb_CAA47962_ (X67733) receptor-like protein
kinase [Zea mays] >gi_226927_prf__1611404A receptor protein
                    kinase [Zea mays]
                    312520
```

Seq. No.

xjt700092841.h1 Seq. ID

Method BLASTX q3927825 NCBI GI 238 BLAST score E value 3.0e-20 50 Match length



```
% identity
NCBI Description
                  (AC005727) putative dTDP-glucose 4-6-dehydratase
                  [Arabidopsis thaliana]
                  312521
Seq. No.
                  xjt700092923.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1076758
BLAST score
                  323
                  3.0e-30
E value
                  99
Match length
                  62
% identity
                  heat-shock protein precursor - rye >gi_2130093_pir__$65776
NCBI Description
                  heat-shock protein, 82K, precursor - rye
                  >gi 556673 emb CAA82945 (Z30243) heat-shock protein
                  [Secale cereale]
                  312522
Seq. No.
                  xjt700092981.h1
Seq. ID
Method
                  BLASTX
                  g3834324
NCBI GI
                  298
BLAST score
                  6.0e-33
E value
Match length
                  96
% identity
                  74
                  (AC005679) Similar to gb X92762 tafazzins protein from Homo
NCBI Description
                  sapiens. [Arabidopsis thaliana]
                  312523
Seq. No.
                  xjt700093008.h1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g115815
BLAST score
                  211
E value
                  5.0e-25
                  75
Match length
                  63
% identity
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                   (CAB-M9) (LHCP) >gi_100866_pir__S13098 chlorophyll
                  a/b-binding protein precursor - maize
                  >gi_22355_emb_CAA39376_ (X55892) light-harvesting
                  chlorophyll a/b binding protein [Zea mays]
                  312524
Seq. No.
                  xjt700093011.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q82080
BLAST score
                  256
E value
                  2.0e-22
```

Match length 69 72 % identity

NCBI Description chlorophyll a/b-binding protein type III precursor - tomato

>gi 226872 prf 1609235A chlorophyll a/b binding protein

[Lycopersicon esculentum]

Seq. No. 312525

Seq. ID xjt700093033.h1

Method BLASTX

44630

```
NCBI GI
                  q3461813
BLAST score
                  338
                  6.0e-32
E value
Match length
                  98
% identity
NCBI Description
                  (AC004138) putative sucrose/H+ symporter [Arabidopsis
                  thaliana]
Seq. No.
                  312526
Seq. ID
                  xjt700093047.h1
Method
                  BLASTX
NCBI GI
                  q4574141
BLAST score
                  227
E value
                  6.0e-19
Match length
                  66
                  65
% identity
NCBI Description
                  (AF073698) cysteine synthase [Oryza sativa]
                  312527
Seq. No.
                  xjt700093075.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g758354
BLAST score
                  78
E value
                  4.0e-36
Match length
                  101
                  96
% identity.
                  Z.mays mRNA for plasma membrane H+ ATPase
NCBI Description
Seq. No.
                  312528
Seq. ID
                  xjt700093077.h1
Method
                  BLASTX
NCBI GI
                  q2529662
BLAST score
                  274
E value
                  2.0e-24
Match length
                  60
% identity
                  87
NCBI Description
                   (AC002535) putative small nuclear ribonucleoprotein, Sm D2
                   [Arabidopsis thaliana] >gi 3738278 (AC005309) putative
                  small nuclear ribonucleoprotein, Sm D2 [Arabidopsis
                  thaliana]
                  312529
Seq. No.
Seq. ID
                  xjt700093091.h1
Method
                  BLASTX
                  g2440042
NCBI GI
BLAST score
                  198
```

E value 1.0e-21 78 Match length 74 % identity

NCBI Description (AJ001292) major intrinsic protein PIPa2 [Craterostigma

plantagineum]

Seq. No. 312530

Seq. ID xjt700093114.h1

BLASTX Method g2129559 NCBI GI BLAST score 141



```
1.0e-11
E value
Match length
                  43
% identity
                  cellulase homolog OR16pep - Arabidopsis thaliana
NCBI Description
                  >gi_1022807 (U37702) cellulase [Arabidopsis thaliana]
                  >gi_3493633 (AF074092) cellulase [Arabidopsis thaliana]
                  >gi_3598956 (AF074375) cellulase [Arabidopsis thaliana]
                  >gi 3978258 (AF073875) endo-1,4-beta-D-glucanase KORRIGAN
                  [Arabidopsis thaliana]
                  312531
Seq. No.
Seq. ID
                  xjt700093324.h1
Method
                  BLASTX
NCBI GI
                  g629669
BLAST score
                  211
                  4.0e-17
E value
Match length
                  87
                  49
% identity
NCBI Description hypothetical protein - tomato
                  312532
Seq. No.
                  xjt700093330.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2190544
BLAST score
                  219
                  5.0e-18
E value
Match length
                  50
                  84
% identity
                  (AC001229) Similar to Saccharomyces hypothetical protein
NCBI Description
                  P9642.2 (gb U40828). [Arabidopsis thaliana]
Seq. No.
                  312533
                  xjt700093385.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1680686
BLAST score
                  281
E value
                  3.0e-25
Match length
                  82
% identity
                  68
NCBI Description
                  (U51330) rust resistance kinase Lr10 [Triticum aestivum]
                  312534
Seq. No.
Seq. ID
                  xjt700093444.h1
Method
                  BLASTX
NCBI GI
                  g2384675
BLAST score
                  253
E value
                  5.0e-22
Match length
                  82
% identity
NCBI Description
                   (AF012659) putative potassium transporter AtKT4p
```

[Arabidopsis thaliana]

Seq. No. 312535

Seq. ID xjt700093477.h1

Method BLASTX
NCBI GI g3927831
BLAST score 145

Method

NCBI GI

BLAST score

BLASTX

330

g3212859

```
2.0e-09
E value
Match length
% identity
                  (AC005727) similar to mouse ankyrin 3 [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  312536
Seq. ID
                  xjt700093513.h1
Method
                  BLASTX
NCBI GI
                  g730125
BLAST score
                  261
E value
                  5.0e-23
Match length
                  62
% identity
                  77
                  NADPH-CYTOCHROME P450 REDUCTASE >gi_322739_pir__$31502
NCBI Description
                  NADPH--ferrihemoprotein reductase (EC 1.6.2.4) - Madagascar
                  periwinkle >gi_18139_emb_CAA49446_ (X69791)
                  NADPH--ferrihemoprotein reductase [Catharanthus roseus]
Seq. No.
                  312537
                  xjt700093545.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g135449
BLAST score
                  199
E value
                  1.0e-15
Match length
                  59
                  73
% identity
                  TUBULIN BETA-1 CHAIN >gi_100932_pir__S14701 tubulin beta-1
NCBI Description
                  chain - maize >gi_295851_emb_CAA37060_ (X52878) beta 1
                  tubulin [Zea mays]
Seq. No.
                  312538
Seq. ID
                  xjt700093573.h1
Method
                  BLASTX
NCBI GI
                  g2244996
BLAST score
                  309
E value
                  1.0e-28
Match length
                  98
% identity
                  54
NCBI Description
                  (Z97341) similarity to a membrane-associated salt-inducible
                  protein [Arabidopsis thaliana]
Seq. No.
                  312539
Seq. ID
                  xjt700093593.h1
Method
                  BLASTX
NCBI GI
                  g4539351
BLAST score
                  324
E value
                  5.0e-32
Match length
                  93
                  78
% identity
NCBI Description
                  (AL035539) putative protein [Arabidopsis thaliana]
Seq. No.
                  312540
                  xjt700093637.h1
Seq. ID
```

44633



E value 5.0e-31
Match length 98
% identity 61

NCBI Description (AC004005) hypothetical protein [Arabidopsis thaliana]

Seq. No. 312541

Seq. ID xjt700093639.h1

Method BLASTX
NCBI GI g1085650
BLAST score 155
E value 2.0e-10
Match length 35
% identity 91

NCBI Description aspartate transcarbomoylase - wheat >gi_688218_bbs_156442

aspartate carbamoyltransferase {C-terminal} {EC 2.1.3.2} [Triticum aestivum=wheat, avalon, seedlings, Peptide

Partial, 233 aa]

Seq. No. 312542

Seq. ID xjt700093666.h1

Method BLASTX
NCBI GI g66009
BLAST score 356
E value 4.0e-34
Match length 69
% identity 99

NCBI Description glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) C,

cytosolic - maize >gi_22238_emb_CAA30151_ (X07156) GADPH

(AA 1-337) [Zea mays]

Seq. No. 312543

Seq. ID xjt700093718.h1

Method BLASTX
NCBI GI g4455338
BLAST score 144
E value 2.0e-09
Match length 74
% identity 41

NCBI Description (AL035525) putative protein [Arabidopsis thaliana]

Seq. No. 312544

Seq. ID xjt700093735.h1

Method BLASTX
NCBI GI g1709000
BLAST score 377
E value 1.0e-36
Match length 75
% identity 93

NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE

ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)

>gi 960357 dbj BAA09895 (D63835) S-adenosylmethionine

synthetase [Hordeum vulgare]

Seq. No. 312545

Seq. ID xjt700093751.h1

Method BLASTX NCBI GI g1076791



```
BLAST score 270
E value 4.0e-30
Match length 67
% identity 94
```

NCBI Description calcium-binding protein - maize >gi_2119370_pir__S58170 Calreticulin precursor - maize >gi_577612_emb_CAA86728_

(Z46772) calcium-binding protein [Zea mays]

>gi_927572_emb_CAA61939_ (X89813) Calreticulin precursor
[Zea mays] >gi_1587033_prf__2205314A calreticulin [Zea

mays]

 Seq. No.
 312546

 Seq. ID
 xjt700093881.hl

 Method
 BLASTX

 NCBI GI
 g3776015

NCBI GI g3776015
BLAST score 304
E value 6.0e-28
Match length 80
% identity 75

NCBI Description (AJ010471) RNA helicase [Arabidopsis thaliana] >gi 4249378 gb AAD14475 (AC005966) Identical to

gb_AJ010471 mRNA for DEAD box RNA helicase (RH22) from Arabidopsis thaliana. EST gb Y11191 comes from this gene.

[Arabidopsis thaliana]

Seq. No. 312547

Seq. ID xjt700093885.h1

Method BLASTX
NCBI GI g2129533
BLAST score 196
E value 3.0e-15
Match length 50
% identity 78

NCBI Description adenine nucleotide translocase - Arabidopsis thaliana

>gi 1051109 emb CAA89201 (Z49227) adenine nucleotide

translocase [Arabidopsis thaliana]

Seq. No. 312548

Seq. ID xjt700093956.h1

Method BLASTX
NCBI GI g116374
BLAST score 395
E value 1.0e-38
Match length 83
% identity 93

NCBI Description CHALCONE SYNTHASE WHP1 (NARINGENIN-CHALCONE SYNTHASE WHP1)

(WHITE POLLEN) >gi_66555_pir__SYZMW1 naringenin-chalcone synthase (EC 2.3.1.74) whp1 - maize >gi_22512_emb_CAA42763_

(X60204) chalcone synthase [Zea mays]

Seq. No. 312549

Seq. ID xjt700093959.h1

Method BLASTX
NCBI GI g3850063
BLAST score 167
E value 7.0e-12
Match length 65



```
% identity
                  (AJ223830) ARE1 [Rattus norvegicus]
NCBI Description
                  312550
Seq. No.
                  xjt700093989.h1
Seq. ID
                  BLASTX
Method
                  g3522943
NCBI GI
                  451
BLAST score
                  3.0e-45
E value
                  102
Match length
                  45
% identity
                  (AC004411) putative p-glycoprotein [Arabidopsis thaliana]
NCBI Description
                  312551
Seq. No.
                  xjt700094037.h1
Seq. ID
                  BLASTX
Method
                   g2342691
NCBI GI
                   154
BLAST score
                   2.0e-10
E value
                   55
Match length
% identity
                   58
                   (AC000106) F7G19.26 [Arabidopsis thaliana]
NCBI Description
                   312552
Seq. No.
                   xjt700094115.h1
Seq. ID
Method
                   BLASTX
                   g2582971
NCBI GI
BLAST score
                   327
                   1.0e-30
E value
                   103
Match length
                   63
% identity
                   (D83711) TKRP125 [Nicotiana tabacum]
NCBI Description
                   312553
Seq. No.
                   xjt700094126.h1
Seq. ID
                   BLASTN
Method
                   g433038
NCBI GI
                   52
BLAST score
                   8.0e-21
E value
                   122
Match length
% identity
                   87
                   Zea mays W-22 clone cDNA7 retroelement PREM-1-containing
NCBI Description
                   mRNA
                   312554
Seq. No.
                   xjt700094136.h1
Seq. ID
Method
                   BLASTX
                   g4263714
NCBI GI
BLAST score
                   164
                   1.0e-11
E value
Match length
                   38
% identity
                   84
                   (AC006223) putative integral membrane protein [Arabidopsis
NCBI Description
                   thaliana]
```

312555

xjt700094138.h1

Seq. No.

Seq. ID

Method BLASTX
NCBI GI g2492504
BLAST score 176
E value 3.0e-13
Match length 38
% identity 95
NCBI Description CELL DIV
>gi_1669

CELL DIVISION CYCLE PROTEIN 48 HOMOLOG

>gi_1669660_emb_CAA70565_ (Y09396) protein of AAA family

[Capsicum annuum]

Seq. No. 312556

Seq. ID xjt700094204.h1

Method BLASTX
NCBI GI g893294
BLAST score 334
E value 2.0e-31
Match length 101
% identity 65

NCBI Description (L43362) 4-coumarate:CoA ligase isoform 2 [Oryza sativa]

Seq. No. 312557

Seq. ID xjt700094293.h1

Méthod BLASTX
NCBI GI g4006918
BLAST score 157
E value 1.0e-10
Match length 48
% identity 56

NCBI Description (Z99708) peroxidase like protein [Arabidopsis thaliana]

Seq. No. 312558

Seq. ID xjt700094363.h1

Method BLASTX
NCBI GI g4544445
BLAST score 382
E value 3.0e-37
Match length 82
% identity 80

NCBI Description (AC006592) putative pyrophosphate--fructose 6-phosphate

1-phosphotransferase [Arabidopsis thaliana]

Seq. No. 312559

Seq. ID xjt700094415.h1

Method BLASTX
NCBI GI g1076758
BLAST score 228
E value 3.0e-24
Match length 67
% identity 88

NCBI Description heat-shock protein precursor - rye >gi_2130093_pir__S65776

heat-shock protein, 82K, precursor - rye

>gi_556673_emb_CAA82945_ (Z30243) heat-shock protein

[Secale cereale]

Seq. No. 312560

Seq. ID xjt700094467.h1

Method BLASTX

```
NCBI GI
                  q2224915
BLAST score
                  273
                  2.0e-24
E value
Match length
                   63
% identity
                  76
NCBI Description (U95968) beta-expansin [Oryza sativa]
Seq. No.
                  312561
                  xjt700094547.h1
Seq. ID
Method
                  BLASTX
                  g2078350
NCBI GI
BLAST score
                   348
E value
                  3.0e-33
Match length
                  95
                  79
% identity
NCBI Description (U95923) transaldolase [Solanum tuberosum]
                  312562
Seq. No.
                  xjt700094552.h1
Seq. ID
Method
                  BLASTX
                  g4105798
NCBI GI
BLAST score
                   161
                   4.0e-11
E value
Match length
                   47
% identity
                   55
NCBI Description
                 (AF049930) PGP237-11 [Petunia x hybrida]
Seq. No.
                   312563
                  xjt700094571.h1
Seq. ID
Method
                  BLASTN
                  g409782
NCBI GI
BLAST score
                   54
                   1.0e-21
E value
Match length
                   70
% identity
                   94
NCBI Description Rice mRNA for ferredoxin-NADP+ reductase, complete cds
                   312564
Seq. No.
                   xjt700094587.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3913464
BLAST score
                   211
E value
                   2.0e-27
Match length
                   76
% identity
                   86
                  BETAINE-ALDEHYDE DEHYDROGENASE (BADH)
NCBI Description
                   >gi_2244604_dbj_BAA21098_ (AB001348) betaine aldehyde
                   dehydrogenase [Oryza sativa]
Seq. No.
                   312565
Seq. ID
                   xit700094593.h1
Method
                   BLASTN
NCBI GI
                   g1206012
BLAST score
                   35
E value
                   3.0e-10
Match length
                   35
% identity
                   100
```

44638



95

partial cds

% identity

NCBI Description

```
Zea mays beta-D-glucosidase precursor (glu2) mRNA, complete
NCBI Description
                   312566
Seq. No.
                   xjt700094619.h1
Seq. ID
Method
                   BLASTX
                   g2306981
NCBI GI
BLAST score
                   172
                   1.0e-12
E value
Match length
                   60
                   58
% identity
                   (AF010321) photosystem I antenna protein [Oryza sativa]
NCBI Description
                   312567
Seq. No.
Seq. ID
                   xjt700094644.h1
Method
                   BLASTN
                   q3821780
NCBI GI
BLAST score
                   36
                   6.0e-11
E value
Match length
                   36
% identity
                   100
                   Xenopus laevis cDNA clone 27A6-1
NCBI Description
                   312568
Seq. No.
                   xjt700094769.h1
Seq. ID
Method
                   BLASTX
                   g129916
NCBI GI
BLAST score
                   323
E value
                   4.0e-30
                   69
Match length
                   94
% identity
                   PHOSPHOGLYCERATE KINASE, CYTOSOLIC >gi 66911 pir TVWTGY
NCBI Description
                   phosphoglycerate kinase (EC 2.7.2.3), cytosolic - wheat
                   >gi 21835 emb CAA33302 (X15232) phosphoglycerate kinase
                   (AA 1 - 401) [Triticum aestivum]
Seq. No.
                   312569
                   xjt700094774.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2760844
BLAST score
                   194
                   5.0e-15
E value
Match length
                   49
                   80
% identity
NCBI Description
                   (AC003105) hypothetical protein [Arabidopsis thaliana]
                   312570
Seq. No.
                   xjt700094938.h1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2981213
BLAST score
                   35
                   2.0e-10
E value
Match length
                   43
```

44639

Zea mays photosystem I complex PsaN subunit precursor

(psaN) mRNA, nuclear gene encoding chloroplast protein,



```
Seq. No.
                  312571
                  xjt700094966.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4262162
BLAST score
                  267
                  1.0e-23
E value
                  86
Match length
% identity
                   (AC005275) putative glycosylation enzyme [Arabidopsis
NCBI Description
                  thaliana]
                  312572
Seq. No.
                  xjt700094969.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1617270
                  387
BLAST score
                 - 1.0e-37
E value
                   97
Match length
                   70
% identity
                  (X94624) acyl-CoA synthetase [Brassica napus]
NCBI Description
Seq. No.
                   312573
                   xjt700095034.h1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3777601
BLAST score
                   60
E value
                   4.0e-25
Match length
                   92
                   91
% identity
                  Oryza sativa clone LS195 50S ribosomal protein L10 (rpl10)
NCBI Description
                   mRNA, nuclear gene encoding chloroplast protein, complete
                   cds
Seq. No.
                   312574
                   xjt700095059.h1
Seq. ID
Method
                   BLASTN
                   g3821780
                                                                   Sil.
NCBI GI
BLAST score
                   36
E value
                   6.0e-11
Match length
                   36
                   100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                   312575
Seq. No.
                   xjt700095071.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2832717
BLAST score
                   488
                   1.0e-49
E value
Match length
                   94
                   98
% identity
NCBI Description (AJ003114) alkaline/neutral invertase [Lolium temulentum]
```

Seq. No. xjt700095106.h1 Seq. ID

312576

Method BLASTX

44640

```
g4314401
NCBI GI
                  144
BLAST score
                  2.0e-09
E value
Match length
                  48
% identity
                  56
                  (AC006232) putative beta-1,3-glucanase [Arabidopsis
NCBI Description
                  thaliana]
                  312577
Seq. No.
                  xjt700095111.hl
Seq. ID
                  BLASTN
Method
                  g168438
NCBI GI
BLAST score
                  57
                  8.0e-24
E value
Match length
                  93
% identity
                   92
                  Zea mays light harvesting chlorophyll a/b binding protein
NCBI Description
                   (cab-m1) gene, 5' end
                   312578
Seq. No.
                   xjt700095137.h1
Seq. ID
Method
                  BLASTX
                   g2058273
NCBI GI
BLAST score
                   329
                   7.0e-31
E value
                   83
Match length
% identity
                   80
NCBI Description
                  (D83527) YK426 [Oryza sativa]
                   312579
Seq. No.
                   xjt700095220.h1
Seq. ID
Method
                   BLASTX
                   g2275199
NCBI GI
BLAST score
                   228
                   4.0e-19
E value
Match length
                   65
% identity
                   75
                   (AC002337) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   312580
Seq. No.
                   xjt700095231.h1
Seq. ID
                   BLASTX
Method
                   q3724087
NCBI GI
                   182
BLAST score
                   1.0e-13
E value
                   38
Match length
                   87
% identity
                   (AJ011840) 1-deoxyxylulose 5-phosphate synthase
NCBI Description
                   [Catharanthus roseus]
```

Seq. No. 312581

Seq. ID xjt700095252.h1 Method BLASTN

Method BLASTN
NCBI GI g564023
BLAST score 57
E value 2.0e-23
Match length 166



% identity NCBI Description Zea mays dihydrolipoamide acetyl transferase (ZM/DHLAAT) mRNA, complete cds 312582 Seq. No. Seq. ID xjt700095318.h1 BLASTX Method NCBI GI q2541876 BLAST score 237 6.0e-20 E value 128 Match length 39 % identity (D26015) CND41, chloroplast nucleoid DNA binding protein NCBI Description [Nicotiana tabacum] 312583 Seq. No. xjt700095345.h1 Seq. ID Method BLASTX g4006905 NCBI GI BLAST score 469 4.0e-47 E value 124 Match length % identity (Z99708) ATPase-like protein [Arabidopsis thaliana] NCBI Description 312584 Seq. No. xjt700095355.h1 Seq. ID BLASTX Method g4006867 NCBI GI BLAST score 333 E value 2.0e-31 106 Match length % identity 67 (Z99707) putative protein [Arabidopsis thaliana] NCBI Description Seq. No. 312585 xjt700095363.h1 Seq. ID Method BLASTX NCBI GI g168586 BLAST score 403 1.0e-39 E value Match length 79 % identity 99 (M58656) pyruvate, orthophosphate dikinase [Zea mays] NCBI Description Seq. No. 312586 xjt700095392.h1 Seq. ID Method BLASTX NCBI GI g3335372 179 BLAST score E value 3.0e-13

78 Match length 45 % identity

(AC003028) putative SRG1 protein [Arabidopsis thaliana] NCBI Description

Seq. No. 312587

xjt700095456.h1 Seq. ID

44642

```
BLASTX
Method
                   g2134385
NCBI GI
                   299
BLAST score
                   2.0e-33
E value
                   98
Match length
                   73
% identity
                  protein kinase - chicken >gi_571460 (U16656) protein kinase
NCBI Description
                   [Gallus gallus]
                   312588
Seq. No.
                   xjt700095464.h1
Seq. ID
Method
                   BLASTX
                   q558367
NCBI GI
                   178
BLAST score
                   4.0e-13
E value
                   33
Match length
                   100
% identity
                   (X81830) cytochrome P450 [Zea mays]
NCBI Description
                   312589
Seq. No.
                   xjt700095471.h1
Seq. ID
Method
                   BLASTN
                   g397395
NCBI GI
                   194
BLAST score
                   1.0e-105
E value
                   194
Match length
                   100
% identity
NCBI Description Z.mays MNB1b mRNA for DNA-binding protein
                   312590
Seq. No.
                   xjt700095480.hl
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4581205
                   221
BLAST score
                   2.0e-19
E value
                   72
Match length
                   68
% identity
                   (Y17913) cyclic nucleotide and calmodulin-regulated ion
NCBI Description
                   channel [Arabidopsis thaliana]
                   312591
Seq. No.
                   xjt700095484.h1
Seq. ID
                   BLASTX
Method
                   g3885896
NCBI GI
                   304
BLAST score
                   5.0e-28
E value
                   93
Match length
                    66
 % identity
                   (AF093636) plastocyanin precursor [Oryza sativa]
 NCBI Description
                    312592
 Seq. No.
 Seq. ID
                    xjt700095507.h1
                    BLASTX
 Method
                    g4455232
 NCBI GI
 BLAST score
                    306
                    4.0e-28
 E value
```

108

Match length

% identity



```
% identity
NCBI Description (AL035523) putative protein [Arabidopsis thaliana]
                  312593
Seq. No.
                  xjt700095534.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3193284
                  207
BLAST score
                  1.0e-24
E value
                  88
Match length
% identity
                  (AF069298) No definition line found [Arabidopsis thaliana]
NCBI Description
                  312594
Seq. No.
                  xit700095543.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2829925
BLAST score
                  159
                   6.0e-11
E value
Match length
                   41
% identity
                   68
                   (AC002291) Similar to dnaj-like protein, gp_Y11969_2230757
NCBI Description
                   [Arabidopsis thaliana]
                   312595
Seq. No.
                   xjt700095546.h1
Seq. ID
Method
                   BLASTX
                   q2499708
NCBI GI
BLAST score
                   164
                   2.0e-11
E value
                   44
Match length
                   86
% identity
                   PHOSPHOLIPASE D PRECURSOR (PLD) (CHOLINE PHOSPHATASE)
NCBI Description
                   (PHOSPHATIDYLCHOLINE-HYDROLYZING PHOSPHOLIPASE D)
                   >qi 1020409 dbj BAA11135_ (D73410) phospholipase D [Zea
                   mays]
                   312596
Seq. No.
Seq. ID
                   xjt700095577.h1
Method
                   BLASTX
                   g1129134
NCBI GI
                   348
BLAST score
                   4.0e-33
E value
Match length
                   87
                   75
% identity
                   (X94105) old yellow enzyme NADPH dehydrogenase [Chenopodium
NCBI Description
                   rubrum]
                   312597
Seq. No.
                   xjt700095591.h1
Seq. ID
                   BLASTX
Method
                   g4587572
NCBI GI
                   200
BLAST score
                   9.0e-16
E value
                   76
Match length
                   57
```

NCBI Description (AC006550) Similar to gb_U70015 lysosomal trafficking



90

63

Match length % identity

NCBI Description

regulator from Mus musculus and contains 2 PF_00400 WD40, G-beta repeats. ESTs gb_T43386 and gb_AA395236 come from this gene. [Arabidopsis thaliana]

312598 Seq. No. Seq. ID xjt700095601.h1 BLASTX Method g3036816 NCBI GI 201 BLAST score 8.0e-16 E value 71 Match length % identity 54 (AL022373) myosin-like protein [Arabidopsis thaliana] NCBI Description 312599 Seq. No. Seq. ID xjt700095620.h1 Method BLASTX NCBI GI g417745 BLAST score 431 7.0e-43 E value 103 Match length 83 % identity ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE NCBI Description HYDROLASE) (ADOHCYASE) >gi 170773 (L11872) S-adenosyl-L-homocysteine hydrolase [Triticum aestivum] 312600 Seq. No. xjt700095629.h1 Seq. ID BLASTX Method NCBI GI g1572819 BLAST score 162 3.0e-11 E value Match length 63 52 % identity (U70855) similar to the RAS gene family [Caenorhabditis NCBI Description elegans] Seq. No. 312601 xjt700095644.h1 Seq. ID Method BLASTX NCBI GI g2708331 BLAST score 209 E value 7.0e-17 Match length 66 59 % identity (AF038557) ligand gated channel-like protein [Arabidopsis NCBI Description thaliana] Seq. No. 312602 xjt700095774.h1 Seq. ID Method BLASTX g543938 NCBI GI BLAST score 293 E value 1.0e-26

44645

CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR



(CAB48) (LHCP) >gi_82681_pir__S22497 chlorophyll a/b-binding protein precursor (cab-48) - maize >gi 22228_emb CAA44888_ (X63205) chlorophyll a /b binding

protein [Zea mays]

312603 Seq. No.

xjt700095819.h1 Seq. ID

BLASTX Method NCBI GI q4587556 392 BLAST score 3.0e-38 E value 100 Match length % identity 71

(AC006577) Similar to gi 1653162 (p)ppGpp NCBI Description

3-pyrophosphohydrolase from Synechocystis sp genome

gb D90911. EST gb W43807 comes from this gene.

[Arabidopsis thaliana]

312604 Seq. No.

xjt700095850.h1 Seq. ID

BLASTX Method g1870700 NCBI GI 181 BLAST score E value 6.0e-1437 Match length 100 % identity

NCBI Description (U84116) cleavage stage histone H3 [Psammechinus miliaris]

312605 Seq. No.

Seq. ID xjt700095856.h1

BLASTN Method NCBI GI g468491 BLAST score 38 4.0e-12 E value 106 Match length % identity 84

NCBI Description Rice mRNA for lipoxygenase

312606 Seq. No.

xjt700095874.h1 Seq. ID

BLASTX Method NCBI GI q3413423 BLAST score 166 E value 8.0e-12 50 Match length 58 % identity

(AJ006309) hypothetical protein [Arabidopsis thaliana] NCBI Description

312607 Seq. No.

xjt700095882.h1 Seq. ID

Method BLASTX q4586056 NCBI GI BLAST score 206 E value 1.0e-16 Match length 77 55 % identity

(AC007020) unknown protein [Arabidopsis thaliana] NCBI Description



```
312608
Seq. No.
                  xjt700095904.h1
Seq. ID
                  BLASTX
Method
                  g4335735
NCBI GI
                  244
BLAST score
                   6.0e-21
E value
Match length
                  93
% identity
                   48
                   (AC006248) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  312609
Seq. No.
                  xjt700095936.h1
Seq. ID
Method
                  BLASTX
                   g283004
NCBI GI
                   153
BLAST score
                   2.0e-10
E value
Match length
                   45
                   67
% identity
                   DNA-binding protein Gt-2 - rice >gi_20249_emb_CAA48328_
NCBI Description
                   (X68261) gt-2 [Oryza sativa]
                   312610
Seq. No.
                   xjt700095940.h1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3789951
BLAST score
                   36
                   7.0e-11
E value
Match length
                   60
                   90
% identity
                   Oryza sativa chlorophyll a/b-binding protein presursor
NCBI Description
                   (Cab27) mRNA, nuclear gene encoding chloroplast protein,
                   complete cds
Seq. No.
                   312611
                   xjt700095947.h1
Seq. ID
                   BLASTX
Method
                   g3445208
NCBI GI
                   186
BLAST score
                   3.0e-14
E value
                   95
Match length
                   48
% identity
                   (AC004786) putative amino-acid acetyltransferase
NCBI Description
                   [Arabidopsis thaliana]
                   312612
Seq. No.
                   xjt700095948.h1
Seq. ID
                   BLASTX
Method
                   g1352468
NCBI GI
                   411
BLAST score
                   1.0e-40
E value
                   96
Match length
                   85
% identity
                   BETA-FRUCTOFURANOSIDASE 1 PRECURSOR (SUCROSE-6-PHOSPHATE
NCBI Description
                   HYDROLASE 1) (INVERTASE 1) >gi_1122439 (U16123) invertase
```

[Zea mays]



```
312613
Seq. No.
                  xjt700095949.h1
Seq. ID
                  BLASTN
Method
                  g556557
NCBI GI
                  38
BLAST score
                  1.0e-12
E value
Match length
                  46
                  96
% identity
                  Rice mRNA for homologue of Tat binding protein, complete
NCBI Description
                  312614
Seq. No.
                  xjt700095983.h1
Seq. ID
                  BLASTX
Method
                  g283004
NCBI GI
                  278
BLAST score
                   7.0e-25
E value
                   58
Match length
                   44
% identity
                  DNA-binding protein Gt-2 - rice >gi_20249_emb_CAA48328_
NCBI Description
                   (X68261) gt-2 [Oryza sativa]
                   312615
Seq. No.
                   xjt700095985.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                 ্র g4539333
                   173
BLAST score
                   1.0e-12
E value
                   88
Match length
                   49
% identity
                   (AL035539) putative amino acid transport protein
NCBI Description
                   [Arabidopsis thaliana]
                   312616
Seq. No.
                   xjt700095994.h1
Seq. ID
                   BLASTX
Method
                   g3242708
NCBI GI
                   163
                                                                ٥,
BLAST score
                   2.0e-11
E value
                   96
Match length
                   36
% identity
                   (AC003040) putative serine/threonine protein kinase
NCBI Description
                   [Arabidopsis thaliana]
                   312617
Seq. No.
                   xit700096064.h1
Seq. ID
                   BLASTX
Method
                   q763046
NCBI GI
BLAST score
                   283
                   2.0e-25
E value
                   87
Match length
% identity
                   (U23787) 4-hydroxycinnamic acid: CoA ligase [Sorghum
NCBI Description
                   bicolor]
```

44648

312618

xjt700096068.hl

Seq. No.

Seq. ID

E value

4.0e-46



```
Method
                  BLASTX
NCBI GI
                  g3128193
                  278
BLAST score
                  7.0e-25
E value
                  101
Match length
                   51
% identity
NCBI Description (AC004521) hypothetical protein [Arabidopsis thaliana]
                  312619
Seq. No.
Seq. ID
                  xjt700096087.h1
                  BLASTX
Method
NCBI GI
                   g4454468
BLAST score
                   332
                   3.0e-31
E value
                   102
Match length
                   59
% identity
                  (AC006234) putative NADH dehydrogenase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   312620
Seq. ID
                  xjt700096091.h1
Method
                  BLASTN
NCBI GI
                   g1870200
BLAST score
                   190
E value
                   1.0e-103
                   238
Match length
                   95
% identity
NCBI Description
                  Z.mays cyp71c2 gene
                   312621
Seq. No.
                   xjt700096114.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3044218
                   289
BLAST score
E value
                   3.0e-26
                   63
Match length
% identity
NCBI Description
                  (AF057144) signal peptidase [Arabidopsis thaliana]
                   312622
Seq. No.
                   xjt700096150.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2388578
BLAST score
                   192
E value
                   8.0e-15
Match length
                   59
                   61
% identity
NCBI Description
                   (AC000098) Similar to Mycobacterium RlpF (gb_Z84395). ESTs
                   gb T75785,gb R30580,gb T04698 come from this gene.
                   [Arabidopsis thaliana]
Seq. No.
                   312623
Seq. ID
                   xjt700096208.h1
Method
                   BLASTX
NCBI GI
                   q554565
BLAST score
                   459
```



```
Match length
                  100
% identity
                  (M24889) glutathione S-transferase [Artificial gene]
NCBI Description
                  312624
Seq. No.
Seq. ID
                  xjt700096286.h1
                  BLASTN
Method
                  g3851002
NCBI GI
BLAST score
                  68
E value
                  4.0e-30
                  194
Match length
                  95
% identity
                  Zea mays pyruvate dehydrogenase E1 beta subunit isoform 3
NCBI Description
                  mRNA, nuclear gene encoding mitochondrial protein, complete
                  cds
```

312625 Seq. No. Seq. ID xjt700096293.h1 Method BLASTN

NCBI GI g1870200 132 BLAST score E value 3.0e-68 Match length 267 91 % identity

Z.mays cyp71c2 gene NCBI Description

312626 Seq. No. Seq. ID xjt700096323.h1 Method BLASTX NCBI GI g2935342 BLAST score 254 E value 4.0e-22 Match length 62

% identity 81

(AF044216) steroid 22-alpha-hydroxylase; DWF4; CYP90B1 NCBI Description

[Arabidopsis thaliana]

312627 Seq. No.

Seq. ID xjt700096368.h1

BLASTX Method g4001805 NCBI GI BLAST score 183 E value 9.0e-14 Match length 46 72 % identity

NCBI Description (AF041476) BAF53a [Mus musculus]

312628 Seq. No.

Seq. ID xjt700096384.h1

Method BLASTX NCBI GI g217909 BLAST score 370 E value 1.0e-35 Match length 82 % identity

(D14044) glycolate oxidase [Cucurbita sp.] NCBI Description

```
312629
Seq. No.
Seq. ID
                  xjt700096447.h1
Method
                  BLASTX
NCBI GI
                   q131772
BLAST score
                   338
E value
                   4.0e-32
                   68
Match length
                   99
% identity
                   40S RIBOSOMAL PROTEIN S14 (CLONE MCH1)
NCBI Description
                   >gi 82723 pir A30097 ribosomal protein S14 (clone MCH1) -
                  maize
                   312630
Seq. No.
                   xjt700096545.h1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g82080
BLAST score
                   212
                   3.0e-17
E value
Match length
                   60
                   70
% identity
                   chlorophyll a/b-binding protein type III precursor - tomato
NCBI Description
                   >qi 226872 prf 1609235A chlorophyll a/b binding protein
                   [Lycopersicon esculentum]
                   312631
Seq. No.
                   xjt700096547.h1
Seq. ID
Method
                   BLASTX
                   g2911052
NCBI GI
                   155
BLAST score
                   1.0e-10
E value
                   94
Match length
% identity
                   (AL021961) putative protein [Arabidopsis thaliana]
NCBI Description
                   312632
Seq. No.
Seq. ID
                   xjt700096581.h1
Method
                   BLASTX
NCBI GI
                   g3153902
BLAST score
                   234
E value
                   1.0e-21
```

Match length 74 % identity 84

(AF066076) 14-3-3-like protein [Helianthus annuus] NCBI Description

Seq. No. 312633

Seq. ID xjt700096610.h1

Method BLASTX NCBI GI g1053047 BLAST score 407 E value 5.0e-40 Match length 81 % identity 100

(U38425) histone H3 [Glycine max] >gi_1053049 (U38426) NCBI Description

histone H3 [Glycine max] >gi_1053051 (U38427) histone H3

[Glycine max]

312634 Seq. No.



```
xjt700096630.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2281090
BLAST score
                  194
E value
                  4.0e-15
Match length
                  87
% identity
                  (AC002333) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  312635
Seq. No.
Seq. ID
                  xjt700096643.h1
                  BLASTX
Method
NCBI GI
                  g1169286
BLAST score
                  142
E value
                  2.0e-09
Match length
                  59
% identity
                  47
NCBI Description
                  BETAINE-ALDEHYDE DEHYDROGENASE PRECURSOR (BADH)
                  >gi_1085671_pir__S49205 betaine-aldehyde dehydrogenase (EC
                  1.2.1.8) precursor - Atriplex hortensis
                  >gi 510574 emb CAA49425 (X69770) betaine-aldehyde
                  dehydrogenase [Atriplex hortensis]
Seq. No.
                  312636
                  xjt700096679.h1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1351904
BLAST score
                  369
E value
                  1.0e-35
Match length
                  76
% identity
                  100
                  ASPARTOKINASE 1 / HOMOSERINE DEHYDROGENASE 1 CHLOROPLAST
NCBI Description
                  PRECURSOR (AK-HSDH 1) (AKHSDH1) >qi 500851 (L33912)
                  aspartate kinase-homoserine dehydrogenase [Zea mays]
Seq. No.
                  312637
Seq. ID
                  xjt700096687.h1
Method
                  BLASTX
NCBI GI
                  q4538968
BLAST score
                  212
E value
                  3.0e-17
Match length
                  83
% identity
NCBI Description
                  (AL049488) putative protein kinase [Arabidopsis thaliana]
Seq. No.
                  312638
                  xjt700096705.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1350821
BLAST score
                  170
                  3.0e-12
E value
```

Match length 42 % identity 79

NCBI Description CHLOROPLAST 31 KD RIBONUCLEOPROTEIN PRECURSOR

>gi 280403 pir S26204 RNA-binding protein 31 -

curled-leaved tobacco >gi 19710 emb CAA46233 (X65117) RNA

binding protein 31 [Nicotiana plumbaginifolia]

```
312639
Seq. No.
Seq. ID
                  xjt700096785.h1
                  BLASTX
Method
NCBI GI
                  g2118425
BLAST score
                  254
                  4.0e-22
E value
                  61
Match length
% identity
                  subtilisin/chymotrypsin inhibitor - maize
NCBI Description
                  >qi 475253 emb CAA55588 (X78988) proteinase inhibitor [Zea
                  mays] >gi 475922 emb CAA49593 (X69972) proteinase
                  inhibitor [Zea mays] >gi_559538_emb_CAA57677_ (X82187)
                  substilin /chymotrypsin-like inhibitor [Zea mays]
                  312640 -
Şeq. No.
                xjt700096789.h1
BLASTX
 · ID
Method
NCBI GI
                  g100226
BLAST score
                  148
                  1.0e-09
E value
                  60
Match length
                  47
% identity
                  hypothetical protein - tomato >gi 19275 emb_CAA78112_
NCBI Description
                  (Z12127) protein of unknown function [Lycopersicon
                  esculentum] >gi 445619 prf 1909366A Leu zipper protein
                  [Lycopersicon esculentum]
                  312641
Seq. No.
Seq. ID
                  xjt700096833.h1
                  BLASTX
Method
NCBI GI
                  g2344901
BLAST score
                  160
                  3.0e-11
E value
Match length
                  81
% identity
                  (AC002388) serine/threonine protein kinase isolog
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  312642
Seq. ID
                  xjt700096845.h1
                  BLASTX
Method
NCBI GI
                  q1168470
BLAST score
                  158
E value
                  7.0e-11
Match length
                  92
% identity
NCBI Description
                  PROTEIN KINASE APK1A >gi 282877 pir S28615 protein kinase,
                  tyrosine/serine/threonine-specific (EC 2.7.1.-) -
                  Arabidopsis thaliana >gi 217829 dbj_BAA02092_ (D12522)
                  protein tyrosine-serine-threonine kinase [Arabidopsis
                  thaliana]
```

 Seq. No.
 312643

 Seq. ID
 xjt700096848.h1

 Method
 BLASTX

 NCBI GI
 g114335



```
BLAST score
  E value
                    2.0e-14
  Match length
                    40
                    95
  % identity
  NCBI Description
                    PLASMA MEMBRANE ATPASE 2 (PROTON PUMP)
                    >gi 67973 pir PXMUP2 H+-transporting ATPase (EC 3.6.1.35)
                    type 2, plasma membrane - Arabidopsis thaliana >gi 166629
                    (J05570) H+-ATPase [Arabidopsis thaliana]
  Seq. No.
                    312644
  Seq. ID
                    xjt700096903.h1
  Method
                    BLASTX
  NCBI GI
                    g2880048
  BLAST score
                    305
  E value
                    5.0e-32
  Match length
                    86
  % identity.
                                                                         NCBI Description
                    (AC002340) unknown protein [Arabidopsis thaliana]
                    312645
  Seq. No.
  Seq. ID
                    xjt700096916.h1
  Method
                    BLASTX
  NCBI GI
                    g1730713
  BLAST score
                    151
  E value
                    6.0e-10
  Match length
                    52
                    50
  % identity
                    HYPOTHETICAL 108.5 KD PROTEIN IN UME3-PUB1 INTERGENIC
  NCBI Description
                    REGION >gi_2131866_pir__S62935 hypothetical protein YNL023c

    yeast (Saccharomyces cerevisiae)

                    >gi 1301855 emb CAA95885 (Z71299) ORF YNL023c
                    [Saccharomyces cerevisiae]
  Seq. No.
                    312646
  Seq. ID
                    xjt700096952.h1
  Method
                    BLASTX
  NCBI GI
                    q4455350
  BLAST score
                    245
  E value
                    5.0e-21
  Match length
                    60
  % identity
  NCBI Description
                    (AL035524) putative protein [Arabidopsis thaliana]
  Seq. No.
                    312647
                    xjt700096967.h1
  Seq. ID
  Method
                    BLASTX
  NCBI GI
                    q2959767
  BLAST score
                    183
  E value
                    8.0e-16
```

Match length 97

% identity 46

(AJ002584) AtMRP4 [Arabidopsis thaliana] >gi 3738292 NCBI Description (AC005309) glutathione-conjugate transporter AtMRP4

[Arabidopsis thaliana]

Seq. No. 312648

xmt700256711.h1 Seq. ID

```
Method
                  BLASTX
NCBI GI
                  g2245135
BLAST score
                  226
E value
                  1.0e-22
Match length
                  96
                  58
% identity
                  (Z97344) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  312649
Seq. No.
                  xmt700256712.h1
Seq. ID
Method
                  BLASTX
                  g2119719
NCBI GI
BLAST score
                  234
                   9.0e-20
E value
Match length
                   56
% identity
                  82
                  heat-shock cognate protein 70-3 - tomato >gi 762844
NCBI Description
                   (L41253) Hsc70 [Lycopersicon esculentum]
Seq. No.
                   312650
Seq. ID
                  xmt700256768.h1
                  BLASTX
Method
                   g1113941
NCBI GI
BLAST score
                   174
E value
                   1.0e-12
Match length
                   54
% identity
                  (U40713) Pv42p [Phaseolus vulgaris]
NCBI Description
                   312651
Seq. No.
                   xmt700256830.h1
Seq. ID
Method
                   BLASTX
                   g3913239
NCBI GI
BLAST score
                   391
                   2.0e-38
E value
Match length
                   81
                   96
% identity
                   PROBABLE 1-DEOXYXYLULOSE-5-PHOSPHATE SYNTHASE (DXP
NCBI Description
                   SYNTHASE) >gi_2612941 (AF024512) CLA1 transketolase-like
                   protein [Oryza sativa]
Seq. No.
                   312652
                   xmt700256866.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4455331
BLAST score
                   153
                   3.0e-10
E value
Match length
                   76
% identity
                   42
NCBI Description
                  (AL035525) putative protein [Arabidopsis thaliana]
```

Seq. No. 312653

Seq. ID xmt700256875.h1

Method BLASTX
NCBI GI g4539005
BLAST score 249
E value 1.0e-21

Match length

% identity

54 91



```
Match length
                  49
% identity
NCBI Description (AL049481) putative oxidoreductase [Arabidopsis thaliana]
Seq. No.
                  312654
                  xmt700256890.h1
Seq. ID
                  BLASTX
Method
                  q2267006
NCBI GI
BLAST score
                  331
                  3.0e-31
E value
Match length
                  66
                  100
% identity
NCBI Description (AF006825) endosperm lumenal binding protein [Oryza sativa]
Seq. No.
                  312655
                  xmt700256923.h1
Seq. ID
                  BLASTX
Method
NĈBI GI
                  g119355
                  169
BLAST score
                  2.0e-12
E value
Match length
                  43
% identity
                  86
                  ENOLASE 1 (2-PHOSPHOGLYCERATE DEHYDRATASE 1)
NCBI Description
                  (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE 1)
                  >gi 100869 pir S16257 phosphopyruvate hydratase (EC
                  4.2.1.11) - maize >gi_22273_emb_CAA39454_ (X55981) enolase
                  [Zea mays]
Seq. No.
                  312656
                  xmt700256931.h1
Seq. ID
Method
                  BLASTN
                  g687244
NCBI GI
BLAST score
                  159
                  2.0e-84
E value
                  202
Match length
% identity
                  95
NCBI Description Zea mays oil body protein 16 kDa oleosin (ole16) gene,
                  complete cds
                  312657
Seq. No.
                  xmt700256940.h1
Seq. ID
                  BLASTN
Method
                  g1129085
NCBI GI
                  49
BLAST score
                  9.0e-19
E value
Match length
                  77
                  91
% identity
NCBI Description Wheat mRNA for protein H2A, complete cds, clone wcH2A-9
                  312658
Seq. No.
                  xmt700257028.h1
Seq. ID
Method
                  BLASTX
                  g1710077
NCBI GI
BLAST score
                  272
                  2.0e-24
E value
```



(

NCBI Description PEROXIREDOXIN (REHYDRIN HOMOLOG) (B15C)

>gi 2130029 pir S60285 B15C protein - barley

>gi_471321 emb_CAA54066 (X76605) HvB15C [Hordeum vulgare]
>gi_1694833_emb_CAA65387 (X96551) peroxiredoxin [Hordeum

vulgare]

Seq. No. 312659

Seq. ID xmt700257203.h1

Method BLASTX
NCBI GI g2501190
BLAST score 195
E value 2.0e-15
Match length 48
% identity 83

NCBI Description THIAMINE BIOSYNTHETIC ENZYME 1-2 PRECURSOR

>gi_2130147_pir__S61420 thiamine biosynthetic enzyme thil-2
- maize >gi_596080 (U17351) thiamine biosynthetic enzyme

[Zea mays]

Seq. No. 312660

Seq. ID xmt700257240.h1

Method BLASTX
NCBI GI g1352681
BLAST score 175
E value 3.0e-13
Match length 41
% identity 80

NCBI Description PROTEIN PHOSPHATASE 2C (PP2C) >gi 1076391 pir __S55457

phosphoprotein phosphatase (EC $3.\overline{1}.3.16$) $\overline{2}C$ - Arabidopsis

thaliana >gi 633028 dbj BAA07287 (D38109) protein

phosphatase 2C [Arabidopsis thaliana]

Seq. No. 312661

Seq. ID xmt700257277.h1

Method BLASTX
NCBI GI g2911067
BLAST score 214
E value 9.0e-18
Match length 48
% identity 79

NCBI Description (AL021960) UV-damaged DNA-binding protein-like [Arabidopsis

thaliana]

Seq. No. 312662

Seq. ID xmt700257310.h1

Method BLASTN
NCBI GI g473602
BLAST score 204
E value 1.0e-111
Match length 261
% identity 95

NCBI Description Zea mays W-22 histone H2A mRNA, complete cds

Seq. No. 312663

Seq. ID xmt700257319.h1

Method BLASTX NCBI GI g2058280

E value

Match length

% identity



```
BLAST score
E value
                  7.0e-15
Match length
                  41
                  88
% identity
NCBI Description
                  (X97381) atran3 [Arabidopsis thaliana]
                  312664
Seq. No.
Seq. ID
                  xmt700257369.h1
Method
                  BLASTN
NCBI GI
                  g3108052
BLAST score
                  36
E value
                   4.0e-11
                   68
Match length
                  88
% identity
                  Zea mays myo-inositol 1-phosphate synthase mRNA, complete
NCBI Description
Seq. No.
                  312665
Seq. ID
                  xmt700257375.h1
Method
                  BLASTN
NCBI GI
                  g2345153
BLAST score
                  195
E value
                  1.0e-106
Match length
                  218
% identity
                   98
NCBI Description
                  Zea mays ribsomal protein S4 (rps4) mRNA, complete cds
                  312666
Seq. No.
Seq. ID
                  xmt700257483.h1
Method
                  BLASTX
NCBI GI
                  g3482916
BLAST score
                  151
                   4.0e-10
E value
                  95
Match length
                   36
% identity
NCBI Description
                  (AC003970) Hypothetical protein [Arabidopsis thaliana]
                  312667
Seq. No.
                  xmt700257707.h1
Seq. ID
Method
                  BLASTX
                   g1336084
NCBI GI
BLAST score
                   151
                   2.0e-10
E value
Match length
                  53
% identity
                  53
                   (U56635) Arabidopsis thaliana glutamate dehydrogenase 2
NCBI Description
                   (GDH2) mRNA, complete cds. [Arabidopsis thaliana]
                   312668
Seq. No.
Seq. ID
                  xmt700257728.h1
Method
                  BLASTX
                   g417154
NCBI GI
BLAST score
                   139
```

6.0e-09

36 83

44658

NCBI Description HEAT SHOCK PROTEIN 82 >gi 100685 pir S25541 heat shock

protein 82 - rice (strain Taichung Native One) >gi 20256 emb_CAA77978_ (Z11920) heat shock protein 82 (HSP82) [Oryza sativa]

Seq. No. 312669

xmt700257736.h1 Seq. ID

BLASTX Method q1710078 NCBI GI BLAST score 161 E value 1.0e-11 Match length 41

% identity 71

NCBI Description RAB24 PROTEIN >gi_971280 dbj_BAA09947 (D63917) RAB24

protein [Oryza sativa]

Seq. No. 312670

xmt700257837.h1 Seq. ID

Method BLASTN NCBI GI g3452291 BLAST score 98 E value 5.0e-48 Match length 152 % identity 92

NCBI Description Zea mays retrotransposon Huck-2 3' LTR, partial sequence

Seq. No. 312671

xmt700258007.h1 Seq. ID

Method BLASTX NCBI GI g3860245 BLAST score 214 2.0e-17 E value Match length 66 59 % identity

(AC005824) putative argonaute protein [Arabidopsis NCBI Description

thaliana]

312672 Seq. No.

xmt700258048.h1 Seq. ID

Method BLASTX g1495768 NCBI GI BLAST score 176 3.0e-13E value Match length 52

% identity 65

(Z68506) chloroplast inner envelope protein, 110 kD NCBI Description

(IEP110) [Pisum sativum]

312673 Seq. No.

xmt700258052.h1 Seq. ID

Method BLASTX g1703574 NCBI GI BLAST score 165 E value 1.0e-11 Match length 80 45 % identity

NCBI Description (U80437) C43E11.9 [Caenorhabditis elegans]



```
312674
Seq. No.
                  xmt700258072.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3452306
BLAST score
                  89
                  2.0e-42
E value
Match length
                  97
                  98
% identity
NCBI Description Zea mays retrotransposon Opie-3 5' LTR, partial sequence
Seq. No.
                  312675
                  xmt700258118.hl
Seq. ID
Method
                  BLASTX
                  g4512698
NCBI GI
BLAST score
                  180
E value
                  9.0e-14
                  53
Match length
% identity
                  68
                  (AC006569) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  312676
                  xmt700258186.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3201541
BLAST score
                  344
E value
                  1.0e-32
Match length
                  74
% identity
                  86
                  (AJ005077) TCTR2 protein [Lycopersicon esculentum]
NCBI Description
                   312677
Seq. No.
                   xmt700258196.h1
Seq. ID
Method
                  BLASTX
                   g3201626
NCBI GI
BLAST score
                   326
                   1.0e-30
E value
Match length
                   94
                   65
% identity
                   (AC004669) putative protein kinase MAP3K [Arabidopsis
NCBI Description
                   thaliana]
                   312678
Seq. No.
                   xmt700258217.h1
Seq. ID
Method
                   BLASTX
                   q3128195
NCBI GI
BLAST score
                   254
E value
                   2.0e-22
Match length
                   56
                   86
% identity
                   (AC004521) putative phosphoribosyl pyrophosphate synthetase
NCBI Description
                   [Arabidopsis thaliana] >gi_3341673 (AC003672) putative
```

phosphoribosyl pyrophosphate synthetase [Arabidopsis

thaliana]

312679 Seq. No.

xmt700258240.h1 Seq. ID

Method BLASTX

```
g2618689
NCBI GI
                  140
BLAST score
                  8.0e-09
E value
                  38
Match length
                  74
% identity
                  (AC002510) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  312680
                  xmt700258275.h1
Seq. ID
                  BLASTN
Method
                  g1620544
NCBI GI
                  34
BLAST score
                  1.0e-09
E value
Match length
                  34
                  100
% identity
NCBI Description Sorghum bicolor hypothetical URF107 mRNA, complete cds
                  312681
Seq. No.
                  xmt700258317.h1
Seq. ID
                  BLASTX
Method
                  g3925225
NCBI GI
BLAST score
                  166
                  8.0e-12
E value
Match length
                  34
                   100
% identity
                   (AF037030) 6-phosphogluconate dehydrogenase isoenzyme B
NCBI Description
                   [Zea mays]
                   312682
Seq. No.
                  xmt700258323.h1
Seq. ID
                  BLASTX
Method
                   g547818
NCBI GI
                   174
BLAST score
                   9.0e-13
E value
Match length
                   40
% identity
                  LATE EMBRYOGENESIS ABUNDANT PROTEIN B19.3 (LEA B19.3)
NCBI Description
                   >gi 542123 pir S36751 embryonic abundant protein B19.3 -
                   barley >gi 19015 emb CAA44623 (X62805) LEA B19.3 [Hordeum
                   vulgare]
                   312683
Seq. No.
                   xmt700258361.h1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g126078
BLAST score
                   161
                   1.0e-11
E value
                   58
Match length
                   53
% identity
```

NCBI Description

LATE EMBRYOGENESIS ABUNDANT PROTEIN D-34 (LEA D-34)
>gi_81554_pir__S04046 embryonic abundant protein gD-34 upland cotton >gi_18501_emb_CAA31594_ (X13206) D-34 Lea
protein [Gossypium hirsutum] >gi_167385 (M19389) storage
protein [Gossypium hirsutum] >gi_226556_prf__1601521F Lea

D-34 gene [Saguinus oedipus]

Seq. No.



```
xmt700258364.h1
Seq. ID
                  BLASTN
Method
                  g1213279
NCBI GI
BLAST score
                  38
E value
                  2.0e-12
Match length
                  38
% identity
                  100
                  Z.mays ZEMc gene
NCBI Description
                  312685
Seq. No.
Seq. ID
                  xmt700258377.h1
                  BLASTX
Method
                   g3287696
NCBI GI
                   398
BLAST score
                   5.0e-39
E value
                   98
Match length
% identity
                   (AC003979) Strong similarity to phosphoribosylanthranilate
NCBI Description
                   transferase gb D86180 from Pisum sativum. This ORF may be
                   part of a larger gene that lies in the overlapping region.
                   [Arabidopsis thaliana]
Seq. No.
                   312686
                   xmt700258392.h1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g584867
BLAST score
                   305
E value
                   4.0e-28
                   93
Match length
% identity
                   CYTOCHROME P450 77A2 (CYPLXXVIIA2) (P-450EG5)
NCBI Description
                   >qi 481959 pir S40266 gene CYP77A2 protein - eggplant
                   >gi_542071_pir__S41598 cytochrome P450 77A2 - eggplant
                   >gi 438241 emb CAA50646 (X71655) CYP77A2 [Solanum
                   melongena]
                   312687
Seq. No.
Seq. ID
                   xmt700258438.h1
Method
                   BLASTX
NCBI GI
                   g2330651
BLAST score
                   281
E value
                   2.0e-25
Match length
                   61
% identity
                   84
                   (Y14559) topoisomerase II [Pisum sativum]
NCBI Description
                   312688
Seq. No.
Seq. ID
                   xmt700258460.h1
Method
                   BLASTN
                   g22340
NCBI GI
BLAST score
                   100
```

E value 2.0e-49 Match length 108 % identity 99

Maize gene for heat shock protein 70 exon 1 (hsp70; clone NCBI Description

pMON 9502)



```
312689
Seq. No.
                  xmt700258480.hl
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4455223
BLAST score
                  137
                  9.0e-09
E value
Match length
                  45
% identity
                  56
                   (AL035440) putative DNA binding protein [Arabidopsis
NCBI Description
                  thaliana]
                  312690
Seq. No.
                  xmt700258512.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3986691
BLAST score
                  389
E value
                   6.0e-38
Match length
                   86
% identity
                   (AF101421) heat shock protein [Cichorium intybus]
NCBI Description
Seq. No.
                  312691
                  xmt700258532.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g4106395
BLAST score
                   171
E value
                   4.0e-13
Match length
                   91
% identity
                   (AF073744) raffinose synthase [Cucumis sativus]
NCBI Description
Seq. No.
                   312692
                   xmt700258637.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g542182
BLAST score
                   350
E value
                   2.0e-33
Match length
                   86
% identity
                   85
                   vicilin-like storage protein Glb1-L, embryo - maize
NCBI Description
                   >gi 22284 emb CAA41809 (X59083) vicilin-like embryo
                   storage protein [Zea mays]
Seq. No.
                   312693
Seq. ID
                   xmt700258659.h1
Method
                   BLASTX
NCBI GI
                   g4580467
BLAST score
                   318
                   1.0e-29
E value
Match length
                   85
                   71
% identity
NCBI Description
                   (AC006081) putative protein phosphatase; similar to protein
                   phosphatase 2C from Mesembryanthemum [Arabidopsis thaliana]
                   312694
```

Seq. No. Seq. ID

xmt700258817.h1

Method BLASTX



```
q3334474
NCBI GI
BLAST score
                  152
                  3.0e-11
E value
Match length
                  61
% identity
                  72
NCBI Description
                  OLEOSIN ZM-I (OLEOSIN 16 KD) (LIPID BODY-ASSOCIATED MAJOR
                  PROTEIN) (LIPID BODY-ASSOCIATED PROTEIN L3)
                  >gi 1076817 pir S52029 oleosin 16 - maize >gi 687245
                  (U13701) 16 kDa oleosin [Zea mays]
Seq. No.
                  312695
Seq. ID
                  xmt700258985.h1
                  BLASTX
Method
NCBI GI
                  g2950395
BLAST score
                  323
E value
                  3.0e-30
Match length
                  97
% identity
                  72
NCBI Description (AJ224847) oxidoreductase [Zea mays]
Seq. No.
                  312696
Seq. ID
                  xmt700259025.h1
Method
                  BLASTX
NCBI GI
                  g100876
                  307
BLAST score
E value
                  2.0e-28
Match length
                  77
                  77
% identity
NCBI Description globulin-2 precursor - maize >gi_228310_prf__1802402A
                  globulin 2 [Zea mays]
Seq. No.
                  312697
Seq. ID
                  xmt700259194.h2
Method
                  BLASTX
NCBI GI
                  g3914425
BLAST score
                  303
E value
                  9.0e-37
Match length
                  96
% identity
NCBI Description
                  PROTEASOME EPSILON CHAIN PRECURSOR (MACROPAIN EPSILON
                  CHAIN) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX EPSILON CHAIN)
                  >gi 2511596 emb CAA74029.1 (Y13695) multicatalytic
                  endopeptidase complex, proteasome precursor, beta subunit
                   [Arabidopsis thaliana] >qi 3421117 (AF043536) 20S
                  proteasome beta subunit PBE1 [Arabidopsis thaliana]
Seq. No.
                  312698
                  xmt700259204.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2191144
BLAST score
                  269
```

E value 4.0e-24 Match length 78 % identity 65

NCBI Description (AF007269) A IG002N01.24 gene product [Arabidopsis

thalianal



```
312699
Seq. No.
                  xmt700259309.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2198853
BLAST score
                  516
                  8.0e-53
E value
                  104
Match length
                  100
% identity
NCBI Description (AF007786) cystathionine gamma-synthase [Zea mays]
Seq. No.
                  312700
                  xmt700259324.h1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g22281
BLAST score
                  74
E value
                   7.0e-34
Match length
                   149
% identity
                   89
                   Zea mays Glb1-0 gene for vicilin-like storage protein
NCBI Description
                   (truncated)
Seq. No.
                   312701
                   xmt700259360.h1
Seq. ID
                   BLASTN
Method
                   q4585620
NCBI GI
BLAST score
                   197
                   1.0e-107
E value
                   250
Match length
                   96
% identity
                   Zea mays hmgi/y gene, exons 1-2
NCBI Description
                   312702
Seq. No.
                   xmt700259428.h1
Seq. ID
Method
                   BLASTN
                   g168512
NCBI GI
BLAST score
                   64
                   4.0e-28
E value
Match length
                   108
% identity
                   90
                   Maize major protein (L3) mRNA from the surface of lipid
NCBI Description
                   bodies, 3' end
                   312703
Seq. No.
                   xmt700259517.h1
Seq. ID
                   BLASTX
Method
                   g3650037
NCBI GI
                   167
BLAST score
                   3.0e-12
E value
                   40
Match length
                   82
% identity
                   (AC005396) auxin-responsive GH3-like protein [Arabidopsis
NCBI Description
                   thaliana]
```

Method BLASTX NCBI GI g3913240

_



BLAST score 285 E value 8.0e-26 Match length 62 % identity 89

NCBI Description MAGNESIUM-CHELATASE SUBUNIT CHLD PRECURSOR

(MG-PROTOPORPHYRIN IX CHELATASE) (MG-CHELATASE SUBUNIT D) >gi_2239151_emb_CAA71128_ (Y10022) CHLD magnesium chelatase

subunit [Nicotiana tabacum]

Seq. No. 312705

Seq. ID xmt700259589.h1

Method BLASTX
NCBI GI g2598227
BLAST score 190
E value 1.0e-14
Match length 56
% identity 71

NCBI Description (AJ222585) AT-hook protein 1 [Arabidopsis thaliana]

Seq. No. 312706

Seq: ID xmt700259603.h1

Method BLASTX
NCBI GI g2462732
BLAST score 302
E value 5.0e-28
Match length 76
% identity 70

NCBI Description (AC002292) Hypothetical Protein [Arabidopsis thaliana]

Seq. No. 312707

Seq. ID xmt700259645.h1

Method BLASTX
NCBI GI g1708311
BLAST score 274
E value 8.0e-25
Match length 63

Match length 63 % identity 86

NCBI Description CHLOROPLAST STROMA 70 KD HEAT SHOCK-RELATED PROTEIN

>gi_170094 (M99565) 80 kDa heat shock protein [Spinacia

oleracea]

Seq. No. 312708

Seq. ID xmt700259653.h1

Method BLASTN
NCBI GI g687244
BLAST score 101
E value 6.0e-50
Match length 172
% identity 90

NCBI Description Zea mays oil body protein 16 kDa oleosin (ole16) gene,

complete cds

Seq. No. 312709

Seq. ID xmt700259667.h1

Method BLASTX
NCBI GI g3108053
BLAST score 293

```
1.0e-26
E value
Match length
                  58
% identity
                  97
                  (AF056326) myo-inositol 1-phosphate synthase; INO1 [Zea
NCBI Description
                  mays]
                  312710
Seq. No.
                  xmt700259733.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g22292
BLAST score
                  97
E value
                  1.0e-47
Match length
                  129
% identity
                  94
NCBI Description Z.mays mRNA for glycine-rich protein
Seq. No.
                  312711
                  xmt700259748.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4336905
BLAST score
                  231
E value
                  9.0e-20
Match length
                   47
                   96
% identity
NCBI Description (AF112244) Ran-related GTP binding protein [Zea mays]
Seq. No.
                  312712
Seq. ID
                  xmt700259846.h1
Method
                  BLASTX
NCBI GI
                   q136063
BLAST score
                   174
E value
                   6.0e-13
Match length
                   58
% identity
                   66
                  TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)
NCBI Description
                   >gi_68426_pir__ISZMT triose-phosphate isomerase (EC
                   5.3.1.1) - maize >gi_168647 (L00371) triosephosphate
                   isomerase 1 [Zea mays] >gi_217974_dbj_BAA00009_ (D00012)
                   triosephosphate isomerase [Zea mays]
Seq. No.
                   312713
                   xmt700259946.h1
Seq. ID
Method
                   BLASTX
                   q4512667
NCBI GI
```

Method BLASTX
NCBI GI g451266'
BLAST score 155
E value 8.0e-11
Match length 74
% identity 45

NCBI Description (AC006931) putative MAP kinase [Arabidopsis thaliana]

Seq. No. Seq. ID

312714 xmt700260149.h1

Method BLASTX
NCBI GI g1839188
BLAST score 174
E value 4.0e-13

Match length 50

```
% identity
NCBI Description (U86081) root hair defective 3 [Arabidopsis thaliana]
Seq. No.
                  312715
                  xmt700260189.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g169818
BLAST score
                  141
                  9.0e-74
E value
Match length
                  173
                  95
% identity
NCBI Description Rice 25S ribosomal RNA gene
Seq. No.
                  312716
Seq. ID
                  xmt700260263.h1
Method
                  BLASTX
                  g132659
NCBI GI
BLAST score
                  351
                  2.0e-33
E value
Match length
                  77
% identity
                  84
NCBI Description
                  50S RIBOSOMAL PROTEIN L13, CHLOROPLAST PRECURSOR (CL13)
                  >gi 81483 pir A32033 ribosomal protein L13 precursor,
                  chloroplast - spinach >gi 170133 (J04461) ribosomal protein
                  L13 [Spinacia oleracea]
Seq. No.
                  312717
Seq. ID
                  xmt700260334.h2
Method
                  BLASTX
NCBI GI
                  g3914685
BLAST score
                  151
E value
                  2.0e-10
Match length
                  39
                  77
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L17 >qi 2668748 (AF034948) ribosomal
                  protein L17 [Zea mays]
Seq. No.
                  312718
Seq. ID
                  xmt700260372.h2
Method
                  BLASTX
NCBI GI
                  g3294467
BLAST score
                  154
                  1.0e-10
E value
Match length
                  34
% identity
                  91
NCBI Description
                 (U89341) phosphoglucomutase 1 [Zea mays]
Seq. No.
                  312719
                  xmt700260445.h1
Seq. ID
                  BLASTX
Method
                  g4559391
NCBI GI
BLAST score
                  154
E value
                  9.0e-11
Match length
                  58
% identity
                  55
NCBI Description
                  (AC006526) putative auxin response factor 1 [Arabidopsis
                  thaliana]
```



```
312720
Seq. No.
Seq. ID
                  xmt700260508.h1
Method
                  BLASTN
NCBI GI
                  q22270
BLAST score
                  59
                   5.0e-25
E value
                  123
Match length
% identity
                  89
NCBI Description Maize mRNA from an embryogenic abscisic acid-inducible gene
                  312721
Seq. No.
                  xmt700260545.h2
Seq. ID
Method
                  BLASTX
                   g4220523
NCBI GI
BLAST score
                  160
                   2.0e-18
E value
Match length
                  70
% identity
                  (AL035356) putative alliin lyase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   312722
                  xmt700260760.h1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3021357
                   289
BLAST score
E value
                   4.0e-26
Match length
                   80
% identity
NCBI Description
                   (AJ005082) UDP-galactose 4-epimerase [Cyamopsis
                   tetragonoloba]
Seq. No.
                   312723
Seq. ID
                   xmt700260839.h1
Method
                   BLASTX
NCBI GI
                   q3249105
BLAST score
                   219
E value
                   2.0e-18
Match length
                   66
% identity
NCBI Description
                   (AC003114) Contains similarity to protein phosphatase 2C
                   (ABI1) gb X78886 from A. thaliana. [Arabidopsis thaliana]
Seq. No.
                   312724
                   xmt700260945.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4510380
BLAST score
                   194
                   4.0e-15
E value
                   90
Match length
% identity
                   46
NCBI Description
                   (AC007017) putative calcium-dependent protein kinase
                   [Arabidopsis thaliana]
```

44669

312725

BLASTN

xmt700260970.h1

Seq. No.

Seq. ID Method

BLAST score

Match length

E value

1.0e-69

166

```
q687244
NCBI GI
                  259
BLAST score
                  1.0e-144
E value
                  282
Match length
                  98
% identity
                  Zea mays oil body protein 16 kDa oleosin (ole16) gene,
NCBI Description
                  complete cds
                  312726
Seq. No.
                  xmt700260982.h1
Seq. ID
                  BLASTX
Method
                  g542182
NCBI GI
                  222
BLAST score
                   2.0e-18
E value
                   54
Match length
                   76
% identity
                  vicilin-like storage protein Glb1-L, embryo - maize
NCBI Description
                   >gi_22284_emb_CAA41809_ (X59083) vicilin-like embryo
                   storage protein [Zea mays]
                   312727
Seq. No.
Seq. ID
                   xmt700260994.h1
                   BLASTX
Method
NCBI GI
                   g3219267
                   145
BLAST score
                   2.0e-09
E value
                   86
Match length
% identity
                   44
                   (AB015313) MAP kinase kinase 2 [Arabidopsis thaliana]
NCBI Description
                   312728
Seq. No.
Seq. ID
                   xmt700261055.hl
Method
                   BLASTN
                   g169818
NCBI GI
                   61
BLAST score
                   4.0e-26
E value
                   69
Match length
                   97
% identity
                   Rice 25S ribosomal RNA gene
NCBI Description
                   312729
Seq. No.
                   xmt700261074.h1
Seq. ID
Method
                   BLASTX
                   q3758833
NCBI GI
BLAST score
                   143
                   2.0e-09
E value
                   37
Match length
                   76
 % identity
                   (Y18225) MtN6 [Medicago truncatula]
NCBI Description
                   312730
 Seq. No.
                   xmt700261079.hl
 Seq. ID
 Method
                   BLASTN
 NCBI GI
                   g1597722
                   134
```



```
% identity
                  Zea mays CRINKLY4 precursor (cr4) mRNA, complete cds
NCBI Description
                  312731
Seq. No.
Seq. ID
                  xmt700261105.hl
Method
                  BLASTX
                  q1698690
NCBI GI
                  215
BLAST score
                  2.0e-17
E value
                  42
Match length
% identity
NCBI Description (U67317) beta-ketoacyl-ACP synthase II [Cuphea wrightii]
                  312732
Seq. No.
                  xmt700261140.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q100876
BLAST score
                  403
                  1.0e-39
E value
Match length
                  75
                  99
% identity
                  globulin-2 precursor - maize >gi_228310 prf__1802402A
NCBI Description
                  globulin 2 [Zea mays]
                  312733
Seq. No.
                  xmt700261141.h1
Seq. ID
Method
                  BLASTX
                  g100876
NCBI GI
                  357
BLAST score
E value
                  3.0e-34
Match length
                  84
% identity
                  globulin-2 precursor - maize >gi_228310_prf__1802402A
NCBI Description
                  globulin 2 [Zea mays]
                   312734
Seq. No.
Seq. ID
                  xmt700261174.hl
Method
                  BLASTX
NCBI GI
                   g312179
BLAST score
                   381
E value
                   7.0e-37
Match length
                   82
% identity
                   90
                   (X73151) glyceraldehyde 3-phosphate dehydrogenase
NCBI Description
                   (phosphorylating) [Zea mays] >gi_1184772 (U45855) cytosolic
                   glyceroldehyde-3-phosphate dehydrogenase GAPC2 [Zea mays]
                   >gi_1185554 (U45858) glyceraldehyde-3-phosphate
                   dehydrogenase [Zea mays]
                   312735
Seq. No.
                   xmt700261339.h1
Seq. ID
                   BLASTX
Method
                   g3108053
NCBI GI
                   285
BLAST score
                   6.0e-26
E value
```

44671

56

96

Match length % identity



NCBI Description (AF056326) myo-inositol 1-phosphate synthase; INO1 [Zea mays]

Seq. No. 312736

Seq. ID xmt700261376.h1

Method BLASTX
NCBI GI g2130082
BLAST score 229
E value 3.0e-19
Match length 83
% identity 55

NCBI Description protein kinase Xa21 (EC 2.7.1.-) - rice >gi_1122443

(U37133) receptor kinase-like protein [Oryza sativa] >gi 2586085 (U72723) receptor kinase-like protein [Oryza

longistaminata] >gi_1586408_prf__2203451A receptor

kinase-like protein [Oryza sativa]

Seq. No. 312737

Seq. ID xmt700261384.h1

Method BLASTX
NCBI GI g1296955
BLAST score 253
E value 5.0e-22
Match length 51
% identity 46

NCBI Description (X95402) duplicated domain structure protein [Oryza sativa]

Seq. No. 312738

Seq. ID xmt700261480.h1

Method BLASTX
NCBI GI g1172818
BLAST score 179
E value 1.0e-13
Match length 54
% identity 72

NCBI Description 40S RIBOSOMAL PROTEIN S16 >gi_538428 (L36313) ribosomal

protein S16 [Oryza sativa] >gi 1096552_prf__2111468A

ribosomal protein S16 [Oryza sativa]

Seq. No. 312739

Seq. ID xmt700261524.h1

Method BLASTX
NCBI GI g1346487
BLAST score 301
E value 6.0e-28
Match length 60
% identity 97

NCBI Description MALATE SYNTHASE, GLYOXYSOMAL >gi 532625 (L35914) malate

synthase [Zea mays]

Seq. No. 312740

Seq. ID xmt700261612.h1

Method BLASTX
NCBI GI g1154954
BLAST score 249
E value 2.0e-21
Match length 52



% identity 98 NCBI Description (X94693) histone H2A [Triticum aestivum] Seq. No. 312741

Method BLASTN
NCBI GI g687244
BLAST score 86
E value 4.0e-41
Match length 122

Seq. ID

% identity 93
NCBI Description Zea mays oil body protein 16 kDa oleosin (ole16) gene,

complete cds

xmt700261784.h1

Seq. No. 312742

Seq. ID xmt700261794.h1

Method BLASTX
NCBI GI g2935573
BLAST score 176
E value 7.0e-25

Match length 76 % identity 83

NCBI Description (AF050180) KNOX class homeodomain protein [Oryza sativa]

Seq. No. 312743

Seq. ID xmt700261864.h1

Method BLASTX
NCBI GI g2462749
BLAST score 268
E value 4.0e-24
Match length 63
% identity 81

NCBI Description (AC002292) Putative Serine/Threonine protein kinase

[Arabidopsis thaliana]

Seq. No. 312744

Seq. ID xmt700261868.h1

Method BLASTN
NCBI GI g687244
BLAST score 156
E value 1.0e-82
Match length 195
% identity 95

NCBI Description Zea mays oil body protein 16 kDa oleosin (ole16) gene,

complete cds

Seq. No. 312745

Seq. ID xmt700261965.h1

Method BLASTX
NCBI GI g3080414
BLAST score 183
E value 6.0e-14
Match length 54
% identity 78

NCBI Description (AL022604) putative protein [Arabidopsis thaliana]

Seq. No. 312746



```
xmt700261975.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4586244
                  290
BLAST score
                  3.0e-26
E value
Match length
                  102
% identity
                  (AL049640) putative protein [Arabidopsis thaliana]
NCBI Description
                  312747
Seq. No.
Seq. ID
                  xmt700261986.h1
Method
                  BLASTN
                  q473602
NCBI GI
                  186
BLAST score
                  1.0e-100
E value
                  222
Match length
                  96
% identity
                  Zea mays W-22 histone H2A mRNA, complete cds
NCBI Description
                  312748
Seq. No.
Seq. ID
                  xmt700261993.h1
                  BLASTX
Method
NCBI GI
                  g730146
BLAST score
                  145
                   1.0e-09
E value
                   49
Match length
                   53
% identity
                  NITRATE REDUCTASE (NR) >gi_632154_pir__S47029 nitrate
NCBI Description
                  reductase (NADH) (EC 1.6.6.1) - Lotus japonicus
                   >gi 517356 emb CAA56696 (X80670) nitrate reductase (NADH)
                   [Lotus japonicus]
Seq. No.
                   312749
Seq. ID
                   xmt700262161.h1
                   BLASTN
Method
                   q687244
NCBI GI
BLAST score
                   202
E value
                   1.0e-110
Match length
                   221
% identity
                  Zea mays oil body protein 16 kDa oleosin (ole16) gene,
NCBI Description
                   complete cds
Seq. No.
                   312750
                   xmt700262163.h1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2119187
BLAST score
                   218
E value
                   1.0e-24
Match length
                   60
                   98
% identity
```

NCBI Description transmembrane protein, glucose starvation-induced - maize >qi 575731 emb CAA57955 (X82633) transmembrane protein

Sdr 2/2/21 Feur CAM2/322 (V05022) Framsmemprane bro

[Zea mays]

Seq. No. 312751

Seq. ID xmt700262211.h1

BLAST score

E value Match length 241 1.0e-20

84



```
Method
                   BLASTX
NCBI GI
                   g2652938
BLAST score
                   159
                   6.0e-17
E value
Match length
                   71
% identity
                   62
NCBI Description (Z47554) orf [Zea mays]
                   312752
Seq. No.
Seq. ID
                   xmt700262230.h1
Method
                   BLASTX
NCBI GI
                   g3914423
BLAST score
                   175
                   4.0e-26
E value
                   62
Match length
% identity
NCBI Description PROFILIN 4 >gi_2642324 (AF032370) profilin [Zea mays]
                   312753
Seq. No.
Seq. ID
                   xmt700262238.h1
Method
                   BLASTX
NCBI GI
                   q4539335
BLAST score
                   244
                   6.0e-21
E value
                   98
Match length
% identity
                   50
NCBI Description (AL035539) putative protein [Arabidopsis thaliana]
                   312754
Seq. No.
Seq. ID
                   xmt700262267.h1
Method
                   BLASTN
NCBI GI
                   q687244
BLAST score
                   291
E value
                   1.0e-163
Match length
                   298
                   100
% identity
NCBI Description Zea mays oil body protein 16 kDa oleosin (ole16) gene,
                   complete cds
                   312755
Seq. No.
Seq. ID
                   xmt700262294.h1
                   BLASTX
Method
NCBI GI
                   g4220474
BLAST score
                   168
E value
                   2.0e-12
Match length
                   56
% identity
                   (AC006069) putative myosin heavy chain [Arabidopsis
NCBI Description
                   thaliana]
                   312756
Seq. No.
                   xmt700262355.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1703227
```



```
3
  % identity
                    ALANINE AMINOTRANSFERASE 2 (GPT) (GLUTAMIC--PYRUVIC
  NCBI Description
                     TRANSAMINASE 2) (GLUTAMIC--ALANINE TRANSAMINASE 2)
                     (ALAAT-2) >gi_629770_pir__S42535 alanine transaminase (EC
                     2.6.1.2) - barley >gi_469148_emb_CAA81231_ (Z26322) alanine
                     aminotransferase [Hordeum vulgare]
  Seq. No.
                     312757
                     xmt700262385.h1
  Seq. ID
  Method
                     BLASTX
                     q633890
  NCBI GI
                     396
  BLAST score
                     8.0e-39
  E value
  Match length
                     90
                     83
  % identity
                     (S72926) glucose and ribitol dehydrogenase homolog [Hordeum
  NCBI Description
                     vulgare]
                     312758
  Seq. No.
                     xmt700262404.h1
  Seq. ID
  Method
                     BLASTN
  NCBI GI
                     g4321977
  BLAST score
                     42
                     9.0e-15
  E value
  Match length
                     70
  % identity
                     90
                     Zea mays beta-amylase (Amy2) gene, complete cds
  NCBI Description
                     312759
  Seq. No.
                     xmt700262437.h1
  Seq. ID
  Method
                     BLASTX
                     g3935141
  NCBI GI
                     159
  BLAST score
   E value
                     5.0e-11
                     92
   Match length
                     39
   % identity
                     (AC005106) T25N20.5 [Arabidopsis thaliana]
   NCBI Description
                     312760
   Seq. No.
                     xmt700262483.h1
   Seq. ID
                     BLASTX
   Method
                     g3928150
   NCBI GI
                     245
   BLAST score
                     4.0e-21
   E value
   Match length
                     62
   % identity
                     73
                     (AJ131049) hypothetical protein [Cicer arietinum]
   NCBI Description
                     312761
   Seq. No.
                     xmt700262520.h1
   Seq. ID
                     BLASTN
   Method
```

NCBI GI g169818
BLAST score 66
E value 8.0e-29
Match length 78
% identity 96

NCBI Description Rice 25S ribosomal RNA gene

```
312762
Seq. No.
                  xmt700262540.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2160190
BLAST score
                  222
                  2.0e-18
E value
                  58
Match length
                  72
% identity
                  (ACO00132) No definition line found [Arabidopsis thaliana]
NCBI Description
                  312763
Seq. No.
                  xmt700262541.h1
Seq. ID
                  BLASTX
Method
                  g4519507
NCBI GI
BLAST score
                  313
E value
                   4.0e-29
Match length
                  78
                   77
% identity
                  (D88434) protein abundantly expressed during apple fruit
NCBI Description
                  development [Malus domestica]
                   312764
Seq. No.
                   xmt700262702.h1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1345588
BLAST score
                   169
E value
                   1.0e-15
                   50
Match length
% identity
                  14-3-3-LIKE PROTEIN GF14-12 >gi 998432 bbs 164524
NCBI Description
                   GF14-12=GRF2 product/14-3-3 protein homolog [Zea mays,
                   XL80, Peptide, 261 aa]
Seq. No.
                   312765
Seq. ID
                   xmt700262768.h1
Method
                   BLASTN
NCBI GI
                   g687244
BLAST score
                   290
E value
                   1.0e-162
Match length
                   297
% identity
                   100
                   Zea mays oil body protein 16 kDa oleosin (ole16) gene,
NCBI Description
                   complete cds
                   312766
Seq. No.
                   xmt700262802.h1
Seq. ID
Method
                   BLASTX
                   g1346760
NCBI GI
```

BLAST score 166 8.0e-12 E value

Match length 49 % identity 63

SERINE/THREONINE PROTEIN PHOSPHATASE PP1 ISOZYME 6 NCBI Description

>gi_829255_emb_CAA86339_ (Z46253) protein phosphatase type
1 [Arabidopsis thaliana] >gi_3153203 (U80921)

serine/threonine protein phosphatase type one [Arabidopsis

NCBI Description

Seq. No. Seq. ID

Method NCBI GI



thaliana]

```
312767
Seq. No.
Seq. ID
                  xmt700262815.h1
Method
                  BLASTN
NCBI GI
                  g22514
                  169
BLAST score
                   2.0e-90
E value
                  211
Match length
                   96
% identity
NCBI Description Maize Zc1 gene for Zein Zc1 (14 kD zein-2)
                   312768
Seq. No.
Seq. ID
                  xmt700262922.h1
                  BLASTX
Method
                   g100876
NCBI GI
BLAST score
                   342
                   2.0e-32
E value
Match length
                   73
                   99
% identity
                   globulin-2 precursor - maize >gi_228310_prf__1802402A
NCBI Description
                   globulin 2 [Zea mays]
                   312769
Seq. No.
Seq. ID
                   xmt700262958.hl
                   BLASTN
Method
                   g2345153
NCBI GI
BLAST score
                   73
                   5.0e-33
E value
                   73
Match length
                   100
% identity
                  Zea mays ribsomal protein S4 (rps4) mRNA, complete cds
NCBI Description
                   312770
Seq. No.
                   xmt700262994.h1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g3819440
BLAST score
                   39
                   9.0e-13
E value
Match length
                   83
                   87
% identity
                  Hordeum vulgare genomic DNA fragment; clone MWG0934.rev
NCBI Description
Seq. No.
                   312771
                   xmt700263019.h1
Seq. ID
                   BLASTX
Method
                   q3212869
NCBI GI
                   254
BLAST score
E value
                   2.0e-22
Match length
                   64
% identity
```

312772

BLASTX

q2369714

xmt700263062.hl

(AC004005) unknown protein [Arabidopsis thaliana]

92

% identity

NCBI Description

```
BLAST score
                  8.0e-11
E value
                   31
Match length
                   97
% identity
NCBI Description (Z97178) elongation factor 2 [Beta vulgaris]
Seq. No.
                   312773
Seq. ID
                  xmt700263090.h1
Method
                  BLASTX
                  q4521249
NCBI GI
BLAST score
                  170
                   1.0e-12
E value
Match length
                   45
                   73
% identity
NCBI Description (AB013912) DNA helicase [Mus musculus]
Seq. No.
                   312774
Seq. ID
                   xmt700263146.h1
Method
                   BLASTN
NCBI GI
                   g902524
BLAST score
                   84
E value
                   7.0e-40
Match length
                   131
                   92
% identity
                   Zea mays clone MubG10 ubiquitin fusion protein gene,
NCBI Description
                   complete cds
Seq. No.
                   312775
                   xmt700263176.h1
Seq. ID
Method
                   BLASTX
                   q960289
NCBI GI
BLAST score
                   159
E value
                   3.0e-11
                   36
Match length
                   83
% identity
                   (L34343) anthranilate synthase alpha subunit [Ruta
NCBI Description
                   graveolens]
Seq. No.
                   312776
Seq. ID
                   xmt700263184.h1
Method
                   BLASTX
NCBI GI
                   g4191616
BLAST score
                   287
E value
                   3.0e-26
Match length
                   76
                   64
% identity
                  (AF120334) GTP-binding protein NGB [Homo sapiens]
NCBI Description
Seq. No.
                   312777
                   xmt700263192.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3157951
BLAST score
                   314
                   2.0e-29
E value
Match length
                   65
```

44679

(AC002131) Contains similarity to vesicle trafficking



protein gb_U91538 from Mus musculus. ESTs gb_F15494 and gb F14097 come from this gene. [Arabidopsis thaliana]

Seq. No. 312778

Seq. ID xmt700263233.h1

Method BLASTN
NCBI GI g687244
BLAST score 164
E value 2.0e-87
Match length 171
% identity 99

NCBI Description Zea mays oil body protein 16 kDa oleosin (ole16) gene,

complete cds

Seq. No. 312779

Seq. ID xmt700263240.h1

Method BLASTX
NCBI GI g2623307
BLAST score 158
E value 3.0e-24
Match length 70
% identity 79

NCBI Description (AC002409) putative ubiquitin protease [Arabidopsis

thaliana]

Seq. No. 312780

Seq. ID xmt700263245.h1

Method BLASTN
NCBI GI g168604
BLAST score 154
E value 1.0e-81
Match length 166
% identity 98

NCBI Description Zea mays viviparous-1 mRNA, complete cds

Seq. No. 312781

Seq. ID xmt700263294.h1

Method BLASTX
NCBI GI 94220529
BLAST score 160
E value 4.0e-11
Match length 69
% identity 42

NCBI Description (AL035356) putative protein [Arabidopsis thaliana]

Seq. No. 312782

Seq. ID xmt700263320.h1

Method BLASTN
NCBI GI g687244
BLAST score 297
E value 1.0e-166
Match length 304
% identity 100

NCBI Description Zea mays oil body protein 16 kDa oleosin (ole16) gene,

complete cds

Seq. No. 312783

```
xmt700263349.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1001311
BLAST score
                  167
                  3.0e-12
E value
Match length
                  40
                  80
% identity
                  (D64006) hypothetical protein [Synechocystis sp.]
NCBI Description
                 312784
Seq. No.
                  xmt700263483.h1
Seq. ID
                  BLASTX
Method
                  g2462927
NCBI GI
BLAST score
                  248
E value
                  2.0e-21
Match length
                  62
                  77
% identity
NCBI Description
                  (Y10342) putative amidase [Arabidopsis thaliana]
Seq. No.
                  312785
                  xmt700263509.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g135430
BLAST score
                  215
E value
                  7.0e-18
Match length
                  42
                  98
% identity
                  TUBULIN ALPHA CHAIN >gi 71576 pir UBURAL tubulin alpha
NCBI Description
                  chain - sea urchin (Lytechinus pictus) (fragment)
Seq. No.
                  312786
                  xmt700263620.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3264765
BLAST score
                  201
                  4.0e-16
E value
Match length
                  45
% identity
                  73
NCBI Description
                  (AF071892) omega-6 fatty acid desaturase [Prunus armeniaca]
Seq. No.
                  312787
                  xmt700263626.h1
Seq. ID
Method
                  BLASTN
                  g2895865
NCBI GI
BLAST score
                  57
                  8.0e-24
E value
Match length
                  77
                  94
% identity
```

NCBI Description Oryza sativa methylmalonate semi-aldehyde dehydrogenase

(MMSDH1) mRNA, complete cds

Seq. No. 312788

Seq. ID xmt700263757.h1

Method BLASTX
NCBI GI g3786009
BLAST score 360
E value 3.0e-38



```
Match length
% identity
NCBI Description
                  (AC005499) unknown protein [Arabidopsis thaliana]
                  312789
Seq. No.
Seq. ID
                  xmt700263778.h1
Method
                  BLASTN
NCBI GI
                  q3452288
                  227
BLAST score
E value
                  1.0e-125
Match length
                  283
% identity
                   95
                  Zea mays retrotransposon Grande-Zm1 3' LTR, partial
NCBI Description
                  sequence
                  312790
Seq. No.
Seq. ID
                  xmt700263783.h1
Method
                  BLASTX
NCBI GI
                  g1749752
                  176
BLAST score
E value
                   2.0e-13
Match length
                   69
% identity
                   46
NCBI Description
                   (D89272) similar to Saccharomyces cerevisiae T-complex
                  protein 1, theta subunit, SWISS-PROT Accession Number P47079
                   [Schizosaccharomyces pombe]
Seq. No.
                   312791
Seq. ID
                  xmt700263835.h1
Method
                  BLASTX
                   g2979549
NCBI GI
BLAST score
                   169
E value
                   4.0e-12
Match length
                   79
% identity
                   41
NCBI Description
                   (AC003680) putative 7-ethoxycoumarin O-deethylase
                   [Arabidopsis thaliana]
Seq. No.
                   312792
Seq. ID
                   xmt700263851.h1
Method
                   BLASTX
NCBI GI
                   g1362064
BLAST score
                   179
                   3.0e-13
E value
Match length
                   42
% identity
                   86
                   small G protein - garden pea >gi 871514_emb CAA90079
NCBI Description
                   (Z49899) small G protein [Pisum sativum]
                   312793
Seq. No.
                   xmt700263860.h1
Seq. ID
```

Method BLASTX
NCBI GI g1945277
BLAST score 170
E value 2.0e-12
Match length 58
% identity 57



NCBI Description (Z94180) branched chain alpha-keto acid dehydrogenase E1-alpha subunit [Lycopersicon esculentum]

Seq. No. 312794

Seq. ID xmt700263862.h1

Method BLASTX
NCBI GI g1169518
BLAST score 180.
E value 2.0e-13
Match length 38
% identity 92

NCBI Description EM PROTEIN H5 >gi_629821_pir__S43332 EmH5 protein - wheat

Seq. No. 312795

Seq. ID xmt700263884.h1

Method BLASTX
NCBI GI g2832685
BLAST score 153
E value 3.0e-10
Match length 36
% identity 81

NCBI Description (AL021712) putative protein [Arabidopsis thaliana]

Seq. No. 312796

Seq. ID xmt700263915.h1

Method BLASTX
NCBI GI g3641252
BLAST score 162
E value 1.0e-11

Match length 65 % identity 52

NCBI Description (AF053127) leucine-rich receptor-like protein kinase [Malus

domestica]

Seq. No. 312797

Seq. ID xmt700263916.h1

Method BLASTX
NCBI GI g1488255
BLAST score 163
E value 8.0e-12
Match length 44
% identity 68

NCBI Description (U38416) ferulate-5-hydroxylase [Arabidopsis thaliana]

>gi 2961381_emb_CAA18128_ (AL022141) ferulate-5-hydroxylase

(FAH1) [Arabidopsis thaliana] >gi 3925365 (AF068574)

ferulate-5-hydroxylase [Arabidopsis thaliana]

Seq. No. 312798

Seq. ID xmt700263930.h1

Method BLASTX
NCBI GI g4455359
BLAST score 176
E value 4.0e-13
Match length 49
% identity 76

NCBI Description (AL035524) putative protein [Arabidopsis thaliana]

```
312799
Seq. No.
                  xmt700263934.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2979554
BLAST score
                  346
                  7.0e-33
E value
                  102
Match length
                  59
% identity
                  (AC003680) CDC4 like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  312800
                  xmt700264050.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                   g2832242
BLAST score
                   76
E value
                   7.0e-35
Match length
                   167
```

312801

% identity 87

Seq. No.

Zea mays 22-kDa alpha zein gene cluster, complete sequence NCBI Description

xmt700264163.h1 Seq. ID Method BLASTX NCBI GI g100876 BLAST score 220 E value 2.0e-18

Match length 56 % identity 73

globulin-2 precursor - maize >gi_228310_prf__1802402A NCBI Description

globulin 2 [Zea mays]

Seq. No. 312802

xmt700264203.h1 Seq. ID

Method BLASTX NCBI GI g2702277 BLAST score 430 8.0e-43 E value Match length 92 % identity 82

NCBI Description (AC003033) putative cyclin g-associated kinase [Arabidopsis

thaliana] >gi 2914689 (AC003974) putative cyclin

g-associated kinase [Arabidopsis thaliana]

Seq. No. 312803

xmt700264216.h1 Seq. ID

Method BLASTX NCBI GI g3445201 BLAST score 158 E value 7.0e-11 Match length 63 % identity 48

NCBI Description (AC004786) unknown protein [Arabidopsis thaliana]

312804 Seq. No.

xmt700264256.h1 Seq. ID

Method BLASTX NCBI GI g3334474



```
BLAST score
                  2.0e-13
E value
Match length
                  75
% identity
                  64
NCBI Description
                  OLEOSIN ZM-I (OLEOSIN 16 KD) (LIPID BODY-ASSOCIATED MAJOR
                  PROTEIN) (LIPID BODY-ASSOCIATED PROTEIN L3)
                  >gi 1076817 pir S52029 oleosin 16 - maize >gi_687245
                  (U1\overline{3}701) 16 kDa oleosin [Zea mays]
Seq. No.
                  312805
Seq. ID
                  xmt700264259.h1
Method
                  BLASTX
NCBI GI
                  g3242783
                  323
BLAST score
E value
                  3.0e-30
Match length
                  89
% identity
NCBI Description
                  (AF055354) respiratory burst oxidase protein B [Arabidopsis
                  thaliana]
                  312806
Seq. No.
Seq. ID
                  xmt700264278.h1
Method
                  BLASTX
NCBI GI
                  g3212873
BLAST score
                  148
E value
                  5.0e-10
Match length
                  32
% identity
NCBI Description (AC004005) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  312807
Seq. ID
                  xmt700264292.h1
Method
                  BLASTX
NCBI GI
                  q4579913
BLAST score
                  244
E value
                  6.0e-21
Match length
                  76
                  59
% identity
NCBI Description (AB023423) sulfate transporter [Arabidopsis thaliana]
Seq. No.
                  312808
                  xmt700264343.h1
Seq. ID
Method
                  BLASTX
                  g4218011
NCBI GI
BLAST score
                  385
E value
                  1.0e-37
Match length
                  87
% identity
                  87
```

(AC006135) putative protein kinase [Arabidopsis thaliana] NCBI Description

>gi_4309721_gb_AAD15491_ (AC006439) putative

serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No. 312809

xmt700264352.h1 Seq. ID

BLASTX Method g4586053 NCBI GI BLAST score 235



```
3.0e-20
                                                                 المنتجع
E value
Match length
                  63
% identity
                   67
                  (AC007020) putative lacasse [Arabidopsis thaliana]
NCBI Description
                  312810
Seq. No.
                  xmt700264362.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4567278
BLAST score
                  155
E value
                  2.0e-10
Match length
                  34
                  91
% identity
                  (AC006841) putative anthracycline associated resistance ARX
NCBI Description
                  protein [Arabidopsis thaliana]
Seq. No.
                  312811
Seq. ID
                  xmt700264367.h1
Method
                  BLASTN
NCBI GI
                  g2738749
BLAST score
                  56
                   8.0e-23
E value
Match length
                  72
                  94
% identity
                  Zea mays ATP sulfurylase mRNA, complete cds
NCBI Description
                   312812
Seq. No.
Seq. ID
                  xmt700264413.h1
Method
                  BLASTX
NCBI GI
                   g461498
BLAST score
                   319
E value
                   1.0e-29
Match length
                  101
                   59
% identity
                  ALANINE AMINOTRANSFERASE 2 (GPT) (GLUTAMIC--PYRUVIC
NCBI Description
                   TRANSAMINASE 2) (GLUTAMIC--ALANINE TRANSAMINASE 2)
                   (ALAAT-2) >gi 320619 pir S28429 alanine transaminase (EC
                   2.6.1.2) - proso millet >gi 296204 emb CAA49199 (X69421)
                   alanine aminotransferase [Panicum miliaceum]
Seq. No.
                   312813
Seq. ID
                  xmt700264420.h1
Method
                  BLASTN
NCBI GI
                   g3650465
BLAST score
                   46
E value
                   7.0e-17
Match length
                   54
% identity
                   96
                  Zea mays histone deacetylase HD2-p39 (HD2) gene, complete
NCBI Description
```

Seq. No. 312814

Seq. ID xmt700264430.h1

Method BLASTX
NCBI GI g418134
BLAST score 140
E value 1.0e-08



Match length 40 % identity NCBI Description ANTHRANILATE SYNTHASE COMPONENT I-2 PRECURSOR >gi 282854 pir S27752 anthranilate synthase (EC 4.1.3.27) alpha chain - Arabidopsis thaliana >qi 166606 (M92354) anthranilate synthase alpha subunit [Arabidopsis thaliana] >gi 3582331 (AC005496) anthranilate synthase [Arabidopsis thaliana] Seq. No. 312815 Seq. ID xmt700264455.hl Method BLASTX NCBI GI g542182 BLAST score 227 E value 3.0e-19 Match length 54 % identity 72 NCBI Description vicilin-like storage protein Glb1-L, embryo - maize >gi 22284 emb CAA41809 (X59083) vicilin-like embryo storage protein [Zea mays] Seq. No. 312816 Seq. ID xmt700264482.h1 Method BLASTN NCBI GI g687244 BLAST score 211 E value 1.0e-115 Match length 218 % identity 100 NCBI Description Zea mays oil body protein 16 kDa oleosin (ole16) gene, complete cds Seq. No. 312817 xmt700264501.h1 Seq. ID Method BLASTX NCBI GI g401161 BLAST score 233 E value 1.0e-19 Match length 43 % identity 100 NCBI Description TUBULIN ALPHA-5 CHAIN >gi_322879_pir__\$28982 tubulin alpha-5 chain - maize >gi_22156_emb_CAA44862_ alpha-tubulin #5 [Zea mays] >gi $450\overline{2}93$ (L278 $\overline{1}5$) alpha-tubulin [Zea mays] $>gi_45\overline{2}474$ (U05258) alpha-tubulin [Zea mays] Seq. No. 312818 xmt700264521.h1 Seq. ID Method BLASTX

35

NCBI GI g4558666 BLAST score 189 E value 2.0e-14 Match length 82 45 % identity

NCBI Description (AC007063) putative Na/H antiporter isolog [Arabidopsis

thaliana]

Seq. No.

Seq. ID

Method

312824

BLASTX

xmt700264641.h1



```
Seq. No.
                   312819
                  xmt700264522.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g4063751
BLAST score
                  162
                   3.0e-11
E value
Match length
                   87
% identity
                   34
                   (AC005851) putative white protein [Arabidopsis thaliana]
NCBI Description
                   >gi_4510409_gb_AAD21495.1_ (AC006929) putative white
                  protein [Arabidopsis thaliana]
                   312820
Seq. No.
Seq. ID
                  xmt700264613.h1
                   BLASTX
Method
NCBI GI
                   g4581164
BLAST score
                   143
                   4.0e-09
E value
Match length
                   70
% identity
                   44
                  (AC006220) putative polyprotein [Arabidopsis thaliana]
NCBI Description
                   312821
Seq. No.
Seq. ID
                   xmt700264622.h1
                   BLASTX
Method
                   g3377509
NCBI GI
                   417
BLAST score
E value
                   3.0e-41
                   95
Match length
                   84
% identity
                  (AF056027) auxin transport protein REH1 [Oryza sativa]
NCBI Description
                   312822
Seq. No.
                   xmt700264637.h1
Seq. ID
                   BLASTX
Method
                   q4154359
NCBI GI
BLAST score
                   140
E value
                   8.0e-09
                   55
Match length
                   55
% identity
                   (AF113541) putative ethylene response sensor [Phalaenopsis
NCBI Description
                   sp. 'KCbutterfly']
Seq. No.
                   312823
Seq. ID
                   xmt700264638.h1
Method
                   BLASTN
NCBI GI
                   q1185553
BLAST score
                   195
E value
                   1.0e-106
                   236
Match length
                   97
% identity
                   Zea mays glyceraldehyde-3-phosphate dehydrogenase (gpc2)
NCBI Description
                   gene, complete cds
```

Seq. ID

Method

NCBI GI



```
NCBI GI
                  q3785980
                  243
BLAST score
                  7.0e-21
E value
                  91
Match length
% identity
NCBI Description (AC005560) hypothetical protein [Arabidopsis thaliana]
                  312825
Seq. No.
                                           X.
Seq. ID
                  xmt700264654.h1
                  BLASTX
Method
NCBI GI
                  q2494417
BLAST score
                  501
                  5.0e-51
E value
                  103
Match length
                  87
% identity
                  FRUCTOSE-1, 6-BISPHOSPHATASE, CYTOSOLIC
NCBI Description
                  (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE)
                  >gi 1364071 pir S57717 fructose-1, 6-bisphosphatase (EC
                  3.1.3.11) - sugarcane hybrid H65-7052
                  >gi 895909 emb CAA61409.1 (X89006) fructose-1,
                  6-bisphosphatase [Saccharum hybrid cultivar H65-7052]
                  312826
Seq. No.
Seq. ID
                  xmt700264667.h1
Method
                  BLASTX
NCBI GI
                  g1542941
                  159
BLAST score
                  6.0e-11
E value
                  48
Match length
                  65
% identity
NCBI Description (X78116) Acetoacetyl-coenzyme A thiolase [Raphanus sativus]
                  312827
Seq. No.
Seq. ID
                  xmt700264685.h1
Method
                  BLASTX
                  q1707642
NCBI GI
BLAST score
                  256
E value
                  2.0e-22
                  94
Match length
                  53
% identity
                  (Y07748) TMK [Oryza sativa]
NCBI Description
Seq. No.
                  312828
Seq. ID
                  xmt700264711.h1
Method
                  BLASTX
NCBI GI
                  q3928084
BLAST score
                  313
E value
                  5.0e-29
Match length
                  97
                  71
% identity
                  (AC005770) retrotransposon-like protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  312829
```

xmt700264747.h1

BLASTX

g2058273



```
BLAST score
                   4.0e-33
E value
                  73
Match length
                  93
% identity
NCBI Description
                  (D83527) YK426 [Oryza sativa]
Seq. No.
                  312830
                  xmt700264760.hl
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3738297
BLAST score
                  313
E value
                  1.0e-29
Match length
                  96
                  20
% identity
NCBI Description (AC005309) unknown protein [Arabidopsis thaliana]
Seq. No.
                   312831
                  xmt700265001.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g100876
BLAST score
                   372
                   5.0e-36
E value
Match length
                   86
                   81
% identity
                  globulin-2 precursor - maize >gi_228310_prf__1802402A
NCBI Description
                  globulin 2 [Zea mays]
Seq. No.
                   312832
Seq. ID
                  xmt700265008.h1
Method
                  BLASTX
NCBI GI
                   g1184776
                   297
BLAST score
E value
                   2.0e-27
                   57
Match length
                   100
% identity
                   (U45857) cytosolic glyceroldehyde-3-phosphate dehydrogenase
NCBI Description
                   GAPC4 [Zea mays]
Seq. No.
                   312833
Seq. ID
                   xmt700265022.h1
Method
                   BLASTX
NCBI GI
                   q2662343
BLAST score
                   398
E value
                   5.0e-39
Match length
                   79
% identity
                   97
                  (D63581) EF-1 alpha [Oryza sativa]
NCBI Description
Seq. No.
                   312834
                   xmt700265135.h1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g687244
BLAST score
                   266
E value
                   1.0e-148
Match length
                   273
                   100
% identity
NCBI Description Zea mays oil body protein 16 kDa oleosin (ole16) gene,
```



```
complete cds
Seq. No.
                  312835
Seq. ID
                  xmt700265206.h1
Method
                  BLASTX
                  g4585977
NCBI GI
BLAST score
                  317
                  2.0e-29
E value
                  100
Match length
% identity
                  54
NCBI Description (AC005287) Unknown protein [Arabidopsis thaliana]
Seq. No.
                  312836
                  xmt700265216.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g167112
BLAST score
                  37
                  1.0e-11
E value
Match length
                  105
% identity
                  84
NCBI Description
                  Bromus inermis aldose reductase-related protein, complete
Seq. No.
                  312837
                  xmt700265237.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2384671
BLAST score
                  290
E value
                   1.0e-26
Match length
                  70
                   77
% identity
NCBI Description
                   [Arabidopsis thaliana]
```

(AF012657) putative potassium transporter AtKT2p

Seq. No. 312838

xmt700265275.h1 Seq. ID

Method BLASTX NCBI GI g2130141 BLAST score 310 · 1.0e-28 E value Match length 97 57 % identity

mudrA protein - maize transposon MuDR >gi_540581 (M76978) NCBI Description mudrA [Zea mays] >gi 595816 (U14597) mudrA gene product

[Zea mays]

312839 Seq. No.

Seq. ID xmt700265286.h1

Method BLASTX NCBI GI g2598151 BLAST score 221 6.0e-22 E value Match length 62 % identity 82

(AF027350) NADPH:protochlorophyllide oxidoreductase porB NCBI Description

[Pinus taeda]



```
312840
Seq. No.
                  xmt700265351.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4585972
BLAST score
                  312
                  4.0e-29
E value
Match length
                  80
% identity
                  74
NCBI Description (AC005287) Putative ATPase [Arabidopsis thaliana]
Seq. No.
                  312841
                  xmt700265383.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1871192
BLAST score
                  165
E value
                  1.0e-11
Match length
                  87
% identity
                  41
                  (U90439) Cys3His zinc finger protein isolog [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  312842
Seq. ID
                  xmt700265393.h1
Method
                  BLASTX
NCBI GI
                  g3834306
BLAST score
                  149
E value
                  7.0e-10
Match length
                  35
% identity
                  71
                  (AC005679) EST gb_R65024 comes from this gene. [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  312843
                  xmt700265413.h1
Seq. ID
Method
                  BLASTX
                  g3193288
NCBI GI
BLAST score
                  170
                  1.0e-12
E value
Match length
                   47
                  68
% identity
                  (AF069298) similar to bacterial and fungi pectinesterases
NCBI Description
                   [Arabidopsis thaliana]
                  312844
Seq. No.
                  xmt700265503.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g551287
BLAST score
                  33
                  2.0e-09
E value
                  53
Match length
                  91
% identity
NCBI Description Z.mays (W22) phosphoglycerate mutase gene (exon 1)
```

312845 Seq. No.

xmt700265528.h1 Seq. ID

Method BLASTN NCBI GI g168508



```
BLAST score
                  2.0e-97
E value
                  248
Match length
% identity
                  93
NCBI Description Maize oleosin KD18 (KD18; L2) gene, complete cds
                  312846
Seq. No.
                  xmt700265601.h1
Seq. ID
                  BLASTN
Method
                  g21399
NCBI GI
BLAST score
                  55
                  2.0e-22
E value
Match length
                  67
                  96
% identity
NCBI Description Solanum tuberosum processed actin pseudogene
                  312847
Seq. No.
                  xmt700265648.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2130141
BLAST score
                  240
                  2.0e-20
E value
Match length
                  93
% identity
                  54
                  mudrA protein - maize transposon MuDR >gi 540581 (M76978)
NCBI Description
                  mudrA [Zea mays] >gi 595816 (U14597) mudrA gene product
                   [Zea mays]
Seq. No.
                  312848
                  xmt700265650.h1
Seq. ID
                  BLASTX
Method
                  q2499535
NCBI GI
BLAST score
                   139
                   6.0e-09
E value
                   32
Match length
                   88
% identity
                  2-OXOGLUTARATE/MALATE TRANSLOCATOR PRECURSOR >gi_595681
NCBI Description
                   (U13238) 2-oxoglutarate/malate translocator [Spinacia
                   oleracea]
                   312849
Seq. No.
                  xmt700265657.h1
Seq. ID
                  BLASTX
Method
                   g3695388
NCBI GI
BLAST score
                   170
                   3.0e-12
E value
Match length
                   35
                   71
% identity
                  (AF096371) No definition line found [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   312850
Seq. ID
                   xmt700265662.h1
```

Method BLASTX g123593 NCBI GI BLAST score 368 E value 2.0e-35 Match length 76

```
% identity
                  HEAT SHOCK 70 KD PROTEIN >gi 82697 pir A25089 heat shock
NCBI Description
                  protein 70 - maize
Seq. No.
                  312851
Seq. ID
                  xmt700265681.h1
Method
                  BLASTN
NCBI GI
                  q687244
BLAST score
                  67
E value
                  7.0e-30
Match length
                  103
% identity
                  92
NCBI Description
                  Zea mays oil body protein 16 kDa oleosin (ole16) gene,
                  complete cds
Seq. No.
                  312852
```

Seq. ID xmt700265693.h1
Method BLASTX
NCBI GI g4325345
BLAST score 146
E value 2.0e-09
Match length 53

Match length 53 % identity 51

NCBI Description (AF128393) similar to thioredoxin-like proteins (Pfam: PF00085, Score=42.9, E=1.4e-11, N=1); contains similarity to dihydroorotases (Pfam: PF00744, Score=154.9, E=1.4e-42,

N=1) [Arabidopsis thaliana]

Seq. No. 312853

Seq. ID xmt700265749.h1

Method BLASTX
NCBI GI g4262233
BLAST score 173
E value 1.0e-12
Match length 59
% identity 63

NCBI Description (AC006200) hypothetical protein [Arabidopsis thaliana]

Seq. No. 312854

Seq. ID xmt700265836.h1

Method BLASTX
NCBI GI g3341692
BLAST score 190
E value 9.0e-15
Match length 86
% identity 52

NCBI Description (AC003672) unknown protein [Arabidopsis thaliana]

Seq. No. 312855

Seq. ID xmt700265901.h1

Method BLASTX
NCBI GI g3334474
BLAST score 146
E value 2.0e-10
Match length 61
% identity 70

NCBI Description OLEOSIN ZM-I (OLEOSIN 16 KD) (LIPID BODY-ASSOCIATED MAJOR



PROTEIN) (LIPID BODY-ASSOCIATED PROTEIN L3) >gi_1076817_pir__S52029 oleosin 16 - maize >gi_687245 (U13701) 16 kDa oleosin [Zea mays]

312856 Seq. No.

xmt700265920.h1 Seq. ID

Method BLASTN NCBI GI q297017 BLAST score 64 7.0e-28 E value 104 Match length % identity 91

NCBI Description Z.mays OBF3.2 mRNA for ocs-element binding factor 3.2

Seq. No. 312857

xmt700265924.h1 Seq. ID

Method BLASTX g3608412 NCBI GI BLAST score 207 E value 5.0e-18 Match length 72 % identity 69

(AF079355) protein phosphatase-2c [Mesembryanthemum NCBI Description

crystallinum]

Seq. No. 312858

xmt700265950.h1 Seq. ID

Method BLASTX NCBI GI g2462736 BLAST score 178 E value 5.0e-23 Match length 64 97 % identity

NCBI Description (AC002292) putative ADP-ribolylation factor [Arabidopsis

thaliana]

312859 Seq. No.

xmt700265968.h1 Seq. ID

Method BLASTX NCBI GI g1272680 BLAST score 177 E value 5.0e-13 Match length 53 % identity 64

(X81072) YTA7 [Saccharomyces cerevisiae] NCBI Description

Seq. No. 312860

xmt700265988.h1 Seq. ID

Method BLASTX g2191135 NCBI GI BLAST score 180 E value 3.0e-15 Match length 93 % identity 45

NCBI Description (AF007269) A IG002N01.14 gene product [Arabidopsis

thaliana]

```
312861
Seq. No.
                   xmt700266006.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3805764
BLAST score
                   150
                   3.0e-10
E value
                   43
Match length
% identity
                   63
                  (AC005693) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   312862
                   xmt700266007.h1
Seq. ID
Method
                   BLASTX
                   g4587990
                   183
```

NCBI GI BLAST score E value 4.0e-14 Match length 49 % identity 63

(AF085279) hypothetical protein [Arabidopsis thaliana] NCBI Description

Seq. No. 312863 xmt700266022.h1 Seq. ID Method BLASTN NCBI GI g3819442 BLAST score 43

E value 4.0e-15 Match length 51 % identity 96

NCBI Description Hordeum vulgare genomic DNA fragment; clone MWG0939.rev

Seq. No. 312864

Seq. ID xmt700266060.h1

Method BLASTX NCBI GI g3334474 BLAST score 158 E value 8.0e-12 Match length 62 % identity 73:

OLEOSIN ZM-I (OLEOSIN 16 KD) (LIPID BODY-ASSOCIATED MAJOR NCBI Description

PROTEIN) (LIPID BODY-ASSOCIATED PROTEIN L3)

>gi 1076817 pir S52029 oleosin 16 - maize >gi 687245

(U13701) 16 kDa oleosin [Zea mays]

312865 Seq. No.

xmt700266073.h1 Seq. ID

Method BLASTX NCBI GI g2394306 BLAST score 355 6.0e-34 E value 96 Match length 67 % identity

NCBI Description (AF017269) 73 kDA subunit of cleavage and polyadenylation

specificity factor [Homo sapiens]

312866 Seq. No.

Seq. ID xmt700266087.h1

Method BLASTX

Method

NCBI GI

BLAST score

BLASTX

147

g120777



```
g388053
NCBI GI
BLAST score
                  297
E value
                  4.0e-27
Match length
                  57
% identity
                  100
                  (L23548) alcohol dehydrogenase [Zea mays]
NCBI Description
                  312867
Seq. No.
                  xmt700266137.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3242789
BLAST score
                  197
E value
                  1.0e-22
Match length
                  71
% identity
NCBI Description
                  (AF055357) respiratory burst oxidase protein D [Arabidopsis
                  thaliana]
                  312868
Seq. No.
Seq. ID
                  xmt700266166.h1
                  BLASTX
Method
NCBI GI
                  q100849
BLAST score
                  162
                  1.0e-11
E value
                  33
Match length
                  97
% identity
NCBI Description
                  acetolactate synthase (EC 4.1.3.18) (clone pSOG108) - maize
                  >gi 22139 emb CAA45116 (X63553) acetohydroxyacid synthase
                   [Zea mays]
                  312869
Seq. No.
Seq. ID
                  xmt700266177.h1
Method
                  BLASTX
NCBI GI
                  q3785984
BLAST score
                  170
E value
                   3.0e-12
Match length
                   90
% identity
                   39
                  (AC005560) putative reverse transcriptase [Arabidopsis
NCBI Description
                  thaliana]
                   312870
Seq. No.
Seq. ID
                  xmt700266187.h1
Method
                  BLASTX
NCBI GI
                   q4204284
BLAST score
                   245
E value
                   5.0e-21
Match length
                   101
% identity
                   48
                   (AC003027) 1cl prt seq No definition line found
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   312871
Seq. ID
                  xmt700266206.h1
```



```
E value
Match length
                  65
% identity
                  SUCCINATE-SEMIALDEHYDE DEHYDROGENASE (NADP+) (SSDH)
NCBI Description
                  >qi 147901 (M88334) succinic semialdehyde dehydrogenase
                  [Escherichia coli] >gi 1789015 (AE000351)
                  succinate-semialdehyde dehydrogenase, NADP-dependent
                  activity [Escherichia coli]
                  312872
Seq. No.
Seq. ID
                  xmt700266217.h1
                  BLASTN
Method
                  g397395
NCBI GI
BLAST score
                  190
E value
                  1.0e-103
Match length
                  190
% identity
                  100
NCBI Description Z.mays MNB1b mRNA for DNA-binding protein
                  312873
Seq. No.
Seq. ID
                  xmt700266260.h1
Method
                  BLASTX
NCBI GI
                  q2832620
BLAST score
                  175
E value
                  8.0e-13
                  64
Match length
% identity
NCBI Description (AL021711) hypothetical protein [Arabidopsis thaliana]
                  312874
Seq. No.
                  xmt700266294.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2649395
                  173
BLAST score
                  1.0e-12
E value
                  99
Match length
                   47
% identity
NCBI Description
                  (AE001022) 3-hydroxyacyl-CoA dehydrogenase (hbd-7)
                   [Archaeoglobus fulgidus]
                   312875
Seq. No.
Seq. ID
                  xmt700266326.h1
Method
                  BLASTX
NCBI GI
                   q4220474
BLAST score
                  198
E value
                   1.0e-15
Match length
                  79
                   53
% identity
```

NCBI Description (AC006069) putative myosin heavy chain [Arabidopsis

thaliana]

Seq. No. 312876

Seq. ID xmt700266348.h1

Method BLASTN
NCBI GI g22292
BLAST score 161
E value 1.0e-85



Match length 173 % identity 98

NCBI Description Z.mays mRNA for glycine-rich protein

Seq. No. 312877

Seq. ID xmt700266465.h1

Method BLASTX
NCBI GI g100876
BLAST score 171
E value 2.0e-12
Match length 64
% identity 98

NCBI Description globulin-2 precursor - maize >gi 228310 prf 1802402A

globulin 2 [Zea mays]

Seq. No. 312878

Seq. ID xmt700266504.h1

Method BLASTX
NCBI GI g3915865
BLAST score 262
E value 3.0e-23
Match length 50
% identity 98

NCBI Description 40S RIBOSOMAL PROTEIN S4

Seq. No. 312879

Seq. ID xmt700266556.h1

Method BLASTX
NCBI GI g2191177
BLAST score 252
E value 6.0e-22
Match length 79
% identity 66

NCBI Description (AF007270) belongs to the SPOU family of rRNA methylases.

[Arabidopsis thaliana]

Seq. No. 312880

Seq. ID xmt700266602.h1

Method BLASTX
NCBI GI g3913791
BLAST score 225
E value 9.0e-39
Match length 91
% identity 93

NCBI Description GLUTAMATE--CYSTEINE LIGASE PRECURSOR

(GAMMA-GLUTAMYLCYSTEINE SYNTHETASE) (GAMMA-ECS) (GCS) >gi_2407615 (AF017983) gamma-glutamylcysteine synthetase

[Lycopersicon esculentum]

Seq. No. 312881

Seq. ID xmt700266631.h1

Method BLASTX
NCBI GI g710308
BLAST score 271
E value 4.0e-24
Match length 57
% identity 96





NCBI Description (U11693) victorin binding protein [Avena sativa]

Seq. No. 312882

Seq. ID xmt700266744.h1

Method BLASTX
NCBI GI g927239
BLAST score 238
E value 4.0e-27
Match length 69
% identity 91

NCBI Description (U28017) globulin1 [Zea mays]

Seq. No. 312883

Seq. ID xmt700266786.h1

Method BLASTX
NCBI GI g3687445
BLAST score 180
E value 2.0e-13
Match length 89
% identity 47

NCBI Description (AL022398) dJ434014.5 (novel PUTATIVE protein similar to

YIL091C yeast hypoyhetical 84 kD protein from SGA1-KTR7

intergenic region) [Homo sapiens]

Seq. No. 312884

Seq. ID xmt700266886.h1

Method BLASTX
NCBI GI g122087
BLAST score 278
E value 3.0e-25
Match length 55
% identity 100

NCBI Description HISTONE H3 >gi 81849 pir S04520 histone H3 (clone pH3c-1)

- alfalfa >gi_82609_pir__A26014 histone H3 - wheat >gi_19607_emb_CAA31964_ (X13673) histone H3 (AA 1-136) [Medicago sativa] >gi_19609_emb_CAA31965_ (X13674) histone H3 (AA 1-136) [Medicago sativa] >gi_21797_emb_CAA25451_ (X00937) H3 histone [Triticum aestivum] >gi_488565 (U09459)

histone H3.1 [Medicago sativa] >gi 2565419 (AF026803)

histone H3 [Onobrychis viciifolia]

Seq. No. 312885

Seq. ID xmt700266936.h1

Method BLASTX
NCBI GI g3850576
BLAST score 350
E value 1.0e-33
Match length 72
% identity 92

NCBI Description (AC005278) Strong similarity to gb U04968 nucleotide

excision repair protein (ERCC2) from Cricetulus grisseus.

[Arabidopsis thaliana]

Seq. No. 312886

Seq. ID xmt700266938.h1

Method BLASTX NCBI GI g4581149



```
BLAST score
E value
                  1.0e-22
Match length
                  71
% identity
                  70
NCBI Description
                  (AC006919) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  312887
                  xmt700266939.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3023816
BLAST score
                  258
                  6.0e-23
E value
Match length
                  52
% identity
                  98
NCBI Description
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
                  >gi 968996 (U31676) glyceraldehyde-3-phosphate
                  dehydrogenase [Oryza sativa]
Seq. No.
                  312888
Seq. ID
                  xmt700267027.h1
Method
                  BLASTX
NCBI GI
                  g2673917
BLAST score
                  314
E value
                  2.0e-29
Match length
                  73
% identity
NCBI Description
                  (AC002561) putative ATP-dependent RNA helicase [Arabidopsis
                  thaliana]
                  312889
Seq. No.
                  xmt700267081.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g112994
BLAST score
                  195
E value
                  1.0e-15
Match length
                  45
                  87
% identity
NCBI Description
                  GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN
                  >gi_82685_pir__S04536 embryonic abundant protein,
                  glycine-rich - maize >gi 22313 emb CAA31077 (X12564)
                  ABA-inducible gene protein [Zea mays]
                  >gi_226091_prf__1410284A abscisic acid inducible gene [Zea
                  mays]
                  312890
Seq. No.
                  xmt700267183.h1
Seq. ID
Method
                  BLASTX
                  g3687654
                  172
```

NCBI GI BLAST score E value 1.0e-12 Match length 95 % identity 47

NCBI Description (AF047975) putative ethylene receptor; ETR2 [Arabidopsis

thaliana]

Seq. No. 312891

Seq. ID xmt700267209.h1

NCBI GI

BLAST score

g3834321

234



```
BLASTX
Method
NCBI GI
                  g3935138
                  161
BLAST score
                  3.0e-11
E value
Match length
                  97
                  34
% identity
                  (AC005106) T25N20.2 [Arabidopsis thaliana]
NCBI Description
                  312892
Seq. No.
                  xmt700267256.h1
Seq. ID
Method
                  BLASTN
                  g3452292
NCBI GI
BLAST score
                  85
                  3.0e-40
E value
Match length
                  240
% identity
                  86
NCBI Description Zea mays retrotransposon Ji-1 3' LTR, partial sequence
Seq. No.
                  312893
                  xmt700267267.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q687244
BLAST score
                  143
                  9.0e-75
E value
Match length
                  214
% identity
                  92
                  Zea mays oil body protein 16 kDa oleosin (ole16) gene,
NCBI Description
                  complete cds
                  312894
Seq. No.
                  xmt700267284.h1
Seq. ID
Method
                  BLASTX
                  q2117937
NCBI GI
BLAST score
                  179
                  2.0e-13
E value
Match length
                  35
% identity
                  94
                  UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) -
NCBI Description
                  barley >gi 1212996_emb_CAA62689_ (X91347) UDP-glucose
                  pyrophosphorylase [Hordeum vulgare]
Seq. No.
                  312895
                  xmt700267319.h1
Seq. ID
                  BLASTN
Method
                  g2781432
NCBI GI
BLAST score
                  45
                  3.0e-16
E value
Match length
                  81
                  89
% identity
                  Oryza sativa subsp. japonica RSW1-like cellulose synthase
NCBI Description
                  catalytic subunit mRNA, partial cds
                  312896
Seq. No.
                  xmt700267328.h1
Seq. ID
Method
                  BLASTX
```



E value 7.0e-26 Match length 79 % identity 78

NCBI Description (AC005679) Strong similarity to F13P17.9 gi_3337356

transport protein SEC61 alpha subunit homolog from Arabidopsis thaliana BAC gb_AC004481. [Arabidopsis

thaliana]

312897

312898

Seq. No.

Seq. ID xmt700267436.h1

Method BLASTX
NCBI GI g3334474
BLAST score 156
E value 1.0e-11
Match length 75
% identity 60

NCBI Description OLEOSIN ZM-I (OLEOSIN 16 KD) (LIPID BODY-ASSOCIATED MAJOR

PROTEIN) (LIPID BODY-ASSOCIATED PROTEIN L3)

>gi 1076817 pir S52029 oleosin 16 - maize >gi 687245

(U13701) 16 kDa oleosin [Zea mays]

Seq. No.

Seq. ID xmt700267449.h1

Method BLASTX
NCBI GI g2130090
BLAST score 297
E value 4.0e-27
Match length 71
% identity 83

NCBI Description 2-oxoglutarate/malate translocator (clone OMT134),

mitochondrial membrane - proso millet

>gi_1100739_dbj_BAA08103_ (D45073) 2-oxoglutarate/malate
translocator [Panicum miliaceum] >gi_1100741_dbj_BAA08104_
(D45074) 2-oxoglutarate/malate translocator [Panicum

miliaceum]

Seq. No. 312899

Seq. ID xmt700267473.h1

Method BLASTX
NCBI GI g4567220
BLAST score 332
E value 3.0e-31
Match length 100
% identity 58

NCBI Description (AC007119) hypothetical protein, 3' partial [Arabidopsis

thaliana]

Seq. No. 312900

Seq. ID xmt700267568.h1

Method BLASTX
NCBI GI g1113941
BLAST score 143
E value 3.0e-13
Match length 64
% identity 70

NCBI Description (U40713) Pv42p [Phaseolus vulgaris]



xmt700267571.h1

Method BLASTX
NCBI GI g1174850
BLAST score 150
E value 6.0e-10
Match length 30
% identity 97

NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-21 KD 2 (UBIQUITIN-PROTEIN

LIGASE 5) (UBIQUITIN CARRIER PROTEIN 5)

Seq. No.

Seq. ID xmt700267592.h1

312902

Method BLASTX
NCBI GI g3024018
BLAST score 382
E value 3.0e-37
Match length 72
% identity 100

NCBI Description INITIATION FACTOR 5A (EIF-5A) (EIF-4D)

>gi_1546919_emb_CAA69225_ (Y07920) translation initiation factor 5A [Zea mays] >gi_2668738 (AF034943) translation

,47

initiation factor 5A [Zea mays]

Seq. No. 312903

Seq. ID xmt700267649.h1

Method BLASTN
NCBI GI g22270
BLAST score 129
E value 9.0e-67
Match length 133
% identity 99

NCBI Description Maize mRNA from an embryogenic abscisic acid-inducible gene

Seq. No.

Seq. ID xmt700267661.h1

312904

Method BLASTX
NCBI GI g2335096
BLAST score 147
E value 1.0e-17
Match length 94
% identity 53

NCBI Description (AC002339) hypothetical protein [Arabidopsis thaliana]

Seq. No. 312905

Seq. ID xmt700267757.h1

Method BLASTX
NCBI GI g1652434
BLAST score 173
E value 6.0e-13
Match length 57
% identity 58

NCBI Description (D90905) N-acetylglutamate kinase [Synechocystis sp.]

Seq. No. 312906

Seq. ID xmt700267786.h1

Method BLASTX



```
NCBI GI
                  q1351136
BLAST score
                  232
E value
                  7.0e-20
Match length
                  46
                  100
% identity
NCBI Description
                  SUCROSE SYNTHASE 2 (SUCROSE-UDP GLUCOSYLTRANSFERASE 2)
                  >gi 514946 (L22296) UDP-glucose:D-fructose
                  2-glucosyl-transferase [Zea mays] >qi 533252 (L33244)
                  sucrose synthase 2 [Zea mays]
Seq. No.
                  312907
Seq. ID
                  xmt700267956.h1
Method
                  BLASTN
NCBI GI
                  g687244
BLAST score
                  124
E value
                  1.0e-63
Match length
                  151
% identity
                  95
NCBI Description
                  Zea mays oil body protein 16 kDa oleosin (ole16) gene,
                  complete cds
Seq. No.
                  312908
Seq. ID
                  xmt700268014.h1
Method
                  BLASTX
NCBI GI
                  g4539005
BLAST score
                  140
E value
                  4.0e-09
Match length
                  62
% identity
                  45
NCBI Description
                  (AL049481) putative oxidoreductase [Arabidopsis thaliana]
Seq. No.
                  312909
                  xmt700268038.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g687244
BLAST score
                  182
E value
                  3.0e-98
Match length
                  193
% identity
                  99
NCBI Description
                  Zea mays oil body protein 16 kDa oleosin (ole16) gene,
                  complete cds
                  312910
Seq. No.
Seq. ID
                  xmt700268057.h1
Method
                  BLASTX
                  g2443329
NCBI GI
BLAST score
                  147
E value
                  6.0e-10
Match length
                  33
% identity
                  82
```

NCBI Description (D86122) Mei2-like protein [Arabidopsis thaliana]

Seq. No.

312911

Seq. ID xmt700268101.h1

Method BLASTN NCBI GI g257809 BLAST score 176



```
E value
                  1.0e-94
Match length
                  195
% identity
                  98
                  cyppdkZm2=orthophosphate dikinase [maize, Genomic, 871 nt]
NCBI Description
                  312912
Seq. No.
                  xmt700268135.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g940880
BLAST score
                  39
                  7.0e-13
E value
Match length
                  83
% identity
                  87
NCBI Description
                  Z.mays zag2 gene
Seq. No.
                  312913
                  xmt700268164.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q3510343
BLAST score
                  42
                  2.0e-14
E value
Match length
                  74
% identity
                  89
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MJC20, complete sequence [Arabidopsis thaliana]
Seq. No.
                  312914
Seq. ID
                  xsy700207333.h1
Method
                  BLASTX
NCBI GI
                  g2583127
BLAST score
                  158
E value
                  6.0e-11
Match length
                  42
% identity
                  71
NCBI Description
                  (AC002387) putative sialoglycoprotease [Arabidopsis
                  thaliana]
Seq. No.
                  312915
                  xsy700207365.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2244772
BLAST score
                  217
E value
                  5.0e-18
Match length
                  77
% identity
                  58
NCBI Description
                  (Z97335) transport protein [Arabidopsis thaliana]
```

Seq. No. 312916

Seq. ID xsy700207394.h1 Method BLASTX

g3298551 NCBI GI BLAST score 152 2.0e-10 E value Match length 74 % identity 21

NCBI Description (AC004681) putative salt-inducible protein [Arabidopsis

thaliana]



```
312917
Seq. No.
                  xsy700207407.hl
Seq. ID
Method
                  BLASTX
                  q2262105
NCBI GI
BLAST score
                  155
                  1.0e-10
E value
Match length
                  69
% identity
                  41
                  (AC002343) unknown protein [Arabidopsis thaliana]
NCBI Description
                  312918
Seq. No.
                  xsy700207415.h1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4336692
BLAST score
                  148
                  1.0e-09
E value
Match length
                  88
                  38
% identity
                  (AF101361) Abnormal X segregation [Drosophila melanogaster]
NCBI Description
                  312919
Seq. No.
                  xsy700207429.h1
Seq. ID
                  BLASTN
Method
                  g3821780
NCBI GI
BLAST score
                  36
                  7.0e-11
E value
Match length
                  36
% identity
                  100
                  Xenopus laevis cDNA clone 27A6-1
NCBI Description
                  312920
Seq. No.
                  xsy700207459.h1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3482977
BLAST score
                  153
                  2.0e-10
E value
Match length
                  39
                  77
% identity
                  (AL031369) putative protein [Arabidopsis thaliana]
NCBI Description
                  312921
Seq. No.
                  xsy700207526.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3924594
BLAST score
                  384
                  2.0e-37
E value
                  95
Match length
                  75
% identity
                  (AF069442) putative ribonucleoprotein [Arabidopsis
NCBI Description
                  thaliana] >gi 4262139 gb AAD14439_ (AC005275) putative
                  ribonucleoprotein [Arabidopsis thaliana]
```

Seq. No. 312922

Seq. ID xsy700207541.h1

Method BLASTX NCBI GI g3724087



```
BLAST score
                  4.0e-32
E value
Match length
                  101
                  64
% identity
                  (AJ011840) 1-deoxyxylulose 5-phosphate synthase
NCBI Description
                  [Catharanthus roseus]
                  312923
Seq. No.
                  xsy700207546.hl
Seq. ID
Method
                  BLASTN
                  g2463511
NCBI GI
                  250
BLAST score
                  1.0e-138
E value
                  288
Match length
% identity
                  97
                  Z.mays small nuclear RNA genes snoR1.4, snoR2.4, snoR3.4,
NCBI Description
                  U14.4 and snoR4.4
                  312924
Seq. No.
                  xsy700207554.h1
Seq. ID
Method
                  BLASTN
                  g22239
NCBI GI
BLAST score
                  44
                  5.0e-16
E value
                  75
Match length
% identity
                  91
                  Maize cytosolic mRNA for subunit A of chloroplast GAPDH
NCBI Description
                   (GapA) glyceraldehyde-3-phosphate dehydrogenase
                  312925
Seq. No.
                  xsy700207577.h1
Seq. ID
                  BLASTX
Method
                  g2960216
NCBI GI
                  158
BLAST score
                  7.0e-11
E value
Match length
                  54
                   56
% identity
                  (AJ223384) 26S proteasome regulatory ATPase subunit 10b
NCBI Description
                   (S10b) [Manduca sexta]
                   312926
Seq. No.
                   xsy700207646.h1
Seq. ID
Method
                   BLASTX
                   q1346057
NCBI GI
BLAST score
                   386
                   1.0e-37
E value
Match length
                   89
% identity
                   82
                  PROTEIN KINASE G11A >gi 100705_pir__B30311 protein kinase C
NCBI Description
                   (EC 2.7.1.-) homolog - rice (fragment) >gi_169788 (J04556)
```

G11A protein [Oryza sativa]

312927 Seq. No.

xsy700207674.h1 Seq. ID

Method BLASTX NCBI GI q4584525 BLAST score 291



104

42

Match length

NCBI Description

% identity

```
2.0e-26
E value
Match length
                   105
% identity
NCBI Description
                   (AL049607) protein phosphatase 2C-like protein [Arabidopsis
                   thaliana]
                   312928
Seq. No.
                  xsy700207707.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2244987
BLAST score
                   181
E value
                   2.0e-13
                   56
Match length
                   55
% identity
                  (Z97340) similarity to protein kinase - slime mold
NCBI Description
                   (Dictyostelium) [Arabidopsis thaliana]
Seq. No.
                   312929
                   xsy700207710.h1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g483409
BLAST score
                   191
                   1.0e-103
E value
                   215
Match length
                   97
% identity
                  Zea Mays calmodulin-binding protein mRNA, 3'end
NCBI Description
                   312930
Seq. No.
Seq. ID
                   xsy700207740.hl
Method
                   BLASTX
NCBI GI
                   q3080374
BLAST score
                   156
E value
                   8.0e-11
Match length
                   79
% identity
                   38
                   (AL022580) putative protein [Arabidopsis thaliana]
NCBI Description
                   312931
Seq. No.
                   xsy700207875.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4510395
BLAST score
                   429
E value
                   2.0e-47
                   102
Match length
                   79
% identity
                   (AC006587) putative beta-galactosidase precursor
NCBI Description
                   [Arabidopsis thaliana]
                   312932
Seq. No.
                   xsy700207934.h1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3128187
BLAST score
                   207
                   1.0e-16
E value
```

(AC004521) putative beta-glucosidase [Arabidopsis thaliana]



Seq. No. 312933

Seq. ID xsy700207989.h1

Method BLASTX
NCBI GI g1730771
BLAST score 171
E value 2.0e-12
Match length 87
% identity 39

NCBI Description HYPOTHETICAL 110.9 KD PROTEIN IN SPC98-TOM70 INTERGENIC

REGION >gi_2132752_pir__S63064 probable membrane protein

YNL123w - yeast (Saccharomyces cerevisiae)

>gi_1183950_emb_CAA93384_ (Z69382) N1897 [Saccharomyces
cerevisiae] >gi_1302054_emb_CAA96004_ (Z71399) ORF YNL123w

[Saccharomyces cerevisiae]

Seq. No. 312934

Seq. ID xsy700208019.h1

Method BLASTX
NCBI GI g3135274
BLAST score 172
E value 2.0e-12
Match length 52
% identity 67

NCBI Description (AC003058) putative beta-1,3-endoglucanase [Arabidopsis

thaliana]

Seq. No. 312935

Seq. ID xsy700208058.h1

Method BLASTX
NCBI GI g2462826
BLAST score 238
E value 3.0e-20
Match length 95
% identity 56

NCBI Description (AF000657) unknown protein [Arabidopsis thaliana]

Seq. No. 312936

Seq. ID xsy700208075.h1

Method BLASTX
NCBI GI g4585977
BLAST score 176
E value 5.0e-13
Match length 47
% identity 68

NCBI Description (AC005287) Unknown protein [Arabidopsis thaliana]

Seq. No. 312937

Seq. ID xsy700208078.h1

Method BLÄSTX
NCBI GI g115865
BLAST score 228
E value 6.0e-21
Match length 84
% identity 62

NCBI Description [Segment 2 of 2] SERINE CARBOXYPEPTIDASE II CHAINS A AND B

(CARBOXYPEPTIDASE D) (CP-MII) >gi_82420_pir__B29640



serine-type carboxypeptidase (EC 3.4.16.1) II B chain -

Seq. No. 312938

Seq. ID xsy700208080.h1

Method BLASTX
NCBI GI g2494113
BLAST score 215
E value 4.0e-19
Match length 82
% identity 61

NCBI Description (AC002376) Strong similarity to Musa pectate lyase

(gb_X92943). ESTs gb_AA042458, gb ATTS4502, gb N38552 come

from this gene. [Arabidopsis thaliana]

Seq. No. 312939

Seq. ID xsy700208093.h1

Method BLASTX
NCBI GI g1321661
BLAST score 326
E value 9.0e-31
Match length 74
% identity 85

NCBI Description (D45423) ascorbate peroxidase [Oryza sativa]

Seq. No. 312940

Seq. ID xsy700208101.h1

Method BLASTX
NCBI GI g1883026
BLAST score 199
E value 1.0e-15
Match length 48
% identity 85

NCBI Description (X91513) histone H4 [Diprion pini]

Seq. No. 312941

Seq. ID xsy700208131.h1

Method BLASTX
NCBI GI g3913427
BLAST score 176
E value 7.0e-13
Match length 50
% identity 72

NCBI Description S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC)

(SAMDC) >gi_1532073_emb_CAA69075_ (Y07767) S-adenosylmethionine decarboxylase [Zea mays]

Seq. No. 312942

Seq. ID xsy700208153.h1

Method BLASTX
NCBI GI g115771
BLAST score 553
E value 4.0e-57
Match length 104
% identity 100

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-1) (LHCP) >gi 82682 pir S04453 chlorophyll



a/b-binding protein precursor - maize >gi 22224_emb_CAA32900_ (X14794) chlorophyll a/b-binding

preprotein (AA 1 - 262) [Zea mays]

Seq. No. 312943

Seq. ID xsy700208156.h1

Method BLASTX
NCBI GI g2984715
BLAST score 146
E value 2.0e-09
Match length 74

% identity 41

NCBI Description (AF053957) dynamin associated protein isoform Dap160-1

[Drosophila melanogaster]

Seq. No. 312944

Seq. ID xsy700208158.h1

Method BLASTX
NCBI GI g2623246
BLAST score 342
E value 2.0e-32
Match length 80
% identity 85

NCBI Description (AF030709) poly(A) polymerase [Pisum sativum]

Seq. No. 312945

Seq. ID xsy700208169.h1

Method BLASTX
NCBI GI g1352427
BLAST score 289
E value 4.0e-26
Match length 55
% identity 96

NCBI Description EUKARYOTIC TRANSLATION INITIATION FACTOR 1A (EIF-1A)

(EIF-4C)

Seq. No. 312946

Seq. ID xsy700208244.h1

Method BLASTX
NCBI GI g130288
BLAST score 152
E value 3.0e-10
Match length 46
% identity 76

NCBI Description PLASTOCYANIN >gi_65843_pir__CUVF plastocyanin - fava bean

Seq. No. 312947

Seq. ID xsy700208264.h1

Method BLASTX
NCBI GI g1632822
BLAST score 193
E value 1.0e-18
Match length 53
% identity 89

NCBI Description (Y08962) transmembrane protein [Oryza sativa] >gi 1667594

(U77297) transmembrane protein [Oryza sativa]



```
Seq. No.
Seq. ID
                  xsy700208278.h1
                  BLASTX
Method
NCBI GI
                  g3122952
BLAST score
                  220
                  7.0e-18
E value
                  137
Match length
                  40
% identity
                  TIPD PROTEIN >qi 2407788 (AF019236) TipD [Dictyostelium
NCBI Description
                  discoideum]
Seq. No.
                  312949
```

Seq. ID xsy700208296.h1

BLASTX Method NCBI GI g1345132 BLAST score 263 E value 2.0e-23 Match length 75 % identity

(U47029) ERECTA [Arabidopsis thaliana] NCBI Description

> >qi 1389566 dbj BAA11869 (D83257) receptor protein kinase [Arabidopsis thaliana] >gi 3075386 (AC004484) receptor

> > 2

protein kinase, ERECTA [Arabidopsis thaliana]

312950 Seq. No.

Seq. ID xsy700208306.h1

Method BLASTX NCBI GI g129916 BLAST score 441 E value 6.0e-44Match length 94 % identity

PHOSPHOGLYCERATE KINASE, CYTOSOLIC >gi 66911 pir TVWTGY NCBI Description phosphoglycerate kinase (EC 2.7.2.3), cytosolic - wheat

>gi 21835 emb CAA33302 (X15232) phosphoglycerate kinase

(AA 1 - 401) [Triticum aestivum]

312951 Seq. No.

xsy700208405.h1 Seq. ID

Method BLASTN NCBI GI g168421 BLAST score 130 6.0e-67 E value Match length 157 96 % identity

NCBI Description Maize auxin-binding protein (ABP) mRNA, complete cds

312952 Seq. No.

xsy700208410.h1 Seq. ID

Method BLASTX NCBI GI g4105772 BLAST score 340 E value 4.0e-32 Match length 78 39 % identity

NCBI Description (AF049917) PGP9B [Petunia x hybrida]



```
312953
Seq. No.
                  xsy700208424.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q473874
BLAST score
                  304
                  6.0e-28
E value
Match length
                  84
% identity
                  68
                   (U08285) a membrane-associated salt-inducible protein
NCBI Description
                   [Nicotiana tabacum]
                  312954
Seq. No.
                  xsy700208437.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2293566
BLAST score
                  253
E value
                  4.0e-22
Match length
                  57
% identity
                  91
                  (AF012896) ADP-ribosylation factor 1 [Oryza sativa]
NCBI Description
                  312955
Seq. No.
                  xsy700208460.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3928142
BLAST score
                  346
E value
                   6.0e-33
Match length
                  73
% identity
                  90
                  (AJ131045) protein phosphatase [Cicer arietinum]
NCBI Description
Seq. No.
                  312956
                  xsy700208488.h1
Seq. ID
Method
                  BLASTX
                  g2191136
NCBI GI
BLAST score
                  139
                  2.0e-09
E value
Match length
                  87
% identity
                  41
                  (AF007269) Similar to UTP-Glucose Glucosyltransferase;
NCBI Description
                  coded for by A. thaliana cDNA T46230; coded for by A.
                  thaliana cDNA H76538; coded for by A. thaliana cDNA H76290
                   [Arabidopsis thaliana]
                  312957
Seq. No.
                  xsy700208530.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2149640
BLAST score
                  243
E value
                  8.0e-21
Match length
                  97
                  79
% identity
```

NCBI Description (U91995) Argonaute protein [Arabidopsis thaliana]

312958 Seq. No.

Seq. ID xsy700208541.h1

Method BLASTX



```
g168489
NCBI GI
BLAST score
                  291
                  2.0e-26
E value
Match length
                  61
% identity
                  92
                  (M16902) glutathione S-transferase I [Zea mays] >gi 168491
NCBI Description
                  (M16901) glutathione S-transferase I [Zea mays]
                  >qi 225458 prf 1303351A transferase,qlutathione S [Zea
                  mays]
                  312959
Seq. No.
                  xsy700208572.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1498596
BLAST score
                  139
E value
                  1.0e-72
                  143
Match length
                  99
% identity
                  Zea mays phospholipid transfer protein mRNA, complete cds
NCBI Description
Seq. No.
                  312960
                  xsy700208578.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3402690
BLAST score
                  140
E value
                  2.0e-10
Match length
                  43
% identity
                  86
NCBI Description
                  (AC004697) hypothetical protein, 3' partial [Arabidopsis
                  thaliana]
                  312961
Seq. No.
                  xsy700208584.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1895083
BLAST score
                  126
                  8.0e-65
E value
Match length
                  142
                  97
% identity
                  Zea mays golgi associated protein se-wap41 mRNA, complete
NCBI Description
                  cds
Seq. No.
                  312962
Seq. ID
                  xsy700208587.hl
Method
                  BLASTX
NCBI GI
                  g3135251
BLAST score
                  142
E value
                  2.0e-09
```

Match length 59 % identity 44

(AC003058) putative receptor protein kinase [Arabidopsis NCBI Description

thaliana] >gi_3176719 (AC002392) putative protein kinase

[Arabidopsis thaliana]

Seq. No. 312963

Seq. ID xsy700208632.hl

Method BLASTX

```
NCBI GI
                  g2832660
BLAST score
                  193
E value
                   6.0e-15
Match length
                  85
% identity
NCBI Description
                  (AL021710) lipase-like protein [Arabidopsis thaliana]
                  312964
Seq. No.
Seq. ID
                  xsy700208639.h1
Method
                  BLASTX
NCBI GI
                  q2897942
BLAST score
                  176
                  6.0e-13
E value
Match length
                  78
% identity
                  42
NCBI Description
                  (AF003938) thioredoxin-like protein [Homo sapiens]
                  >gi_2961254 (AF051896) thioredoxin homolog [Hômo sapiens]
                  >gi_2970689 (AF052659) thioredoxin-related protein [Homo
                  sapiens]
                  312965
Seq. No.
Seq. ID
                  xsy700208645.h1
Method
                  BLASTX
NCBI GI
                  g3269290
BLAST score
                  309
E value
                  2.0e-28
Match length
                  88
% identity
                   68
NCBI Description
                   (AL030978) putative receptor like kinase [Arabidopsis
                  thaliana]
Seq. No.
                   312966
Seq. ID
                  xsy700208665.h1
                  BLASTX
```

Method BLASTX
NCBI GI g3548810
BLAST score 190
E value 1.0e-17
Match length 82
% identity 55

NCBI Description (AC005313) putative chloroplast nucleoid DNA binding

protein [Arabidopsis thaliana]

Seq. No. 312967

Seq. ID xsy700208733.h1

Method BLASTX
NCBI GI g4115379
BLAST score 163
E value 2.0e-11
Match length 90
% identity 41

NCBI Description (AC005967) putative carbonyl reductase [Arabidopsis

thaliana]

Seq. No.

312968

Seq. ID

xsy700208751.h1

Method NCBI GI BLASTX g4454463



BLAST score 169 E value 4.0e-12 Match length 98 % identity 38

NCBI Description (AC006234) putative leucine rich protein kinase

[Arabidopsis thaliana]

Seq. No. 312969

Seq. ID xsy700208752.h1

Method BLASTX
NCBI GI g3893860
BLAST score 483
E value 6.0e-49
Match length 100
% identity 98

NCBI Description (AF058708) RNA polymerase sigma factor 1 [Zea mays]

Seq. No. 312970

Seq. ID xsy700208802.h1

Method BLASTX
NCBI GI g3860272
BLAST score 512
E value 3.0e-52
Match length 105
% identity 94

NCBI Description (AC005824) putative suppressor protein [Arabidopsis

thaliana] >gi_4314399_gb_AAD15609_ (AC006232) putative skd1

protein [Arabidopsis thaliana]

Seq. No. 312971

Seq. ID xsy700208807.h1

Method BLASTX
NCBI GI g3334120
BLAST score 162
E value 2.0e-11
Match length 58
% identity 71

NCBI Description BETA-AMYLASE (1,4-ALPHA-D-GLUCAN MALTOHYDROLASE)

>gi_1771782_emb_CAA67128_ (X98504) beta-amylase [Triticum

aestivum]

312972

Seq. No.

Seq. ID xsy700208829.h1

Method BLASTX
NCBI GI g3024018
BLAST score 437
E value 2.0e-43
Match length 84
% identity 98

NCBI Description INITIATION FACTOR 5A (EIF-5A) (EIF-4D)

>gi_1546919_emb_CAA69225_ (Y07920) translation initiation factor 5A [Zea mays] >gi_2668738 (AF034943) translation

initiation factor 5A [Zea mays]

Seq. No. 312973

Seq. ID xsy700208832.h1

Method BLASTN

```
NCBI GI
                   q1944204
BLAST score
                   45
E value
                   3.0e-16
Match length
                   68
                   91
% identity
NCBI Description
                   Oryza sativa mRNA for RicMT, complete cds
                   312974
Seq. No.
                   xsy700208843.hl
Seq. ID
                   BLASTN
Method
                   g3639088
NCBI GI
BLAST score
                   38
                   3.0e-12
E value
Match length
                   74
% identity
                   88
                   Brassica oleracea phospholipase D1 (PLD1) mRNA, complete
NCBI Description
                   cds
                   312975
Seq. No.
                   xsy700208847.h1
Seq. ID
Method
                   BLASTX
                   g1076580
NCBI GI
BLAST score
                   151
                   4.0e-10
E value
Match length
                   39
% identity
                   64
NCBI Description
                   alcohol dehydrogenase homolog ADH3b - tomato
                   >gi_913446_bbs_160508 (S75487) alcohol dehydrogenase ADH
                    {EC 1.1.1.1} [Lycopersicon esculentum=tomatoes, cv. red
                   cherry, Peptide, 390 aa] [Lycopersicon esculentum]
                   312976
Seq. No.
                   xsy700208858.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2501189
BLAST score
                   349
                   3.0e-33
E value
Match length
                   69
                   100
% identity
                   THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR
NCBI Description
                   >gi 2130146 pir S61419 thiamine biosynthetic enzyme thi1-1
                    - \overline{\text{maize}} > \overline{\text{gi}} 596\overline{078} (U17350) thiamine biosynthetic enzyme
                    [Zea mays]
                   312977
Seq. No.
Seq. ID
                   xsy700208895.h1
Method
                   BLASTX
NCBI GI
                   g3482974
BLAST score
                   253
                   2.0e-22
E value
Match length
                   53
% identity
                   89
```

NCBI Description (AL031369) ATP-dependent Clp proteinase-like protein

[Arabidopsis thaliana]

Seq. No. 312978

Seq. ID xsy700208908.h1

% identity

73

```
BLASTX
Method
NCBI GI
                  q2668742
BLAST score
                  208
                  3.0e-17
E value
Match length
                  66
% identity
                  76
NCBI Description
                  (AF034945) glycine-rich RNA binding protein [Zea mays]
Seq. No.
                  312979
                  xsy700208921.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g397395
BLAST score
                  193
E value
                  1.0e-104
Match length
                  193
                  100
% identity
NCBI Description
                  Z.mays MNB1b mRNA for DNA-binding protein
Seq. No.
                  312980
Seq. ID
                  xsy700208940.h1
Method
                  BLASTX
                  g3080450
NCBI GI
BLAST score
                  154
E value
                  2.0e-10
Match length
                  55
% identity
                  58
                  (AL022605) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  312981
Seq. No.
                  xsy700208949.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1621463
BLAST score
                  184
E value
                  2.0e-14
Match length
                  82
% identity
                  60
NCBI Description
                  (U73104) laccase [Liriodendron tulipifera]
                  312982
Seq. No.
Seq. ID
                  xsy700208983.h1
Method
                  BLASTN
                  g633094
NCBI GI
BLAST score
                  33
E value
                  4.0e-09
Match length
                  65
                  88
% identity
                  Panicum miliaceum mRNA for plastidic aspartate
NCBI Description
                  aminotransferase, complete cds
Seq. No.
                  312983
Seq. ID
                  xsy700208992.h1
Method
                  BLASTX
                  q3779218
NCBI GI
BLAST score
                  328
E value
                  1.0e-30
Match length
                  84
```

Seq. ID

Method

NCBI GI



NCBI Description (AF030879) protein kinase CPK1 [Solanum tuberosum] 312984 Seq. No. xsy700208994.h1 Seq. ID Method BLASTX g2924503 NCBI GI BLAST score 223 E value 2.0e-18 Match length 93 47 % identity NCBI Description (AL022019) glucosyltransferase [Schizosaccharomyces pombe] Seq. No. 312985 xsy700209058.h1 Seq. ID Method BLASTX NCBI GI g100664 BLAST score 321 E value 2.0e-30 Match length 73 79 % identity NCBI Description beta-glucanase - rice Seq. No. 312986 Seq. ID xsy700209073.h1 Method BLASTX NCBI GI g4469021 BLAST score 239 E value 3.0e-20 Match length 91 % identity 56 NCBI Description (AL035602) hypothetical protein [Arabidopsis thaliana] Seq. No. 312987 Seq. ID xsy700209082.h1 Method BLASTX NCBI GI g3894187 BLAST score 251 5.0e-22 E value Match length 52 % identity 92 (AC005662) hypothetical protein [Arabidopsis thaliana] NCBI Description Seq. No. 312988 xsy700209087.h1 Seq. ID Method BLASTX NCBI GI g1314712 BLAST score 330 E value 5.0e-31 Match length 96 % identity 68 NCBI Description (U54615) calcium-dependent protein kinase [Arabidopsis thaliana] Seq. No. 312989

g3297816

BLASTX

xsy700209152.h1



```
BLAST score
E value
                   2.0e-13
Match length
                  84
                   48
% identity
NCBI Description
                  (AL031032) putative protein [Arabidopsis thaliana]
                  312990
Seq. No.
                  xsy700209218.hl
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3668086
BLAST score
                   175
E value
                  1.0e-15
                  100
Match length
% identity
                   50
                  (AC004667) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   312991
                  xsy700209235.h1
```

Seq. ID Method BLASTN NCBI GI q1839596 BLAST score 169 E value 3.0e-90 Match length 219

94 % identity

calcium/calmodulin-dependent protein kinase homolog CaM NCBI Description kinase homolog MCK1 [Zea mays=maize, cv. Merit, root caps,

mRNA, 2483 nt]

Seq. No. 312992

xsy700209244.h1 Seq. ID

Method BLASTN NCBI GI g22229 BLAST score 118 E value 8.0e-60 Match length 164 % identity 93

Z.mays cab-m7 gene for light harvesting chlorophyll a/b NCBI Description

binding protein

Seq. No. 312993

Seq. ID xsy700209246.h1

Method BLASTN g3618311 NCBI GI BLAST score 38 E value 4.0e-12

Match length 66 89 % identity

NCBI Description Oryza sativa mRNA for zinc finger protein, complete cds,

clone:R1479

Seq. No. 312994

Seq. ID xsy700209321.h1

Method BLASTX NCBI GI q3695389 BLAST score 289 E value 2.0e-26 Match length 82

```
% identity
NCBI Description
                  (AF096371) contains similarity to D-isomer specific
                  2-hydroxyacid dehydrogenases (Pfam: 2-Hacid DH.hmm, score:
                  19.11) [Arabidopsis thaliana]
Seq. No.
                  312995
                  xsy700209350.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3821780
BLAST score
                  36
E value
                  8.0e-11
Match length
                  48
% identity
                  67
NCBI Description
                  Xenopus laevis cDNA clone 27A6-1
Seq. No.
                  312996
                  xsy700209364.hl
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4587570
BLAST score
                  155
E value
                  2.0e-10
Match length
                  109
% identity
                  35
                  (AC006550) Strong similarity to gi 2244833 centromere
NCBI Description
                  protein homolog from Arabidopsis thaliana chromosome 4
                  contig gb Z97337. ESTs gb T20765 and gb AA586277 come from
                  this gene
                  312997
Seq. No.
Seq. ID
                  xsy700209373.h1
Method
                  BLASTN
NCBI GI
                  q3821780
BLAST score
                  36
E value
                  7.0e-11
Match length
                  48
```

% identity 67

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 312998

Seq. ID xsy700209396.h1

Method BLASTX NCBI GI g3962377 BLAST score 347 E value 5.0e-33 Match length 67 % identity 97

NCBI Description (AJ002551) heat shock protein 70 [Arabidopsis thaliana]

Seq. No. 312999

Seq. ID xsy700209401.h1

Method BLASTX NCBI GI q2723471 BLAST score 374 E value 4.0e-36 Match length 88 % identity 78

NCBI Description (D87819) sucrose transporter [Oryza sativa]



```
313000
Seq. No.
                  xsy700209414.hl
Seq. ID
Method
                  BLASTN
                  g3821780
NCBI GI
BLAST score
                  34
                  8.0e-10
E value
Match length
                  34
                  100
% identity
NCBI Description
                  Xenopus laevis cDNA clone 27A6-1
                  313001
Seq. No.
                  xsy700209425.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3063709
BLAST score
                  141
E value
                  8.0e-09
Match length
                  102
% identity
                  (AL022537) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  313002
                  xsy700209438.h1
Seq. ID
Method
                  BLASTN
                  g1205985
NCBI GI
BLAST score
                  91
                  9.0e-44
E value
Match length
                  207
% identity
                   92
                  Zea mays sulfur starvation induced isoflavone
NCBI Description
                  reductase-like IRL (IRL) mRNA, complete cds
                  313003
Seq. No.
                  xsy700209461.hl
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2194128
                   200
BLAST score
E value
                   5.0e-16
Match length
                  72
                   50
% identity
                   (AC002062) Strong similarity to Arabidopsis receptor-like
NCBI Description
                   kinase (qb ATLECGENE) and F20P5.15. [Arabidopsis thaliana]
                   313004
Seq. No.
                  xsy700209470.h1
Seq. ID
Method
                   BLASTX
                   g4138265
NCBI GI
BLAST score
                   329
                   3.0e-31
E value
Match length
                   64
```

91 % identity

NCBI Description (AJ006228) Avr9 elicitor response protein [Nicotiana

tabacum]

313005 Seq. No.

xsy700209503.hl Seq. ID

Method BLASTN



```
NCBI GI
                  g1245938
BLAST score
                   34
E value
                   9.0e-10
Match length
                   34
% identity
                   100
NCBI Description
                  rabClC-2 beta=chloride channel ClC-2G isoform [rabbits,
                  heart atrium, mRNA, 2998 nt]
                  313006
Seq. No.
Seq. ID
                  xsy700209515.h1
Method
                  BLASTX
NCBI GI
                   g1213460
BLAST score
                   251
E value
                   1.0e-21
Match length
                   92
% identity
                   55
                  (U03374) C subunit of V-ATPase [Amblyomma americanum]
NCBI Description
Seq. No.
                   313007
Seq. ID
                  xsy700209536.h1
Method
                  BLASTX
NCBI GI
                   g1402918
BLAST score
                   202
E value
                   7.0e-18
Match length
                   64
                   71
% identity
NCBI Description
                   (X98320) peroxidase [Arabidopsis thaliana]
                   >gi_1429215_emb_CAA67310_ (X98774) peroxidase ATP6a
                   [Arabidopsis thaliana]
Seq. No.
                   313008
Seq. ID
                   xsy700209548.h1
Method
                   BLASTN
NCBI GI
                   q4240034
BLAST score
                   58
E value
                   5.0e-24
Match length
                   66
% identity
                   97
NCBI Description
                  Zea mays ZmGR1b mRNA, complete cds
Seq. No.
                   313009
Seq. ID
                   xsy700209575.h1
Method
                   BLASTN
NCBI GI
                   q3618311
BLAST score
                   84
                   2.0e-39
E value
Match length
                   96
% identity
                   97
                  Oryza sativa mRNA for zinc finger protein, complete cds,
NCBI Description
                   clone:R1479
                   313010
Seq. No.
```

Seq. ID xsy700209639.h1

Method BLASTX NCBI GI q1076315 BLAST score 148 E value 1.0e-09



Match length 36 % identity 69

NCBI Description cytochrome P450 - Arabidopsis thaliana

>gi 853719 emb CAA60793 (X87367) CYP90 protein

[Arabidopsis thaliana] >gi_871988_emb_CAA60794_ (X87368)

CYP90 protein [Arabidopsis thaliana]

Seq. No. 313011

Seq. ID xsy700209684.h1

Method BLASTX
NCBI GI g3080374
BLAST score 147
E value 1.0e-09
Match length 90
% identity 32

NCBI Description (AL022580) putative protein [Arabidopsis thaliana]

Seq. No. 313012

Seq. ID xsy700209704.h1

Method BLASTN
NCBI GI g3851002
BLAST score 236
E value 1.0e-130
Match length 240

NCBI Description Zea mays pyruvate dehydrogenase El beta subunit isoform 3

mRNA, nuclear gene encoding mitochondrial protein, complete

cds

100

Seq. No. 313013

% identity

Seq. ID xsy700209733.h1

Method BLASTN
NCBI GI g21446
BLAST score 84
E value 2.0e-39
Match length 84
% identity 100

NCBI Description S.tuberosum gene for U6 small nuclear RNA

Seq. No. 313014

Seq. ID xsy700209738.h1

Method BLASTX
NCBI GI g3868758
BLAST score 200
E value 9.0e-16
Match length 40
% identity 90

NCBI Description (D89802) elongation factor 1B gamma [Oryza sativa]

Seq. No. 313015

Seq. ID xsy700209751.h1

Method BLASTX
NCBI GI g2497747
BLAST score 149
E value 4.0e-10
Match length 56
% identity 57



NONSPECIFIC LIPID-TRANSFER PROTEIN 3 PRECURSOR (LTP 3) NCBI Description >gi_510337_emb_CAA80809 (Z23271) lipid transfer protein [Oryza sativa] 313016 Seq. No. xsy700209759.h1 Seq. ID Method BLASTN NCBI GI g170772

BLAST score 46 E value 5.0e-17 Match length 86 % identity 88

NCBI Description Triticum aestivum S-adenosyl-L-homocysteine hydrolase

(SH6.2) mRNA, complete cds

Seq. No. 313017

Seq. ID xsy700209795.h1

Method BLASTX NCBI GI g3688186 BLAST score 426 E value 3.0e-42Match length 100 % identity 71

NCBI Description (AL031804) putative protein [Arabidopsis thaliana]

Seq. No. 313018

Seq. ID xsy700209815.h1

Method BLASTX NCBI GI g2160185 BLAST score 301 E value 7.0e-28 Match length 76 % identity 68

NCBI Description (AC000132) Similar to S. pombe ISP4 (gb D83992).

[Arabidopsis thaliana]

Seq. No. 313019

Seq. ID xsy700209864.h1

Method BLASTX NCBI GI g4585873 BLAST score 209 E value 3.0e-17 Match length 70 % identity 57

NCBI Description (AC005850) Putative protein kinase [Arabidopsis thaliana]

Seq. No. 313020

Seq. ID xsy700209902.h1

Method BLASTX NCBI GI g2662341 BLAST score 252 E value 3.0e-22 Match length 47 % identity 100

NCBI Description (D63580) EF-1 alpha [Oryza sativa]

>gi_2662345_dbj BAA23659 (D63582) EF-1 alpha [Oryza sativa] >gi 2662347 dbj BAA23660 (D63583) EF-1 alpha



[Oryza sativa]

 Seq. No.
 313021

 Seq. ID
 xsy700209927.h1

 Method
 BLASTX

 NCBI GI
 g3292849

 NLAST access
 450

BLAST score 450 E value 5.0e-45 Match length 98 % identity 85

NCBI Description (AJ007582) arginine methyltransferase [Arabidopsis

thaliana]

Seq. No. 313022

Seq. ID xsy700209940.h1

Method BLASTX
NCBI GI g2833460
BLAST score 174
E value 8.0e-13
Match length 71
% identity 48

NCBI Description RIBOFLAVIN-SPECIFIC DEAMINASE >qi 1001153 dbj BAA10295

(D64001) riboflavin biosynthesis protein [Synechocystis

sp.]

Seq. No. 313023

Seq. ID xsy700209949.h1

Method BLASTX
NCBI GI g3080450
BLAST score 253
E value 3.0e-22
Match length 72

% identity 68

NCBI Description (AL022605) hypothetical protein [Arabidopsis thaliana]

Seq. No. 313024

Seq. ID xsy700209964.h1

Method BLASTX
NCBI GI g2668744
BLAST score 216
E value 1.0e-17
Match length 40
% identity 100

NCBI Description (AF034946) ubiquitin conjugating enzyme [Zea mays]

Seq. No. 313025

Seq. ID xsy700209977.h1

Method BLASTX
NCBI GI g3687445
BLAST score 180
E value 1.0e-13
Match length 88
% identity 36

NCBI Description (AL022398) dJ434014.5 (novel PUTATIVE protein similar to

YILO91C yeast hypoyhetical 84 kD protein from SGA1-KTR7

intergenic region) [Homo sapiens]



```
Seq. No.
                   313026
Seq. ID
                  xsy700209991.h1
Method
                  BLASTX
NCBI GI
                  q4558460
BLAST score
                  505
E value
                  2.0e-51
                  - 96
Match length
                   99
% identity
NCBI Description
                  (AF073775) replication origin activator ROA2 [Zea mays]
Seq. No.
                  313027
Seq. ID
                  xsy700210088.h1
Method
                  BLASTX
NCBI GI
                  g534982
BLAST score
                  324
E value
                   3.0e-30
Match length
                  101
% identity
                   55
                  (X75898) phosphoglucomutase [Spinacia oleracea]
NCBI Description
Seq. No.
                  313028
Seq. ID
                  xsy700210226.h1
Method
                  BLASTX
NCBI GI
                  q3695403
BLAST score
                  192
E value
                   7.0e-15
Match length
                   49
% identity
                   73
                   (AF096373) contains similarity to the pfkB family of
NCBI Description
                   carbohydrate kinases (Pfam: PF00294, E=1.6e-75)
                   [Arabidopsis thaliana] >gi 4538955 emb CAB39779.1
                   (AL049488) fructokinase-like protein [Arabidopsis thaliana]
Seq. No.
                   313029
Seq. ID
                  xsy700210245.h1
Method
                  BLASTX
NCBI GI
                   g2058498
BLAST score
                   251
E value
                   9.0e-22
Match length
                   71
% identity
                   70
NCBI Description
                   (U76029) hemoglobin 1 [Oryza sativa] >gi 2058500 (U76030)
                  hemoglobin 1 [Oryza sativa]
Seq. No.
                   313030
Seq. ID
                  xsy700210279.h1
Method
                  BLASTX
                  g4056503
                  163
                  2.0e-11
                  36
% identity
                  83
```

NCBI GI BLAST score E value Match length

NCBI Description (AC005896) unknown protein [Arabidopsis thaliana]

Seq. No. 313031

xsy700210308.h1 Seq. ID

Method BLASTX

```
NCBI GI
                  q3551960
BLAST score
                  365
                  4.0e-35
E value
Match length
                  96
% identity
                  76
                  (AF082033) senescence-associated protein 15 [Hemerocallis
NCBI Description
                  hybrid cultivar]
                  313032
Seq. No.
Seq. ID
                  xsy700210364.h1
                  BLASTX
Method
NCBI GI
                  g4467153
BLAST score
                  263
                  4.0e-23
E value
Match length
                  82
% identity
                  57
NCBI Description
                  (AL035540) putative thaumatin-like protein [Arabidopsis
                  313033
Seq. No.
Seq. ID
                  xsy700210379.h1
Method
                  BLASTX
NCBI GI
                  g2829880
BLAST score
                  161
E value
                  1.0e-11
Match length
                  43
% identity
                  79
NCBI Description
                  (AC002396) glucose-6-phosphate 1-dehydrogenase [Arabidopsis
                  thaliana]
Seq. No.
                  313034
Seq. ID
                  xsy700210418.h1
                  BLASTN
Method
                  g20193
NCBI GI
BLAST score
                  44
E value
                  6.0e-16
Match length
                  100
% identity
                  86
NCBI Description
                 O.sativa mRNA for cdc2+/CDC28-related protein kinase
                  313035
Seq. No.
Seq. ID
                  xsy700210459.h1
Method
                  BLASTX
NCBI GI
                  g169673
BLAST score
                  145
E value
                  3.0e-11
Match length
                  56
% identity
                  61
                  (M96071) tyrosine decarboxylase [Petroselinum crispum]
NCBI Description
                  >gi 169675 (M96072) tyrosine decarboxylase [Petroselinum
```

crispum]

Seq. No.

313036

xsy700210540.h1 Seq. ID

Method BLASTX NCBI GI g3776559 BLAST score 287



E value 2.0e-26 Match length 68 % identity 78

NCBI Description (AC005388) Strong similarity to gene F14J9.26 gi 3482933

cdc2 protein kinase homolog from A. thaliana BAC

gb_AC003970. ESTs gb_Z35332 and gb_F19907 come from this

gene. [Arabidopsis thaliana]

Seq. No. 313037

Seq. ID xsy700210561.h1

Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 7.0e-11
Match length 36
% identity 100

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 313038

Seq. ID xsy700210602.h1

Method BLASTX
NCBI GI 94406816
BLAST score 443
E value 3.0e-44
Match length 83
% identity 98

NCBI Description (AC006201) 60S ribosomal protein L2 [Arabidopsis thaliana]

Seq. No. 313039

Seq. ID xsy700210605.h1

Method BLASTX
NCBI GI g3355486
BLAST score 199
E value 1.0e-15
Match length 103
% identity 43

NCBI Description (AC004218) unknown protein [Arabidopsis thaliana]

Seq. No. 313040

Seq. ID xsy700210608.h1

Method BLASTX
NCBI GI g2499873
BLAST score 144
E value 4.0e-09
Match length 67
% identity 48

NCBI Description HYPOTHETICAL SUBTILASE-TYPE PROTEINASE F21H12.6 IN

CHROMOSOME II >gi_726410 (U23176) similar to H. sapiens

tripeptidyl-peptidase II (SP:TPP2_HUMAN, P29144)

[Caenorhabditis elegans]

Seq. No. 313041

Seq. ID xsy700210668.h1

Method BLASTX
NCBI GI g3559814
BLAST score 283
E value 2.0e-25



Match length 59 % identity 90

NCBI Description (Y15781) transketolase 1 [Capsicum annuum]

Seq. No.

313042

Seq. ID

xsy700210710.hl

Method BLASTN
NCBI GI g3342822
BLAST score 253
E value 1.0e-140
Match length 273
% identity 99

NCBI Description Zea mays eukaryotic translation initiation factor p28

subunit (eIFiso-4E) mRNA, complete cds

Seq. No.

313043

Seq. ID

xsy700210721.h1

Method BLASTX
NCBI GI g1737222
BLAST score 275
E value 6:0e-25
Match length 60
% identity 78

NCBI Description (U79958) BP-80 vacuolar sorting receptor [Pisum sativum]

Seq. No.

313044

Seq. ID

xsy700210726.h1

Method BLASTX
NCBI GI g3415134
BLAST score 251
E value 8.0e-22
Match length 65
% identity 71

NCBI Description (AF082024) Phyb1 [Pimpinella brachycarpa]

Seq. No.

313045

Seq. ID

xsy700210793.h1

Method BLASTN
NCBI GI g4539654
BLAST score 52
E value 2.0e-20
Match length 88
% identity 90

NCBI Description Sorghum bicolor 22 kDa kafirin cluster

Seq. No.

313046

Seq. ID

xsy700210842.h1

Method BLASTN
NCBI GI g2642323
BLAST score 37
E value 1.0e-11
Match length 124
% identity 83

NCBI Description Zea mays profilin (PRO4) mRNA, complete cds

Seq. No.

313047

Seq. ID

xsy700210856.hl



```
Method
                  BLASTX
NCBI GI
                  g3986695
BLAST score
                  143
E value
                  2.0e-09
Match length
                  57
% identity
                  53
                  (AF101423) ribosomal protein L12 [Cichorium intybus]
NCBI Description
Seq. No.
                  313048
Seq. ID
                  xsy700210857.h1
Method
                  BLASTX
NCBI GI
                  g4587558
BLAST score
                  141
E value
                  4.0e-09
Match length
                  73
% identity
                  42
                  (AC006577) Contains similarity to gb U45880 X-linked
NCBI Description
                  inhibitor of apotosis protein from Homo sapiens and
                  contains PF_00097 Zinc finger C3HC4 (Ring finger) domain.
                  [Arabidopsis thaliana]
                  313049
Seq. No.
Seq. ID
                  xsy700210870.h1
Method
                  BLASTX
NCBI GI
                  g2344894
BLAST score
                  216
E value
                  1.0e-17
Match length
                  100
% identity
NCBI Description
                  (AC002388) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  313050
Seq. ID
                  xsy700210879.h1
Method
                  BLASTX
NCBI GI
                  g4098333
BLAST score
                  429
E value
                  1.0e-42
Match length
                  82
% identity
                  99
NCBI Description
                  (U76897) beta-tubulin 6 [Triticum aestivum]
Seq. No.
                  313051
Seq. ID
                  xsy700210919.h1
Method
                  BLASTX
NCBI GI
                  q3242705
BLAST score
                  196
E value
                  3.0e-15
Match length
                  39
% identity
                  90
NCBI Description
                  (AC003040) putative nicotinate phosphoribosyltransferase
                  [Arabidopsis thaliana]
```

Method BLASTX NCBI GI g3913651 BLAST score 311



```
7.0e-29
E value
Match length
                   66
% identity
                   83
                  FERREDOXIN--NADP REDUCTASE, LEAF-TYPE ISOZYME PRECURSOR
NCBI Description
                   (FNR) >gi_2225993_emb_CAA74359_ (Y14032)
                   ferredoxin--NADP(+) reductase [Nicotiana tabacum]
                   313053
Seq. No.
                  xsy700211044.h1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1524370
BLAST score
                   157
                   9.0e-11
E value
Match length
                   55
% identity
                   62
NCBI Description
                  (X92491) TOM20 [Solanum tuberosum]
Seq. No.
                   313054
Seq. ID
                   xsy700211142.h1
Method
                   BLASTX
NCBI GI
                   q1706260
BLAST score
                   335
E value
                   1.0e-31
Match length
                   84
% identity
                   79
NCBI Description
                  CYSTEINE PROTEINASE 1 PRECURSOR >gi 2118131 pir S59597
                   cysteine proteinase 1 precursor - maize
                   >gi_643597_dbj_BAA08244_ (D45402) cysteine proteinase [Zea
                   mays]
                   313055
Seq. No.
Seq. ID
                   xsy700211159.h1
                   BLASTX
Method
                   g2462925
NCBI GI
BLAST score
                   368
E value
                   2.0e-35
                   89 -
Match length
                   83
% identity
NCBI Description
                   (AJ000053) GTP cyclohydrolase II /
                   3,4-dihydroxy-2-butanone-4-phoshate synthase [Arabidopsis
                   thaliana]
                   313056
Seq. No.
                   xsy700211177.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4406764
BLAST score
                   277
                   8.0e-25
E value
Match length
                   82
                   66
% identity
```

NCBI Description

313057 Seq. No. xsy700211194.h1

Seq. ID Method BLASTX NCBI GI g1814403

thaliana]

(AC006836) putative uridylyl transferase [Arabidopsis



```
BLAST score 406
E value 5.0e-40
Match length 84
% identity 96
```

NCBI Description (U84889) methionine synthase [Mesembryanthemum

crystallinum]

Seq. No. 313058

Seq. ID xsy700211235.h1

Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 7.0e-11
Match length 36
% identity 100

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 313059

Seq. ID xsy700211255.h1

Method BLASTN
NCBI GI g4138731
BLAST score 217
E value 1.0e-119
Match length 221
% identity 100

NCBI Description Zea mays mRNA for proline-rich protein .

Seq. No. 313060

Seq. ID xsy700211259.h1

Method BLASTN
NCBI GI g3821780
BLAST score 36
E value 7.0e-11
Match length 48
% identity 67

NCBI Description Xenopus laevis cDNA clone 27A6-1

Seq. No. 313061

Seq. ID xsy700211270.h1

Method BLASTX
NCBI GI g1945281
BLAST score 383
E value 3.0e-37
Match length 70
% identity 89

NCBI Description (Y11352) myb factor [Oryza sativa]

Seq. No. 313062

Seq. ID xsy700211277.h1

Method BLASTX
NCBI GI g3548818
BLAST score 364
E value 5.0e-35
Match length 86
% identity 84

NCBI Description (AC005313) unknown protein [Arabidopsis thaliana]



```
      Seq. No.
      313063

      Seq. ID
      xsy700211311.h1

      Method
      BLASTX

      NCBI GI
      g4006829

      BLAST
      149
```

BLAST score 149
E value 6.0e-13
Match length 91
% identity 51

NCBI Description (AC005970) putative protein kinase [Arabidopsis thaliana]

Seq. No. 313064

Seq. ID xsy700211352.h1

Method BLASTX
NCBI GI g129916
BLAST score 399
E value 4.0e-39
Match length 86
% identity 93

NCBI Description PHOSPHOGLYCERATE KINASE, CYTOSOLIC >gi_66911_pir__TVWTGY

phosphoglycerate kinase (EC 2.7.2.3), cytosolic - wheat
>gi_21835_emb_CAA33302_ (X15232) phosphoglycerate kinase

(AA 1 - 401) [Triticum aestivum]

Seq. No. 313065

Seq. ID xsy700211388.h1

Method BLASTX
NCBI GI g2494620
BLAST score 235
E value 2.0e-20
Match length 73
% identity 68

NCBI Description SUCCINATE DEHYDROGENASE IRON-SULFUR PROTEIN >gi 975319

(U31902) succinate dehydrogenase iron-sulfur protein

subunit [Paracoccus denitrificans]

Seq. No. 313066

Seq. ID xsy700211414.h1

Method BLASTN
NCBI GI g1628481
BLAST score 264
E value 1.0e-147
Match length 264
% identity 100

NCBI Description Z.mays dek34 gene

Seq. No. 313067

Seq. ID xsy700211440.h1

Method BLASTX
NCBI GI g4262186
BLAST score 301
E value 1.0e-27
Match length 71
% identity 76

NCBI Description (AC005508) Highly similar to cullin 3 [Arabidopsis

thaliana]

Seq. No. 313068

```
xsy700211459.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4531444
BLAST score
                   239
E value
                   2.0e-20
Match length
                   74
% identity
NCBI Description
                  (AC006224) putative protein kinase [Arabidopsis thaliana]
Seq. No.
                   313069
Seq. ID
                   xsy700211463.hl
Method
                   BLASTX
NCBI GI
                   g1172836
BLAST score
                   379
E value
                   3.0e-37
Match length
                   79
% identity
                   95
                  GTP-BINDING NUCLEAR PROTEIN RAN-B1 >gi 496272 (L16787)
NCBI Description
                   small ras-related protein [Nicotiana tabacum]
Seq. No.
                   313070
Seq. ID
                   xsy700211612.h1
Method
                   BLASTX
NCBI GI
                   q66615
BLAST score
                   398
E value
                   6.0e-39
Match length
                   75
% identity
                   100
NCBI Description
                  glutathione transferase (EC 2.5.1.18) I - maize
Seq. No.
                   313071
Seq. ID
                   xsy700211635.h1
Method
                   BLASTX
NCBI GI
                   q3786007
BLAST score
                   350
E value
                   2.0e-33
Match length
                   102
% identity
                   68
NCBI Description
                  (AC005499) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   313072
Seq. ID
                   xsy700211652.h1
Method
                   BLASTX
NCBI GI
                   g131772
BLAST score
                   300
E value
                   1.0e-27
Match length
                   62
% identity
                   98
NCBI Description
                  40S RIBOSOMAL PROTEIN S14 (CLONE MCH1)
                  >gi 82723 pir A30097 ribosomal protein S14 (clone MCH1) -
                  maize
Seq. No.
                  313073
```

Seq. ID

xsy700211684.h1

Method

BLASTX

NCBI GI BLAST score g2306981



```
2.0e-21
E value
Match length
% identity
                  68
NCBI Description
                  (AF010321) photosystem I antenna protein [Oryza sativa]
Seq. No.
                  313074
Seq. ID
                  xsy700211709.h1
Method
                  BLASTX
NCBI GI
                  g629592
BLAST score
                  163
E value
                  8.0e-12
Match length
                  40
% identity
                  78
NCBI Description hypothetical protein - rape
                  313075
Seq. No.
Seq. ID
                  xsy700211767.hl
Method
                  BLASTX
NCBI GI
                  q1351642
BLAST score
                  144
                  4.0e-09
E value
Match length
                  84
% identity
                  43
NCBI Description
                  HYPOTHETICAL HELICASE C8A4.08C IN CHROMOSOME I
                  >gi 2130449 pir S62524 hypothetical protein SPAC8A4.08c -
                  fission yeast (Schizosaccharomyces pombe)
                  >gi 1052539 emb CAA91518 (Z66569) unknown
                  [Schizosaccharomyces pombe] >gi_4456833_emb_CAB37423.1_
                  (AL032824) ribonuclease [Schizosaccharomyces pombe]
Seq. No.
                  313076
Seq. ID
                  xsy700211777.h1
Method
                  BLASTX
NCBI GI
                  g115815
BLAST score
                  552
E value
                  5.0e-57
Match length
                  102
% identity
                  100
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                  (CAB-M9) (LHCP) >gi_100866_pir__S13098 chlorophyll
                  a/b-binding protein precursor - maize
                  >gi_22355_emb_CAA39376_ (X55892) light-harvesting
                  chlorophyll a/b binding protein [Zea mays]
Seq. No.
                  313077
Seq. ID
                  xsy700211802.h1
Method
                  BLASTX
NCBI GI
                  g2246625
```

BLAST score 399 E value 4.0e-39 Match length 99 % identity 77

NCBI Description (AF004947) protein kinase [Oryza sativa]

Seq. No. 313078

Seq. ID xsy700211810.h1

Method BLASTX



```
g1172995
NCBI GI
BLAST score
                  159
                  7.0e-11
E value
Match length
                  71
% identity
                  49
                  60S RIBOSOMAL PROTEIN L22 >gi 1083790_pir__S52084 ribosomal
NCBI Description
                  protein L22 - rat >gi_710295_emb_CAA55204_ (X78444)
                  ribosomal protein L22 [Rattus norvegicus]
                  >gi 1093952_prf__2105193A ribosomal protein L22 [Rattus
                  norvegicus]
                  313079
Seq. No.
                  xsy700211823.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4580455
BLAST score
                  187
E value
                  2.0e-14
Match length
                  48
% identity
                  75
                  (AC006081) unknown protein [Arabidopsis thaliana]
NCBI Description
                  313080
Seq. No.
                  xsy700211848.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4314378
BLAST score
                  198
E value
                  2.0e-15
Match length
                  79
% identity
                  (AC006232) putative lipase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  313081
                  xsy700211880.hl
Seq. ID
Method
                  BLASTX
                  g1705677
NCBI GI
BLAST score
                  235
E value
                  5.0e-20
Match length
                  60
                  88
% identity
                  CELL DIVISION CYCLE PROTEIN 48 HOMOLOG
NCBI Description
                  >gi 2118115 pir S60112 cell division control protein CDC48
                  homolog - Arabidopsis thaliana >gi 1019904 (U37587) cell
                  division cycle protein [Arabidopsis thaliana]
                  313082
Seq. No.
                  xsy700211909.h1
Seq. ID
                  BLASTN
Method
```

NCBI GI g3264597
BLAST score 40
E value 3.0e-13
Match length 88
% identity 86

NCBI Description Zea mays trypsin inhibitor mRNA, complete cds

Seq. No. 313083

Seq. ID xsy700211949.h1

Method BLASTX

```
g1742955
NCBI GI
BLAST score
                  142
                  3.0e-09
E value
Match length
                  33
% identity
                  85
                   (Z71446) CLC-b chloride channel protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  313084
Seq. ID
                  xsy700211955.h1
Method
                  BLASTX
NCBI GI
                   g1346487
BLAST score
                  329
E value
                  2.0e-31
Match length
                  104
% identity
                  75
```

NCBI Description MALATE SYNTHASE, GLYOXYSOMAL >gi_532625 (L35914) malate synthase [Zea mays]

Seq. ID xsy700211966.h1
Method BLASTN
NCBI GI g286033
BLAST score 37
E value 2.0e-11
Match length 53
% identity 92

Seq. No.

NCBI Description Ipomoea batatas (sweet potato) mRNA for F1-ATPase

gamma-subunit

313085

 Seq. No.
 313086

 Seq. ID
 xsy700212015.h1

 Method
 BLASTX

 MCDI GI
 22236247

Method BLASTX
NCBI GI g3236247
BLAST score 304
E value 6.0e-28
Match length 84
% identity 69

NCBI Description (AC004684) SCARECROW-like protein [Arabidopsis thaliana]

Seq. No. 313087

Seq. ID xsy700212050.h1

Method BLASTX
NCBI GI 94584524
BLAST score 158
E value 8.0e-11
Match length 80
% identity 38

NCBI Description (AL049607) putative protein [Arabidopsis thaliana]

Seq. No. 313088

Seq. ID xsy700212053.h1

Method BLASTX
NCBI GI g3036951
BLAST score 513
E value 2.0e-52
Match length 100



% identity (AB012639) light harvesting chlorophyll a/b-binding protein NCBI Description [Nicotiana sylvestris] Seq. No. 313089 Seq. ID xsy700212062.hl Method BLASTX NCBI GI q115815 BLAST score 324 E value 9.0e-37 Match length 82 98

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-M9) (LHCP) >gi_100866_pir__S13098 chlorophyll

a/b-binding protein precursor - maize

>gi_22355_emb CAA39376 (X55892) light-harvesting

chlorophyll a/b binding protein [Zea mays]

313090 Seq. No.

% identity

Seq. ID xsy700212063.h1

Method BLASTX NCBI GI q4510424 BLAST score 235 E value 7.0e-20 Match length 70 % identity 66

NCBI Description (AC006929) putative carboxypeptidase [Arabidopsis thaliana]

313091 Seq. No.

Seq. ID xsy700212068.h1

Method BLASTX NCBI GI g1773014 BLAST score 245 E value 5.0e-21 Match length 100 % identity 47

NCBI Description (Y10338) chloride channel Stclc1 [Solanum tuberosum]

Seq. No. 313092

Seq. ID xsy700212127.h1

Method BLASTX NCBI GI g2497756 BLAST score 163 E value 2.0e-11 Match length 46 % identity 63

NONSPECIFIC LIPID-TRANSFER PROTEIN 2 PRECURSOR (LTP 2) NCBI Description

> >gi 422011 pir S33461 lipid transfer protein - sorghum >gi 311333 emb CAA50661 (X71668) lipid transfer protein

[Sorghum bicolor]

313093 Seq. No.

Seq. ID xsy700212143.h1

Method BLASTX q3927831 NCBI GI BLAST score 217 E value 8.0e-18



Match length 70 % identity 60 NCBI Description

(AC005727) similar to mouse ankyrin 3 [Arabidopsis

thaliana]

Seq. No.

313094

Seq. ID

xsy700212223.h1

Method BLASTX NCBI GI g2245378 BLAST score 223 1.0e-18 E value

Match length 75 % identity 64

NCBI Description (U83245) auxin response factor 1 [Arabidopsis thaliana]

Seq. No.

313095

Seq. ID

xsy700212230.h1

Method BLASTX q4455159 NCBI GI BLAST score 219 E value 2.0e-18 Match length 55 % identity 73

(AL021687) putative protein [Arabidopsis thaliana] NCBI Description

Seq. No.

313096

Seq. ID

xsy700212235.h1

Method BLASTX q4454459 NCBI GI BLAST score 206 E value 7.0e-17 Match length 54 74 % identity

NCBI Description

(AC006234) unknown protein [Arabidopsis thaliana]

Seq. No.

313097

Seq. ID

xsy700212273.h1

Method BLASTX g4539324 NCBI GI BLAST score 307 E value 2.0e-28 Match length 101 % identity 65

NCBI Description (AL035679) kinesin like protein [Arabidopsis thaliana]

Seq. No.

313098

Seq. ID

...

xsy700212282.h1

Method BLASTX NCBI GI g115815 BLAST score 350 E value 2.0e-33 Match length 91 % identity 73

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-M9) (LHCP) >gi_100866_pir__S13098 chlorophyll

a/b-binding protein precursor - maize

>gi 22355 emb CAA39376 (X55892) light-harvesting

E value

Match length

9.0e-25

105





chlorophyll a/b binding protein [Zea mays]

Seq. No. 313099 xsy700212284.h1 Seq. ID Method BLASTX NCBI GI g585629 BLAST score 372 E value 6.0e-36 Match length 72 97 % identity NCBI Description SERINE/THREONINE PROTEIN PHOSPHATASE PP2A-2 CATALYTIC SUBUNIT >gi_418778 pir S31161 phosphoprotein phosphatase (EC 3.1.3.16) 2A-alpha catalytic chain (clone EP8a) -Arabidopsis thaliana >gi 166821 (M96732) protein phosphatase [Arabidopsis thaliana] Seq. No. 313100 Seq. ID xsy700212292.h1 Method BLASTX NCBI GI g3875740 BLAST score 145 E value 2.0e-09 Match length 45 % identity 53 NCBI Description (Z81497) similar to mannosyl-oligosaccharide alpha-1, 2-mannosidase; cDNA EST EMBL: D67155 comes from this gene; cDNA EST EMBL: D64219 comes from this gene; cDNA EST yk260e12.3 comes from this gene; cDNA EST yk260e12.5 comes from Seq. No. 313101 Seq. ID xsy700212331.h1 Method BLASTX NCBI GI g4582787 BLAST score 260 E value 4.0e-23 Match length ; 53 % identity 100 NCBI Description (AJ012281) adenosine kinase [Zea mays] Seq. No. 313102 Seq. ID xsy700212367.h1 Method BLASTX NCBI GI g4467124 BLAST score 190 E value 1.0e-14 Match length 96 % identity 38 NCBI Description (AL035538) hypothetical protein [Arabidopsis thaliana] Seq. No. 313103 Seq. ID xsy700212412.h1 Method BLASTN NCBI GI g4105114 BLAST score 59



% identity

Hordeum vulgare dehydrin 8 (dhn8) gene, complete cds NCBI Description

Seq. No.

313104

Seq. ID

xsy700212422.h1

Method NCBI GI BLASTX g4587525

BLAST score

141

E value

3.0e-09

Match length

48

% identity

54

NCBI Description

(AC007060) Contains the PF_00650 CRAL/TRIO

phosphatidyl-inositol-transfer protein domain. ESTs gb T76582, gb N06574 and gb Z25700 come from this gene.

[Arabidopsis thaliana]

Seq. No.

313105

Seq. ID

xsy700212432.hl

Method

BLASTX

NCBI GI

q626032

BLAST score

169

E value

6.0e-25

Match length

% identity

84 68

NCBI Description

lipoxygenase L-2 - rice

Seq. No.

313106

Seq. ID

xsy700212448.h1

Method

BLASTX

NCBI GI

q3024018

BLAST score

458

E value

5.0e-46

Match length

86

% identity

99 INITIATION FACTOR 5A (EIF-5A) (EIF-4D)

NCBI Description

>gi_1546919_emb_CAA69225_ (Y07920) translation initiation factor 5A [Zea mays] >gi_2668738 (AF034943) translation

initiation factor 5A [Zea mays]

Seq. No.

313107

Seq. ID

xsy700212449.h1

Method

BLASTN

NCBI GI

g2326946

BLAST score

211 1.0e-115

E value Match length

251

% identity

NCBI Description

97 Z.mays mRNA for chlorophyll a/b-binding protein CP29

Seq. No.

313108

Seq. ID

xsy700212481.h1

Method NCBI GI BLASTX g4454567

BLAST score E value

143

2.0e-09

Match length % identity

54 50





```
NCBI Description
                  (AF128407) lipase homolog [Arabidopsis thaliana]
                  313109
Seq. No.
                  xsy700212549.h1
Seq. ID
Method
                  BLASTX
                   g2369714
NCBI GI
BLAST score
                   278
                   2.0e-29
E value
Match length
                  72
% identity
                   89
                  (Z97178) elongation factor 2 [Beta vulgaris]
NCBI Description
                   313110
Seq. No.
                   xsy700212558.h1
Seq. ID
Method
                  BLASTX
                   g3935183
NCBI GI
BLAST score
                   238
                   2.0e-20
E value
                  83
Match length
                   57
% identity
NCBI Description
                  (AC004557) F17L21.26 [Arabidopsis thaliana]
Seq. No.
                   313111
                   xsy700212570.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2979544
BLAST score
                   164
E value
                   1.0e-11
Match length
                   81
                   43
% identity
                   (AC003680) putative cytochrome P-450 [Arabidopsis thaliana]
NCBI Description
                   313112
Seq. No.
                   xsy700212580.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g320130
BLAST score
                   362
E value
                   8.0e-35
Match length
                   71
% identity
                   97
                  acetolactate synthase (EC 4.1.3.18) (clone pSOG109) - maize
NCBI Description
                   >gi 22141 emb CAA45117 (X63554) acetohydroxyacid synthase
                   [Zea mays]
                   313113
Seq. No.
                   xsy700212617.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g115771
BLAST score
                   514
E value
                   1.0e-52
Match length
                   100
% identity
                   99
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                   (CAB-1) (LHCP) >gi_82682_pir__S04453 chlorophyll
                   a/b-binding protein precursor - maize
```

44744

>gi_22224_emb_CAA32900_ (X14794) chlorophyll a/b-binding
preprotein (AA 1 - 262) [Zea mays]

NCBI GI

BLAST score

g22227

78

```
313114
Seq. No.
                  xsy700212622.hl
Seq. ID
Method
                  BLASTN
NCBI GI
                  g434333
                  92
BLAST score
                  1.0e-44
E value
                  115
Match length
% identity
                  95
NCBI Description Z.mays mRNA gs2 for glutamine synthatase
Seq. No.
                  313115
                  xsy700212668.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2459446
BLAST score
                  174
                  8.0e-13
E value
Match length -
                   64
% identity
                   48
                   (AC002332) putative cinnamoyl-CoA reductase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  313116
                  xsy700212687.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2244971
BLAST score
                   413
E value
                  7.0e-41
Match length
                  90
% identity
                  83
NCBI Description (Z97340) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  313117
                  xsy700212771.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2262105
BLAST score
                  175
E value
                   5.0e-13
Match length
                   63
% identity
                  51
NCBI Description (AC002343) unknown protein [Arabidopsis thaliana]
Seq. No.
                  313118
                  xsy700212774.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2605887
BLAST score
                  142
                   4.0e-09
E value
Match length
                   52
% identity
                   63
NCBI Description (AF029242) dormancy-associated protein [Pisum sativum]
                  313119
Seq. No.
                  xsy700212823.h1
Seq. ID
Method
                  BLASTN
```

```
3.0e-36
E value
Match length
                   169
                   87
% identity
                  Z.mays CAB48 gene for chlorophyll a/b binding protein
NCBI Description
                   313120
Seq. No.
                  xsy700212828.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4588012
BLAST score
                   155
                   7.0e-11
E value
                   54
Match length
                   59
% identity
                   (AF085717) putative callose synthase catalytic subunit
NCBI Description
                   [Gossypium hirsutum]
                   313121
Seq. No.
                   xsy700212923.hl
Seq. ID
Method
                   BLASTN
                   g168470
NCBI GI
BLAST score
                   136
E value
                   9.0e-71
Match length
                   171
% identity
                   95
NCBI Description Maize ferredoxin I (Fd) isoprotein mRNA, pFD1'
Seq. No.
                   313122
Seq. ID
                   xsy700212967.hl
Method
                   BLASTX
                   g2791278
NCBI GI
BLAST score
                   166
                   7.0e-12
E value
Match length
                   77
                   45
% identity
                  (Z69257) beta-xylosidase [Hypocrea jecorina]
NCBI Description
Seq. No.
                   313123
                   xsy700212977.h1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g2668739
```

NCBI GI g2668739
BLAST score 94
E value 1.0e-45

Match length 249 % identity 91

NCBI Description Zea mays translation initiation factor GOS2 (TIF) mRNA,

complete cds

Seq. No. 313124

Seq. ID xsy700212982.h1

Method BLASTX
NCBI GI g115786
BLAST score 169
E value 3.0e-12
Match length 51
% identity 71

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB) (LHCP) >gi_82680_pir__A29119 chlorophyll a/b-binding



```
protein - maize >gi_22357_emb_CAA68451_ (Y00379) LHCP [Zea
mays]
```

Seq. No. 313125

Seq. ID xsy700212992.h1

Method BLASTN
NCBI GI g397395
BLAST score 131
E value 1.0e-67
Match length 131
% identity 100

NCBI Description Z.mays MNB1b mRNA for DNA-binding protein

Seq. No. 313126

Seq. ID xsy700213008.h1

Method BLASTX
NCBI GI g115771
BLAST score 504
E value 2.0e-51
Match length 101
% identity 98

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-1) (LHCP) >gi_82682_pir__S04453 chlorophyll

a/b-binding protein precursor - maize

>gi_22224_emb_CAA32900_ (X14794) chlorophyll a/b-binding

preprotein (AA 1 - 262) [Zea mays]

Seq. No. 313127

Seq. ID xsy700213086.h1

Method BLĀSTX
NCBI GI g730536
BLAST score 328
E value 6.0e-31
Match length 67
% identity 96

NCBI Description 60S RIBOSOMAL PROTEIN L23 >gi_310933 (L18915) 60S ribosomal

protein subunit L17 [Nicotiana tabacum]

Seq. No. 313128

Seq. ID xsy700213117.h1

Method BLASTN
NCBI GI g2981206
BLAST score 200
E value 1.0e-108
Match length 242
% identity 96

NCBI Description Zea mays photosystem I complex PsaH subunit precursor

(psaH) mRNA, nuclear gene encoding chloroplast protein,

complete cds

Ş

Seq. No. 313129

Seq. ID xsy700213118.h1

Method BLASTX
NCBI GI g3600032
BLAST score 160
E value 5.0e-11
Match length 46



```
% identity
NCBI Description
                   (AF080119) contains similarity to tropomyosin (Pfam:
                  Tropomyosin.hmm, score: 14.57) and ATP synthase (Pfam:
                  ATP-synt B.hmm, score: 10.89) [Arabidopsis thaliana]
Seq. No.
                  313130
Seq. ID
                  xsy700213139.h1
Method
                  BLASTX
NCBI GI
                  g4455359
BLAST score
                  245
E value
                  5.0e-21
Match length
                  70
% identity
                  69
NCBI Description
                  (AL035524) putative protein [Arabidopsis thaliana]
Seq. No.
                  313131
Seq. ID
                  xsy700213143.hl
Method
                  BLASTX
NCBI GI
                  g4567250
BLAST score
                  194
E value
                  4.0e-15
Match length
                  70
% identity
                  61
NCBI Description
                  (AC007070) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  313132
Seq. ID
                  xsy700213147.h1
Method
                  BLASTX
NCBI GI
                  q4581164
BLAST score
                  287
E value
                  6.0e-26
                  99
Match length
% identity
                  54
NCBI Description
                  (AC006220) putative polyprotein [Arabidopsis thaliana]
Seq. No.
                  313133
                                                - 4
                  xsy700213155.h1
Seq. ID
Method
                  BLASTN
                  g248338
NCBI GI
BLAST score
                  114
E value
                  2.0e-57
Match length
                  237
% identity
                  12
NCBI Description polyubiquitin [maize, Genomic, 3439 nt]
Seq. No.
                  313134
Seq. ID
                  xsy700213192.h1
Method
                  BLASTX
NCBI GI
                  g3914020
BLAST score
                  214
                  2.0e-17
E value
Match length
                  86
% identity
                  58
NCBI Description
                  (R)-MANDELONITRILE LYASE ISOFORM 1 PRECURSOR
                  (HYDROXYNITRILE LYASE 1) ((R)-OXYNITRILASE 1)
```

44748

[Prunus dulcis]

>gi_1561641 emb CAA69388 (Y08211) mandelonitrile lyase

Seq. ID

Method

```
313135
Seq. No.
Seq. ID
                  xsy700213204.h1
Method
                  BLASTX
NCBI GI
                  g3786011
BLAST score
                  368
                  2.0e-35
E value
Match length
                  90
                  76
% identity
                  (AC005499) putative elongation factor [Arabidopsis
NCBI Description
                  thaliana]
                  313136
Seq. No.
Seq. ID
                  xsy700213211.h1
Method
                  BLASTN
NCBI GI
                  g6598670
BLAST score
                  33
                  4.0e-09
E value
Match length
                  61
% identity
                  89
                  Arabidopsis thaliana chromosome II BAC T23A1 genomic
NCBI Description
                  sequence, complete sequence
Seq. No.
                  313137
Seq. ID
                  xsy700213214.h1
Method
                  BLASTX
NCBI GI
                  g4218121
BLAST score
                  153
E value
                  1.0e-10
Match length
                  55
                  49
% identity
                  (AL035353) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  313138
Seq. ID
                  xsy700213227.h1
Method
                  BLASTX
NCBI GI
                  g3341695 '
BLAST score
                  344
                  1.0e-32
E value
Match length
                  101
% identity
                   (AC003672) putative thiamin pyrophosphokinase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  313139
Seq. ID
                  xsy700213242.h1
Method
                  BLASTX
NCBI GI
                  g3445201
BLAST score
                  268
                  9.0e-24
E value
Match length
                  54
                  89
% identity
                  (AC004786) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  313140
```

44749

xsy700213246.hl

BLASTN



```
g3821780
NCBI GI
BLAST score
                  36
E value
                  5.0e-11
Match length
                  36
                  100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                  313141
                  xsy700213304.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4185136
BLAST score
                  181
E value
                  8.0e-14
Match length
                  60
% identity
                  53
                  (AC005724) putative trehalose-6-phosphate synthase
NCBI Description
                   [Arabidopsis thaliana]
                  313142
Seq. No.
Seq. ID
                  xsy700213338.h1
Method
                  BLASTX
NCBI GI
                  g3402719
BLAST score
                  191
                  1.0e-14
E value
                  59
Match length
% identity
                  63
NCBI Description
                  (AC004261) unknown protein [Arabidopsis thaliana]
Seq. No.
                  313143
Seq. ID
                  xsy700213393.h1
Method
                  BLASTX
                  g3341696
NCBI GI
BLAST score
                  194
E value
                  3.0e-15
Match length
                  66
% identity
                  58
NCBI Description (AC003672) unknown protein [Arabidopsis thaliana]
Seq. No.
                  313144
                  xsy700213395.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2632105
BLAST score
                  324
                  2.0e-30
E value
Match length
                  88
% identity
                  64
                  (Z98760) arginyl-tRNA synthetase [Arabidopsis thaliana]
NCBI Description
                  >gi_4539426_emb_CAB38959.1_ (AL049171) arginyl-tRNA
                  synthetase [Arabidopsis thaliana]
Seq. No.
                  313145
Seq. ID
                  xsy700213413.hl
Method
                  BLASTX
NCBI GI
                  g3142301
```

Match length 38

182

5.0e-14

BLAST score

E value



% identity (AC002411) Contains similarity to neural cell adhesion NCBI Description molecule 2, large isoform precursor gb M76710 from Xenopus laevis, and beta transducin from S. cerevisiae gb_Q05946. ESTs qb N65081 qb Z30910, qb Z34190, qb Z34611, qb R30101, gb H3630 313146 Seq. No. Seq. ID xsy700213444.h1 Method BLASTX g115864 NCBI GI BLAST score 179 1.0e-13 E value Match length 51 % identity 63 NCBI Description [Segment 1 of 2] SERINE CARBOXYPEPTIDASE II CHAINS A AND B (CARBOXYPEPTIDASE D) (CP-MII) >gi 82419 pir A29640 serine-type carboxypeptidase (EC 3.4.16.1) II A chain barley >qi 226038 prf 1408163A CPase II A [Hordeum vulgare var. distichum] Seq. No. 313147 Seq. ID xsy700213496.h1 Method BLASTX NCBI GI q2660670 BLAST score 238 E value 2.0e-20 Match length 77 % identity (AC002342) putative Cu2+-transporting ATPase [Arabidopsis NCBI Description thaliana] Seq. No. 313148 Seq. ID xsy700213562.h1 Method BLASTX NCBI GI g115815 BLAST score ...470 2.0e-47 E value Match length 90 98 % identity NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-M9) (LHCP) >gi 100866 pir S13098 chlorophyll a/b-binding protein precursor - maize >gi 22355 emb CAA39376_ (X55892) light-harvesting chlorophyll a/b binding protein [Zea mays] Seq. No. 313149 Seq. ID xsy700213565.h1

Method

NCBI GI

BLASTX q3036955

BLAST score E value

459 3.0e-46

Match length % identity

88 99

NCBI Description

(AB012641) light harvesting chlorophyll a/b-binding protein [Nicotiana sylvestris]

BLAST score

E value

192

4.0e-15



```
313150
Seq. No.
                  xsy700213566.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3582333
BLAST score
                  189
                  1.0e-14
E value
Match length
                  88
                  43
% identity
NCBI Description
                  (AC005496) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  313151
                  xsy700213576.hl
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3212851
BLAST score
                  172
E value
                  1.0e-12
Match length
                  43
% identity
                  70
                  (AC004005) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   313152
                  xsy700213589.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2062705
BLAST score
                   37
E value
                   1.0e-11
Match length
                   37
% identity
                  100
NCBI Description
                  Human butyrophilin (BTF5) mRNA, complete cds
Seq. No.
                   313153
Seq. ID
                   xsy700213605.hl
Method
                  BLASTX
NCBI GI
                   g4467359
BLAST score
                   231
E value
                   2.0e-19
Match length
                  97
                   48
% identity
                  (AJ002685) Phosphatidylinositol 4-kinase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   313154
                   xsy700213634.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2098705
BLAST score
                   144
                   3.0e-09
E value
Match length
                  83
                   40
% identity
NCBI Description
                  (U82973) pectinesterase [Citrus sinensis]
                  313155
Seq. No.
Seq. ID
                  xsy700213695.h1
Method
                   BLASTX
NCBI GI
                   g482311
```

Match length

% identity

48

65



```
39
Match length
                   92
% identity
                  photosystem II oxygen-evolving complex protein 1 - rice
NCBI Description
                   (strain Nihonbare) >gi 739292_prf__2002393A oxygen-evolving
                   complex protein 1 [Oryza sativa]
Seq. No.
                   313156
                   xsy700213768.hl
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1762142
BLAST score
                   149
                   6.0e-10
E value
Match length
                   60
% identity
                   48
NCBI Description
                   (U48434) putative cytochrome P450 [Solanum chacoense]
                   313157
Seq. No.
Seq. ID
                   xsy700213781.h1
Method
                   BLASTX
NCBI GI
                   q629692
BLAST score
                   180
E value
                   1.0e-16
Match length
                   78
                   63
% identity
                   hypothetical protein - common tobacco
NCBI Description
                   >qi 506471 emb CAA56189 (X79794) unnamed protein product
                   [Nicotiana tabacum]
Seq. No.
                   313158
                   xsy700213791.hl
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1890577
BLAST score
                   185
                   4.0e-14
E value
Match length
                   48
                   65
% identity
                   (X93175) xyloglucan endotransglycosylase (XET) [Hordeum
NCBI Description
                   vulgare]
Seq. No.
                   313159
Seq. ID
                   xsy700213863.h1
Method
                   BLASTX
                   q1644291
NCBI GI
BLAST score
                   264
                   2.0e-23
E value
Match length
                   60
% identity
                   77
                   (Z73295) receptor-like protein kinase [Catharanthus roseus]
NCBI Description
                   313160
Seq. No.
                   xsy700213865.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g401161
BLAST score
                   160
                   2.0e-11
E value
```

20

TUBULIN ALPHA-5 CHAIN >gi_322879_pir S28982 tubulin NCBI Description alpha-5 chain - maize $>gi_22156$ emb $\overline{CA}A44862$ (X63177) alpha-tubulin #5 [Zea mays] $>gi_450\overline{2}93$ (L278 $\overline{1}5$) alpha-tubulin [Zea mays] >gi 452474 (U05258) alpha-tubulin [Zea mays] Seq. No. 313161 xsy700213924.h1 Seq. ID Method BLASTX NCBI GI g2497756 BLAST score 151 E value 4.0e-10 Match length 64 % identity 44 NCBI Description NONSPECIFIC LIPID-TRANSFER PROTEIN 2 PRECURSOR (LTP 2)

>gi_422011_pir__S33461 lipid transfer protein - sorghum >gi 311333 emb CAA50661 (X71668) lipid transfer protein

[Sorghum bicolor]

Seq. No. 313162

Seq. ID xsy700213933.hl

Method BLASTX NCBI GI g4586021 BLAST score 160 E value 2.0e-11 Match length 38 % identity 79

(AC007170) putative cytoplasmic aconitate hydratase NCBI Description

[Arabidopsis thaliana]

Seq. No. 313163

Seq. ID xsy700214035.h1

Method BLASTX NCBI GI g135060 BLAST score 174 4.0e-13 E value Match length 49 76 % identity

SUCROSE SYNTHASE 1 (SUCROSE-UDP GLUCOSYLTRANSFERASE 1) NCBI Description (SHRUNKEN-1) >gi_66570_pir__YUZMS sucrose synthase (EC

2.4.1.13) - maize >gi_22486 emb CAA26247 (X02400) sucrose

synthase [Zea mays] >gi 22488 emb CAA26229 (X02382)

sucrose synthase [Zea mays]

Seq. No. 313164

Seq. ID xsy700214042.h1

Method BLASTX NCBI GI g322701 BLAST score 151 E value 2.0e-10 Match length 47 % identity 70

NCBI Description Tubulin beta-2 chain - soybean

Seq. No. 313165

Seq. ID xsy700214122.h1

Method BLASTX



NCBI GI g232033 BLAST score 268 E value 9.0e-24 Match length 64 % identity 80

NCBI Description ELONGATION FACTOR 1 BETA' >gi 479830 pir S35501

translation elongation factor eEF-1 beta' chain - wheat >gi_218341_dbj_BAA02436_ (D13147) elongation factor 1 beta'

[Triticum aestivum]

Seq. No. 313166

Seq. ID xsy700214232.h1

Method BLASTX
NCBI GI g113621
BLAST score 289
E value 2.0e-26
Match length 64
% identity 88

NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME

>gi_68196_pir__ADZM fructose-bisphosphate aldolase (EC
4.1.2.13), cytosolic - maize >gi_168420 (M16220) aldolase
[Zea mays] >gi_295850_emb_CAA31366_ (X12872) fructose
bisphosphate aldolase [Zea mays] >gi_225624_prf__1307278A

cytoplasmic aldolase [Zea mays]

Seq. No. 313167

Seq. ID xsy700214282.h1

Method BLASTX
NCBI GI g134101
BLAST score 233
E value 1.0e-19
Match length 73
% identity 66

NCBI Description RUBISCO SUBUNIT BINDING-PROTEIN ALPHA SUBUNIT (60 KD

CHAPERONIN ALPHA SUBUNIT) (CPN-60 ALPHA)

>gi_72958_pir__HHCSBA ribulose-bisphosphate carboxylase

subunit-binding protein alpha chain - castor bean

(fragment)

Seq. No. 313168

Seq. ID xsy700214322.h1

Method BLASTX
NCBI GI g2501011
BLAST score 334
E value 2.0e-31
Match length 100
% identity 64

NCBI Description ISOLEUCYL-TRNA SYNTHETASE (ISOLEUCINE--TRNA LIGASE) (ILERS)

>gi_1652625_dbj_BAA17545_ (D90907) isoleucyl-tRNA

synthetase [Synechocystis sp.]

Seq. No. 313169

Seq. ID xsy700214335.h1

Method BLASTX
NCBI GI g2982431
BLAST score 146
E value 3.0e-12

% identity

50



```
Match length
% identity
                   49
NCBI Description
                   (AL022224) leucine rich repeat-like protein [Arabidopsis
                   thaliana]
Seq. No.
                   313170
Seq. ID
                   xsy700214342.h1
Method
                   BLASTX
NCBI GI
                   g1619602
BLAST score
                   234
E value
                   9.0e-20
Match length
                   63
% identity
                   65
                  (Y08726) MtN3 [Medicago truncatula]
NCBI Description
Seq. No.
                   313171
Seq. ID
                   xsy700214367.h1
Method
                   BLASTX
                   g4191791
NCBI GI
BLAST score
                   310
                   9.0e-29
E value
Match length
                   74
% identity
                   73
NCBI Description
                   (AC005917) putative sf21 {Helianthus annuus} protein
                   [Arabidopsis thaliana]
Seq. No.
                   313172
Seq. ID
                   xsy700214370.h1
Method
                   BLASTX
                   g1346057
NCBI GI
BLAST score
                   154
                   2.0e-10
E value
Match length
                   40
% identity
                   65
NCBI Description
                   PROTEIN KINASE G11A >gi_100705_pir__B30311 protein kinase C
                   (EC 2.7.1.-) homolog - rice (fragment) >gi 169788 (J04556)
                   G11A protein [Oryza sativa]
Seq. No.
                   313173
                   xsy700214405.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3036946
BLAST score
                   339
E value
                   3.0e-32
Match length
                   74
% identity
                   86
NCBI Description
                   (AB012637) light harvesting chlorophyll a/b-binding protein
                   [Nicotiana sylvestris]
Seq. No.
                  313174
Seq. ID
                  xsy700214454.h1
Method
                  BLASTX
NCBI GI
                  q2829864
BLAST score
                  151
E value
                  2.0e-10
Match length
                  54
```

NCBI Description



```
NCBI Description
                   (AC002396) similar to zinc metalloproteinases [Arabidopsis
                   thaliana]
Seq. No.
                   313175
                   xsy700214470.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2213547
BLAST score
                   248
                   2.0e-21
E value
Match length
                   77
% identity
                   64
                   (Z97052) putative ubiquinone biosynthesis methyltransferase
NCBI Description
                   [Schizosaccharomyces pombe]
Seq. No.
                   313176
Seq. ID
                   xsy700214475.h1
Method
                   BLASTX
NCBI GI
                   g550438
BLAST score
                   361
E value
                   1.0e-34
Match length
                   76
% identity
                   96
NCBI Description
                   (X81829) cytochrome P450 [Zea mays]
                   >gi 1870201 emb CAA72208 (Y11404) cytochrome p450 [Zea
                   mays]
Seq. No.
                   313177
Seq. ID
                   xsy700214479.h1
Method
                   BLASTN
NCBI GI
                   g2231164
BLAST score
                   85
E value
                   4.0e-40
Match length
                   201
% identity
                   86
NCBI Description
                   Oryza sativa integral membrane protein (OsNramp2) mRNA,
                   complete cds
                   313178
Seq. No.
Seq. ID
                   xsy700214558.h1
Method
                   BLASTX
NCBI GI
                   g2829918
BLAST score
                   201
                   3.0e-16
E value
Match length
                   38
% identity
                   95
NCBI Description
                   (AC002291) similar to "tub" protein gp U82468 2072162
                   [Arabidopsis thaliana]
Seq. No.
                   313179
Seq. ID
                   xsy700214560.h1
Method
                   BLASTX
NCBI GI
                   q2582800
BLAST score
                   157
E value
                   8.0e-11
Match length
                   71
% identity
                   49
```

(Y11607) protein phosphatase 2C [Medicago sativa]

```
Seq. No.
                   313180
Seq. ID
                  xsy700214572.h1
Method
                  BLASTX
NCBI GI
                  q3881189
BLAST score
                   210
E value
                   5.0e-17
Match length
                   58
% identity
                   64
NCBI Description
                  (Z99281) similar to ADP-ribosylation factor; cDNA EST
                  EMBL: C08179 comes from this gene; cDNA EST EMBL: C08337
                   comes from this gene; cDNA EST EMBL: C09829 comes from this
                  gene; cDNA EST yk291b4.5 comes from this gene; cDNA EST yk4
Seq. No.
                  313181
Seq. ID
                  xsy700214586.h1
Method
                  BLASTX
NCBI GI
                  q3152600
BLAST score
                  152
E value
                  3.0e-10
Match length
                  40
% identity
                   68
NCBI Description
                  (AC002986) Contains similarity to S. cerevisiae
                  hypothetical protein YOR197w, gb_Z75105. ESTs gb_H37409,
                  gb_AA395290, and gb_T43907 come from this gene.
                   [Arabidopsis thaliana]
Seq. No.
                  313182
Seq. ID
                  xsy700214625.h1
Method
                  BLASTN
NCBI GI
                  g1129083
BLAST score
                  75
E value
                  4.0e-34
Match length
                  134
% identity
                  90
                  Wheat mRNA for protein H2A, complete cds, clone wcH2A-2
NCBI Description
Seq. No.
                  313183
Seq. ID
                  xsy700214663.h1
Method
                  BLASTX
NCBI GI
                  q3176874
BLAST score
                  222
E value
                  2.0e-18
Match length
                  62
% identity
NCBI Description
                  (AF065639) cucumisin-like serine protease [Arabidopsis
                  thaliana]
Seq. No.
                  313184
Seq. ID
                  xsy700214675.h1
Method
                  BLASTX
NCBI GI
                  q4521190
BLAST score
                  206
E value
                  1.0e-16
Match length
                  87
% identity
                  43
NCBI Description (AB013448) Pib [Oryza sativa] >gi 4521192 dbj BAA76282.1
```

Seq. ID



(AB013449) Pib [Oryza sativa]

```
Seq. No.
                  313185
                  xsy700214676.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3511285
BLAST score
                  416
E value
                  3.0e-41
Match length
                  86
                  88
% identity
                  (AF081534) cellulose synthase [Populus alba x Populus
NCBI Description
                  tremula]
Seq. No.
                  313186
Seq. ID
                  xsy700214704.h1
Method
                  BLASTX
NCBI GI
                  g3913808
BLAST score
                  284
                  5.0e-26
E value
Match length
                  63
% identity
                  92
                  FERROCHELATASE PRECURSOR (PROTOHEME FERRO-LYASE) (HEME
NCBI Description
                  SYNTHETASE) >gi_2429618_dbj_BAA22284_ (AB007120)
                  ferrochelatase [Oryza sativa]
Seq. No.
                  313187
Seq. ID
                  xsy700214730.h1
                  BLASTX
Method
                  g4490736
NCBI GI
BLAST score
                  171
                  9.0e-13
E value
Match length
                  43
% identity
                  86
NCBI Description (AL035708) putative protein [Arabidopsis thaliana]
                  313188
Seq. No.
                  xsy700214756.h1
Seq. ID
Method
                  BLASTX
                  g4539343
NCBI GI
BLAST score
                  355
E value
                  5.0e - 34
Match length
                  85
% identity
                  81
NCBI Description (AL035539) putative protein [Arabidopsis thaliana]
Seq. No.
                  313189
                  xsy700214824.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4587560
BLAST score
                  148
                  7.0e-10
E value
Match length
                  39
% identity
                  69
NCBI Description (AC006577) F15I1.27 [Arabidopsis thaliana]
Seq. No.
                  313190
```

xsy700214825.h1

% identity

```
Method
                   BLASTX
NCBI GI
                   g1835731
BLAST score
                   371
E value
                   8.0e-36
Match length
                   84
% identity
                   81
                   (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
NCBI Description
Seq. No.
                   313191
Seq. ID
                   xsy700214836.h1
Method
                   BLASTN
NCBI GI
                   g1370602
BLAST score
                   105
E value
                   3.0e-52
Match length
                   130
% identity
                   94
NCBI Description
                   Z.mays mRNA for annexin p35
Seq. No.
                   313192
Seq. ID
                   xsy700214877.h1
Method
                   BLASTX
NCBI GI
                   q3549666
BLAST score
                   181
E value
                   1.0e-13
Match length
                   45
% identity
                   73
NCBI Description
                   (AL031394) putative protein [Arabidopsis thaliana]
Seq. No.
                   313193
Seq. ID
                   xsy700214903.h1
Method
                   BLASTX
NCBI GI
                   g2996096
BLAST score
                   266
E value
                   8.0e-24
Match length
                   53
% identity
                   98
NCBI Description
                   (AF030517) translation elongation factor-1 alpha; EF-1
                   alpha [Oryza sativa]
Seq. No.
                   313194
Seq. ID
                   xsy700214944.h1
Method
                   BLASTN
NCBI GI
                   g21800
BLAST score
                   97
E value
                   3.0e-47
Match length
                   220
% identity
                   78
NCBI Description
                  T.aestivum L mRNA for histone H2B
Seq. No.
                   313195
Seq. ID
                   xsy700214954.hl
Method
                   BLASTX
                   g2842469
NCBI GI
BLAST score
                   190
E value
                   1.0e-14
Match length
                   83
```



(AL021747) hypothetical protein [Schizosaccharomyces pombe] NCBI Description 313196 Seq. No. Seq. ID xsy700214974.h1 Method BLASTN NCBI GI q21843 BLAST score 35 3.0e-10 E value 67 Match length 88 % identity Wheat PsbO mRNA for 33kDa oxygen evolving protein of NCBI Description photosystem II 313197 Seq. No. xsy700214976.hl Seq. ID Method BLASTN NCBI GI g473602 BLAST score 147 4.0e-77 E value 243 Match length 90 % identity NCBI Description Zea mays W-22 histone H2A mRNA, complete cds 313198 Seq. No. xsy700214985.h1 Seq. ID BLASTX Method NCBI GI g1706260 BLAST score 311 7.0e-29 E value Match length 80 76 % identity NCBI Description CYSTEINE PROTEINASE 1 PRECURSOR >gi 2118131 pir S59597 cysteine proteinase 1 precursor - maize >gi_643597_dbj_BAA08244_ (D45402) cysteine proteinase [Zea mays] Seq. No. 313199 xsy700217005.h1 Seq. ID Method BLASTX NCBI GI g2781362 BLAST score 206 2.0e-16 E value Match length 87 45 % identity

(AC003113) F2401.18 [Arabidopsis thaliana] NCBI Description

313200 Seq. No.

Seq. ID xsy700217014.h1

Method BLASTX NCBI GI g4038034 BLAST score 202 E value 4.0e-16 Match length 46 74 % identity

(AC005936) unknown protein [Arabidopsis thaliana] NCBI Description

313201 Seq. No.

```
xsy700217026.h1
Seq. ID
Method
                   BLASTX
                   g4583546
NCBI GI
                   218
BLAST score
                   6.0e-18
E value
Match length
                   57
                   77
% identity
NCBI Description
                   (AJ010819) GrpE protein [Arabidopsis thaliana]
                   313202
Seq. No.
                   xsy700217113.h1
Seq. ID
Method
                   BLASTX
                   g1079321
NCBI GI
BLAST score
                   192
                   6.0e-15
E value
Match length
                   76
```

% identity 49
NCBI Description XPMC2 protein - African clawed frog >gi_595380 (U10185)

XPMC2 protein [Xenopus laevis]

 Seq. No.
 313203

 Seq. ID
 xsy700217161.h1

 Method
 BLASTX

 NCBI GI
 g1706260

 BLAST score
 308

 E value
 2.0e-28

E value 2.0e-28
Match length 79
% identity 77
NCBI Description CYSTEIN

NCBI Description CYSTEINE PROTEINASE 1 PRECURSOR >gi_2118131_pir__S59597

cysteine proteinase 1 precursor - maize

>gi_643597_dbj_BAA08244_ (D45402) cysteine proteinase [Zea

mays]

Seq. No. 313204

Seq. ID xsy700217167.h1

Method BLASTX
NCBI GI g2244898
BLAST score 263
E value 3.0e-23
Match length 88
% identity 55

NCBI Description (Z97338) strong similarity to protein phosphatase 2A

regulatory chain, 74K [Arabidopsis thaliana]

Seq. No. 313205

Seq. ID xsy700217169.h1

Method BLASTX
NCBI GI g3785989
BLAST score 177
E value 3.0e-13
Match length 44
% identity 75

NCBI Description (AC005560) unknown protein [Arabidopsis thaliana]

Seq. No. 313206

Seq. ID xsy700217212.h1

Method BLASTX

```
g1052960
 NCBI GI
BLAST score
                    246
 E value
                    4.0e-21
 Match length
                    58
 % identity
                    (U37437) PNIL34 [Ipomoea nil]
 NCBI Description
 Seq. No.
                    313207
 Seq. ID
                   xsy700217236.hl
 Method
                   BLASTX
 NCBI GI
                    g2795807
 BLAST score
                    241
                    1.0e-20
 E value
 Match length
                    77
 % identity
                    (AC003674) hypothetical protein [Arabidopsis thaliana]
 NCBI Description
 Seq. No.
                    313208
 Seq. ID
                    xsy700217245.h1
 Method
                    BLASTX
 NCBI GI
                    q4467111
 BLAST score
                    290
                    2.0e-26
 E value
 Match length
                    70
 % identity
 NCBI Description
                    (AL035538) putative protein [Arabidopsis thaliana]
 Seq. No.
                    313209
 Seq. ID
                    xsy700217253.h1
 Method
                    BLASTN
 NCBI GI
                    q2062705
 BLAST score
                    36
                    6.0e-11
 E value
 Match length
                    36
                    100
 % identity
                    Human butyrophilin (BTF5) mRNA, complete cds
 NCBI Description
                    313210
 Seq. No.
                    xsy700217282.h1
 Seq. ID
 Method
                    BLASTX
                    g3928519
 NCBI GI
 BLAST score
                    362
                    6.0e-35
 E value
 Match length
                    79
```

92 % identity

(AB011670) wpk4 protein kinase [Triticum aestivum] NCBI Description

313211 Seq. No. xsy700217288.h1 Seq. ID Method BLASTN NCBI GI g2062705 BLAST score 37

1.0e-11 E value Match length 37 100 % identity

NCBI Description Human butyrophilin (BTF5) mRNA, complete cds



```
313212
Seq. No.
                  xsy700217348.hl
Seq. ID
Method
                  BLASTX
                  g4115383
NCBI GI
                  173
BLAST score
                  1.0e-12
E value
                  71
Match length
% identity
                  45
                   (AC005967) receptor-like protein kinase [Arabidopsis
NCBI Description
                  thaliana]
                  313213
Seq. No.
                  xsy700217350.h1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1352186
BLAST score
                   302
                   7.0e-28
E value
                   79
Match length
                   72
% identity
                  ALLENE OXIDE SYNTHASE PRECURSOR (HYDROPEROXIDE DEHYDRASE)
NCBI Description
                   (CYTOCHROME P450 74) >gi 404866 (U00428) allene oxide
                   synthase [Linum usitatissimum]
Seq. No.
                   313214
                   xsy700217432.h1
Seq. ID
Method
                  BLASTX
                   g3386604
NCBI GI
BLAST score
                   164
                   1.0e-11
E value
Match length
                   70
                   53
% identity
                   (AC004665) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                   313215
Seq. No.
                   xsy700217455.h1
Seq. ID
Method
                   BLASTX
                   g3335060
NCBI GI
BLAST score
                   325
                   2.0e-30
E value
Match length
                   87
                   71
% identity
                   (AF025842) plasma membrane-type calcium ATPase [Arabidopsis
NCBI Description
                   thaliana] >gi 4468989 emb CAB38303 (AL035605) plasma
                   membrane-type calcium ATPase (ACA2) [Arabidopsis thaliana]
Seq. No.
                   313216
                   xsy700217468.h1
Seq. ID
Method
                   BLASTX
                   g2281115
NCBI GI
BLAST score
                   292
E value
                   1.0e-26
Match length
                   75
                   75
% identity
                   (AC002330) putative cullin-like 1 protein [Arabidopsis
NCBI Description
```

Seq. No. 313217

thaliana]

```
Seq. ID xsy700217482.h1
Method BLASTX
NCBI GI g3789942
BLAST score 271
E value 9.0e-30
```

% identity 16 NCBI Description (AF093505) polyubiquitin [Saccharum hybrid cultivar

H32-8560]

Seq. No. 313218 Seq. ID xsy700

Match length

Seq. ID xsy700217484.h1

Method BLASTX
NCBI GI g1168529
BLAST score 182
E value 5.0e-16
Match length 56
% identity 79

NCBI Description SERINE/THREONINE-PROTEIN KINASE ASK1 >gi 541890 pir S36944

probable serine/threonine-specific protein kinase (EC
2.7.1.-) (clone ASK1) - Arabidopsis thaliana >gi_166882
(M91548) serine/threonine kinase [Arabidopsis thaliana]
>gi_1931648 (U95973) Ser/Thr kinase [Arabidopsis thaliana]

Seq. No. 313219

Seq. ID xsy700217555.h1

Method BLASTX
NCBI GI g1853968
BLAST score 208
E value 8.0e-17
Match length 67
% identity 64

NCBI Description (D88121) CPRD12 protein [Vigna unquiculata]

Seq. No. 313220

Seq. ID xsy700217568.h1

Method BLASTN
NCBI GI g3043528
BLAST score 62

E value 2.0e-26
Match length 150
% identity 85

NCBI Description Zea mays mRNA for flavin containing polyamine oxidase (PAO)

Seq. No.

313221

Seq. ID xsy700217572.h1

Method BLASTX
NCBI GI g1617270
BLAST score 147
E value 1.0e-09
Match length 40
% identity 62

NCBI Description (X94624) acyl-CoA synthetase [Brassica napus]

Seq. No.

313222

Seq. ID xsy700217589.h1

Method

BLASTX

```
g4539460
  NCBI GI
                    156
  BLAST score
                     1.0e-10
  E value
  Match length
                     84
  % identity
                     (AL049500) putative protein [Arabidopsis thaliana]
  NCBI Description
                     313223
Seq. No.
                     xsy700217604.h1
  Seq. ID
  Method
                     BLASTX
                     g2341042
  NCBI GI
  BLAST score
                     197
                     3.0e-16
  E value
  Match length
                     83
  % identity
                     59
  NCBI Description
                     (AC000104) F19P19.26 [Arabidopsis thaliana]
  Seq. No.
                     313224
  Seq. ID
                     xsy700217619.h1
  Method
                     BLASTX
  NCBI GI
                     q168404
  BLAST score
                     173
  E value
                     1.0e-12
  Match length
                     35
  % identity
  NCBI Description
                    (J01238) actin [Zea mays]
  Seq. No.
                     313225
  Seq. ID
                     xsy700217629.hl
  Method
                     BLASTN
                     g1890576
  NCBI GI
  BLAST score
                     39
                     9.0e-13
  E value
  Match length
                     91
                     86
  % identity
                     H.vulgare mRNA for xyloglucan endotransglycosylase-like
  NCBI Description
                     protein (XEB)
  Seq. No.
                     313226
                     xsy700217637.h1
  Seq. ID
  Method
                     BLASTN
  NCBI GI
                     g1777929
  BLAST score
                     41
                     6.0e-14
  E value
                     93
  Match length
                     97
  % identity
                     Saccharum officinarum nucleoside diphosphate kinase
  NCBI Description
                     (SoNDPK1) mRNA, complete cds
```

Method BLASTX
NCBI GI g4220521
BLAST score 187
E value 2.0e-14

Match length 52 % identity 65



```
NCBI Description (AL035356) putative protein [Arabidopsis thaliana]
                  313228
Seq. No.
                  xsy700217663.hl
Seq. ID
Method
                  BLASTX
                  g4191791
NCBI GI
BLAST score
                   246
                   8.0e-26
E value
Match length
                   76
                   76
% identity
NCBI Description
                   (AC005917) putative sf21 {Helianthus annuus} protein
                   [Arabidopsis thaliana]
                   313229
Seq. No.
                   xsy700217726.h1
Seq. ID
Method
                   BLASTX
                   g1890573
NCBI GI
BLAST score
                   151
                   2.0e-10
E value
Match length
                   44
% identity
                   60
                   (X93173) xyloglucan endotransglycosylase (XET) [Hordeum
NCBI Description
                   vulgare]
Seq. No.
                   313230
Seq. ID
                   xsy700217728.h1
Method
                   BLASTX
NCBI GI
                   g1184774
BLAST score
                   356
                   3.0e-34
E value
Match length
                   68
                   100
% identity
                   (U45856) cytosolic glyceroldehyde-3-phosphate dehydrogenase
NCBI Description
                   GAPC3 [Zea mays]
Seq. No.
                   313231
Seq. ID
                   xsy700217789.hl
Method
                   BLASTN
NCBI GI
                   q2062705
BLAST score
                   36
E value
                   6.0e-11
Match length
                   36
% identity
                   100
NCBI Description
                  Human butyrophilin (BTF5) mRNA, complete cds
Seq. No.
                   313232
Seq. ID
                   xsy700217831.h1
Method
                   BLASTX
NCBI GI
                   g1575595
BLAST score
                   394
                   1.0e-38
E value
Match length
                   81
% identity
                   96
NCBI Description
                   (U67717) fimbrin/plastin-like [Triticum aestivum]
```

xsy700217867.h1

Seq. No.

Seq. ID

Method

NCBI GI

BLASTX

q4378066



```
BLASTX
Method
NCBI GI
                  q1362065
BLAST score
                  282
E value
                  2.0e-25
Match length
                  77
                  75
% identity
                  small GTP-binding protein - garden pea
NCBI Description
                  >gi 871506 emb CAA90081 (Z49901) small GTP-binding protein
                  [Pisum sativum]
Seq. No.
                  313234
                  xsy700217955.h1
Seq. ID
Method
                  BLASTX
                  g3970689
NCBI GI
BLAST score
                  159
                  5.0e-11
E value
Match length
                  96
                  38
% identity
                  (Y18484) (+)-delta-cadinene synthase [Gossypium arboreum]
NCBI Description
                  313235
Seq. No.
                  xsy700217962.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1353193
BLAST score
                  306
                  3.0e-28
E value
Match length
                  96
                  61
% identity
                  O-METHYLTRANSFERASE ZRP4 (OMT) >gi 542186 pir JQ2268
NCBI Description
                  O-methyltransferase (EC 2.1.1.-) - maize >gi 404070
                  (L14063) O-methyltransferase [Zea mays]
                  313236
Seq. No.
                  xsy700217971.h1
Seq. ID
Method
                  BLASTN
                  g551482
NCBI GI
BLAST score
                  136
                  1.0e-70
E value
Match length
                  228
% identity
                  91
                  Zea mays ABA- and ripening-inducible-like protein mRNA,
NCBI Description
                  complete cds
                  313237
Seq. No.
Seq. ID
                  xtd700282204.h2
Method
                  BLASTX
NCBI GI
                  g2462756
                  267
BLAST score
E value
                  1.0e-23
                  96
Match length
% identity
                  61
NCBI Description
                  (AC002292) putative receptor kinase [Arabidopsis thaliana]
                  313238
Seq. No.
Seq. ID
                  xtd700282223.h2
```



```
BLAST score 292
E value 1.0e-26
Match length 93
% identity 56
NCBI Description (AF098806) polyprotein [Sorghum bicolor]
```

Seq. No. 313239
Seq. ID xtd700282235.h2

Method BLASTX
NCBI GI g2244836
BLAST score 353
E value 1.0e-33
Match length 99
% identity 70

NCBI Description (Z97337) RNA helicase homolog [Arabidopsis thaliana]

Seq. No. 313240
Seq. ID xtd700282237.h2

Method BLASTX
NCBI GI g3176686
BLAST score 394

E value 2.0e-38
Match length 99
% identity 67

NCBI Description (AC003671) Similar to high affinity potassium transporter,

HAK1 protein gb_U22945 from Schwanniomyces occidentalis.

[Arabidopsis thaliana]

Seq. No.

Seq. ID xtd700282303.h2

313241

Method BLASTX
NCBI GI g3688350
BLAST score 218
E value 7.0e-18
Match length 101
% identity 47

NCBI Description (AL030996) dJ1189B24.4 (novel PUTATIVE protein similar to

hypothetical proteins S. pombe C22F3.14C and C. elegans

C16A3.8) [Homo sapiens]

Seq. No. 313242

Seq. ID xtd700282317.h2

Method BLASTX
NCBI GI g2829910
BLAST score 238
E value 5.0e-33
Match length 102
% identity 24

NCBI Description (AC002291) Unknown protein, contains regulator of

chromosome condensation motifs [Arabidopsis thaliana]

Seq. No. 313243

Seq. ID xtd700282325.h2

Method BLASTX
NCBI GI g3269285
BLAST score 248
E value 2.0e-21



Match length % identity

(AL030978) hypothetical protein [Arabidopsis thaliana] NCBI Description

Seq. No.

313244

Seq. ID

xtd700282329.h2

Method NCBI GI BLASTX q1297187

BLAST score E value Match length

264 3.0e-23 95

54

% identity

(U53501) similar to protein encoded by GenBank Accession NCBI Description Number U41815, nucleoporin 98 [Arabidopsis thaliana]

Seq. No.

313245

Seq. ID

xtd700282336.h2

Method BLASTX NCBI GI g3482913 BLAST score 193 E value 6.0e-15 Match length 76 % identity

NCBI Description (AC003970) Similar to MtN21, gi 2598575, Megicago

truncatula nodulation induced gene [Arabidopsis thaliana]

Seq. No.

313246 Seq. ID xtd700282351.h2

Method BLASTN

NCBI GI q1244652 BLAST score 51

E value 5.0e-20 Match length 103 % identity 87

NCBI Description Zea mays copia-type retroelement PREM-2 gag gene, complete

Seq. No.

313247

Seq. ID

xtj700377208.h1

Method BLASTN NCBI GI g3217024 BLAST score 51

E value 2.0e-20 95 Match length 88 % identity

Homo sapiens DNA sequence from PAC 97D16 on chromosome NCBI Description

6p21.3-22.2. Contains an unknown pseudogene, a 60S Ribosomal protein L24 (L30) LIKE pseudogene and histone genes H2BFC (H2B/c), H4FFP (H4/f pseudogene), H2AFC (H2A/c

Seq. No.

313248

Seq. ID xtj700377240.h1

Method BLASTN NCBI GI g575730 BLAST score 78 3.0e-36 E value Match length 114



```
% identity
NCBI Description Z.mays mRNA for transmembrane protein
Seq. No.
                  313249
                  xtj700377333.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4530611
BLAST score
                  173
E value
                  6.0e-13
Match length
                  32
                  97
% identity
NCBI Description
                  (AF134552) serine/threonine protein phosphatase PP2A-2
                  catalytic subunit [Oryza sativa subsp. indica]
Seq. No.
                  313250
Seq. ID
                  xtj700377405.h1
Method
                  BLASTN
NCBI GI
                  q34621
BLAST score
                  148
E value
                  8.0e-78
Match length
                  179
% identity
                  97
NCBI Description Human mRNA for melanoma growth stimulatory activity (MGSA)
Seq. No.
                  313251
Seq. ID
                  xtj700377407.h1
Method
                  BLASTN
NCBI GI
                  g7124014
BLAST score
                  99
                  9.0e-49
E value
Match length
                  140
% identity
                  91
                  Homo sapiens Chromosome 22 Cosmid Clone 46a9 In DGCR
NCBI Description
                  Region, complete sequence [Homo sapiens]
Seq. No.
                  313252
                  xtj700377417.h1
Seq. ID
Method
                  BLASTN
                  g285966
NCBI GI
BLAST score
                  99
E value
                  9.0e-49
Match length
                  151
                  98
% identity
NCBI Description
                  Human mRNA for KIAA0110 gene, complete cds
                  >gi 1408437 gb G28622 G28622 human STS SHGC-35799
Seq. No.
                  313253
Seq. ID
                  xtj700377421.h1
Method
                  BLASTX
NCBI GI
                  q417523
BLAST score
                  203
```

E value 2.0e-21

Match length 54 96 % identity

SERINE/THREONINE PROTEIN PHOSPHATASE 4 (PP4) (PROTEIN NCBI Description

PHOSPHATASE X) (PP-X) >gi_346323_pir__S28173 phosphoprotein

phosphatase (EC 3.1.3.16) X - human



```
Seq. No.
                  313254
                  xtj700377435.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3894217
BLAST score
                  51
                  5.0e-20
E value
Match length
                  163
% identity
                  90
                  Homo sapiens mRNA for Asparaginyl tRNA Synthetase, complete
NCBI Description
Seq. No.
                  313255
                  xtj700377448.h1
Seq. ID
Method
                  BLASTX
                  g3024432
NCBI GI
BLAST score
                  231
                  9.0e-20
E value
Match length
                  47
% identity
                  98
                  PROTEASOME, ALPHA SUBUNIT (MULTICATALYTIC ENDOPEPTIDASE
NCBI Description
                  COMPLEX ALPHA SUBUNIT) >gi 1930070 (U92540) proteasome
                  alpha subunit [Oryza sativa]
Seq. No.
                  313256
Seq. ID
                  xtj700377456.h1
Method
                  BLASTX
                  g4503479
NCBI GI
BLAST score
                  218
                  3.0e-18
E value
Match length
                  44
                  93
% identity
                  eukaryotic translation elongation factor 1 delta (guanine
NCBI Description
                  nucleotide exchange protein)
                  >gi 461994 sp P29692 EF1D HUMAN ELONGATION FACTOR 1-DELTA
                   (EF-1-DELTA) >gi_1085404_pir__S34626 translation elongation
                   factor eEF-1 delta chain - human >gi_38522_emb_CAA79716_
                  (Z21507) human elongation factor-1-delta [Homo sapiens]
Seq. No.
                  313257
Seq. ID
                  xtj700377463.h1
Method
                  BLASTN
NCBI GI
```

g3882212 BLAST score 101

E value 6.0e-50Match length 159 % identity 93

NCBI Description Homo sapiens mRNA for KIAA0746 protein, partial cds

Seq. No. 313258

Seq. ID xtj700377473.h1

Method BLASTN NCBI GI q3289992 BLAST score 138 6.0e-72 E value Match length 188 % identity 92



NCBI Description Homo sapiens chromosome 19, cosmid R30783, complete sequence [Homo sapiens]

Seq. No. 313259

xtj700377490.h1 Seq. ID

Method BLASTN g2795898 NCBI GI BLAST score 141 8.0e-74 E value Match length 170 % identity 94

NCBI Description Homo sapiens clone 23912 mRNA sequence

Seq. No. 313260

xtj700377505.h1 Seq. ID

Method BLASTN g6249668 NCBI GI BLAST score 47 E value 8.0e-18 Match length 114 93 % identity

NCBI Description Homo sapiens chromosome 10 clone CIT-HSP-1338F24 map

10p11.2-10p12.1, complete sequence [Homo sapiens]

Seq. No. 313261

xtj700377506.h1 Seq. ID

Method BLASTN NCBI GI q598714 BLAST score 34 4.0e-10 E value Match length 42 95 % identity

NCBI Description Human HepG2 3' region cDNA, clone hmd3b09

Seq. No.

313262 xtj700377521.h1 Seq. ID

Method BLASTN NCBI GI g1550813 BLAST score 59 E value 6.0e-25 Match length 63 % identity 98

NCBI Description Z.mays mRNA for acidic ribosomal protein PO

Seq. No. 313263

Seq. ID xtj700377526.h1

Method BLASTN NCBI GI g2618577 BLAST score 36 E value 3.0e-11Match length 64 % identity 91

Homo sapiens mRNA for OTK27, complete cds NCBI Description

Seq. No. 313264

Seq. ID xtj700377530.h1

Method BLASTN

```
q1658192
NCBI GI
BLAST score
                  52
                  9.0e-21
E value
Match length
                  64
% identity
                  Sorghum bicolor obtusifoliol 14-alpha demethylase CYP51
NCBI Description
                  (CYP51) mRNA, complete cds
                  313265
Seq. No.
                  xtj700377547.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g514945
BLAST score
                  53
E value
                  2.0e-21
                  136
Match length
                  94
% identity
NCBI Description Zea mays sucrose synthase (Sus1) mRNA, complete cds
                  313266
Seq. No.
                  xtj700377548.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4504330
BLAST score
                  50
E value
                  1.0e-19
Match length
                  66
                  94
% identity
                  Homo sapiens hakata antigen (member of the Ficolin/Opsonin
NCBI Description
                  p35 Lectin Family) (HAKA1) mRNA
                  >gi 3413515 dbj D88587 D88587 Homo sapiens mRNA for Hakata
                  antigen, complete cds
                   313267
Seq. No.
                  xtj700377561.hl
Seq. ID
Method
                  BLASTN
NCBI GI
                  g34235
BLAST score
                   52
E value
                  8.0e-21
Match length
                  128
% identity
                   95
NCBI Description Human mRNA for nuclear envelope protein lamin C precursor
                   313268
Seq. No.
                   xtj700377579.h1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g338048
                   37
BLAST score
                   7.0e-12
E value
Match length
                   128
% identity
                  Human pulmonary surfactant-associated protein SP-A (SFTP1)
NCBI Description
                   gene, complete cds
```

313269 Seq. No. xtj700377626.h1 Seq. ID

Method BLASTN g4240034 NCBI GI BLAST score 124

```
E value
                  1.0e-63
Match length
                  164
                  93
% identity
NCBI Description
                  Zea mays ZmGR1b mRNA, complete cds
                  313270
Seq. No.
                  xtj700377635.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1477785
BLAST score
                  180
                  2.0e-16
E value
Match length
                  43
                  84
% identity
NCBI Description
                  (U60093) suppressor of hairless protein 1 [Xenopus laevis]
Seq. No.
                  313271
                  xtj700377668.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q3283881
BLAST score
                  138
                  5.0e-72
E value
Match length
                  163
                  94
% identity
                  Homo sapiens clone 24772 BDP-1 protein mRNA, partial cds
NCBI Description
Seq. No.
                  313272
                  xtj700377683.h1
Seq. ID
Method
                  BLASTN
                  g4755126
NCBI GI
BLAST score
                  73
                  3.0e-33
E value
Match length
                  154
% identity
                  97
                  Homo sapiens ADP-ribosylation factor-like 1 (ARL1) mRNA
NCBI Description
                  >gi 607027 gb L28997 HUMARL1A Homo sapiens ARL1 mRNA,
                  complete cds
Seq. No.
                  313273
```

Seq. ID xtj700377707.h1 Method BLASTX

Method BLASTX
NCBI GI g2497486
BLAST score 196
E value 1.0e-17
Match length 80
% identity 56

NCBI Description URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP KINASE) >gi_2121275 (AF000147) UMP/CMP kinase [Arabidopsis

thaliana]

Seq. No.

Seq. ID xtj700377721.h1

313274

Method BLASTN
NCBI GI g4502678
BLAST score 112
E value 2.0e-56
Match length 175
% identity 92

% identity

NCBI Description

97



```
NCBI Description Homo sapiens CD63 antigen (melanoma 1 antigen) (CD63) mRNA
                  313275
Seq. No.
                  xtj700377732.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3831470
BLAST score
                  170
E value
                  1.0e-12
Match length
                  83
                  40
% identity
                  (AC005700) unknown protein, 3' partial [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  313276
                  xtj700377741.h1
Seq. ID
                  BLASTN
Method
                  g602605
NCBI GI
BLAST score
                  76
E value
                  6.0e-35
                  160
Match length
                  87
% identity
NCBI Description Zea mays tandem genes for alphal-tubulin and alpha2-tubulin
                  313277
Seq. No.
Seq. ID
                  xtj700377764.h1
Method
                  BLASTX
                  g632220
NCBI GI
BLAST score
                  161
                  1.0e-11
E value
Match length
                  60
                  57
% identity
NCBI Description
                  ribosomal protein L2 - evening primrose mitochondrion
                  >gi_516394_emb_CAA56451_ (X80170) 70s mitochondrial
                  ribosomal protein L2 [Oenothera berteriana]
Seq. No.
                  313278
                  xtj700377812.h1
Seq. ID
Method
                  BLASTX
                  g3063706
NCBI GI
BLAST score
                  258
E value
                  4.0e-26
Match length
                  99
% identity
NCBI Description
                  (AL022537) putative protein [Arabidopsis thaliana]
                  313279
Seq. No.
                  xtj700377816.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q187507
BLAST score
                  224
E value
                   1.0e-123
Match length
                   301
```

antigen (Mea) mRNA, complete cds

Human male-enhanced antigen mRNA (Mea), complete cds.

>gi 187509 gb L10400 HUMMEAA Homo sapiens male-enhanced



```
Seq. No.
                  313280
                  xtj700377839.hl
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4337095
BLAST score
                  238
E value
                  1.0e-131
                  293
Match length
% identity
                  96
                  Homo sapiéns Mut S homolog 5 gene, partial cds; and NCC27,
NCBI Description
                  NG30, NG31, NG24, NG25, NG32, NG26, NG33, casein kinase II
                  beta subunit, BAT4, NG34, Apo M, BAT3, BAT2, AIF-1, 1C7,
                  LST-1, lymphotoxin beta, tumor necrosis facto
Seq. No.
                  313281
                  xtj700377843.h1
Seq. ID
Method
                  BLASTX
                  g3881836
NCBI GI
                  393
BLAST score
                  2.0e-38
E value
Match length
                  97
                  75
% identity
                  (Z78019) Similarity to Yeast LPG22P protein (TR:G1151240);
NCBI Description
                  cDNA EST EMBL: T00686 comes from this gene; cDNA EST
                  EMBL:C12415 comes from this gene; cDNA EST EMBL:C12728
                  comes from this gene; cDNA EST EMBL:C10626 comes from this
                  313282
Seq. No.
                  xtj700377856.h1
Seq. ID
Method
                  BLASTX
                  g2583079
NCBI GI
                  166
BLAST score
                   7.0e-12
E value
Match length
                  35
% identity
                   91
                  (AF026816) putative oncogene protein [Homo sapiens]
NCBI Description
Seq. No.
                  313283
                  xtj700377868.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g577294
BLAST score
                   244
                   1.0e-135
E value
Match length
                   296
                   96
% identity
NCBI Description Human mRNA for KIAA0088 gene, partial cds
                   313284
Seq. No.
Seq. ID
                   xtj700377883.h1
Method
                   BLASTX
```

NCBI GI q4506273 BLAST score 192 E value 2.0e-23 68 Match length 93 % identity

NCBI Description PTK7 protein tyrosine kinase 7 >gi_2136061_pir_ protein-tyrosine kinase-related receptor PTK7 - human



>qi 1322232 (U40271) transmembrane receptor precursor [Homo sapiens] >qi 1587324 prf 2206402A receptor Tyr kinase [Homo sapiens]

Seq. No. 313285

Seq. ID xtj700377885.h1

BLASTX Method NCBI GI g135398 293 BLAST score 9.0e-27 E value 56 Match length

95 % identity

TUBULIN ALPHA-1 CHAIN >gi 82731 pir__S15773 tubulin alpha-1 NCBI Description

chain - maize >gi 22147_emb_CAA33734_ (X15704)

alphal-tubulin [Zea mays]

Seq. No. 313286

Seq. ID xtj700377923.h1

Method BLASTN NCBI GI q3687210 BLAST score 133 E value 4.0e-69 Match length 144 99 % identity

Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), NCBI Description

complete sequence [Homo sapiens]

313287 Seq. No.

xtj700377926.h1 Seq. ID

Method BLASTX g2345154 NCBI GI 337 BLAST score E value 7.0e-32 Match length 66 % identity

(AF015522) ribsomal protein S4 [Zea mays] NCBI Description

Seq. No. 313288

xtj700377955.h1 Seq. ID

Method BLASTX NCBI GI g3163946 BLAST score 281 E value 2.0e-25 Match length 54 % identity

(AJ005599) alpha-tubulin 1 [Eleusine indica] NCBI Description

Seq. No. 313289

xtj700377975.h1 Seq. ID

Method BLASTN NCBI GI g3811348 BLAST score 240 E value 1.0e-132 Match length 275 97 % identity

Homo sapiens cytosolic phospholipase A2 beta (cPLA2 beta) NCBI Description

precursor RNA, complete sequence

Seq. No.

Seq. ID

313295

xyt700342344.h1



```
313290
Seq. No.
                  xtj700377983.h1
Seq. ID
Method
                  BLASTN
                  g190089
NCBI GI
                  83
BLAST score
                   3.0e-39
E value
                   142
Match length
                   99
% identity
                  Human pulmonary surfactant protein C (SP-C) and pulmonary
NCBI Description
                   surfactant protein C1 (SP-C1) genes, complete cds
                   313291
Seq. No.
                   xtj700378029.hl
Seq. ID
Method
                   BLASTX
                   g2492504
NCBI GI
                   317
BLAST score
                   2.0e-36
E value
                   83
Match length
% identity
                   86
                   CELL DIVISION CYCLE PROTEIN 48 HOMOLOG
NCBI Description
                   >gi_1669660_emb_CAA70565_ (Y09396) protein of AAA family
                   [Capsicum annuum]
                   313292
Seq. No.
Seq. ID
                   xtj700378120.h1
Method
                   BLASTX
                   g4006924
NCBI GI
BLAST score
                   186
                   2.0e-14
E value
                   36
Match length
                   89
% identity
                   (Z99708) beta-galactosidase like protein [Arabidopsis
NCBI Description
                   thaliana]
                   313293
Seq. No.
                   xtj700378121.h1
Seq. ID
                   BLASTX
Method
                   g1743277
NCBI GI
BLAST score
                   166
                   4.0e-12
E value
                   29
Match length
                   100
% identity
                   (Y09741) beta-tubulin 1 [Hordeum vulgare]
NCBI Description
                   313294
Seq. No.
                   xtj700378373.h1
Seq. ID
Method
                   BLASTX
                   g2921304
NCBI GI
BLAST score
                   432
E value
                   5.0e-43
Match length
                   92
                   97
% identity
                   (AF033496) herbicide safener binding protein [Zea mays]
NCBI Description
```



```
BLASTX
Method
                  q1770190
NCBI GI
                  220
BLAST score
                  3.0e-18
E value
                  69
Match length
                  58
% identity
                  (Y10162) cyclin-D like protein [Chenopodium rubrum]
NCBI Description
                  313296
Seq. No.
Seq. ID
                  xyt700342345.hl
Method
                  BLASTN
NCBI GI
                  q4416300
BLAST score
                  63
                  5.0e-27
E value
                  209
Match length
                   44
% identity
                  Zea mays chromosome 4 22 kDa zein-associated intercluster
NCBI Description
                  region, complete sequence
                   313297
Seq. No.
                  xyt700342379.hl
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2500399
BLAST score
                   408
                   3.0e-40
E value
                   91
Match length
% identity
                   40S RIBOSOMAL PROTEIN S3 >gi 1836060 bbs 179561 (S83098)
NCBI Description
                   ribosomal protein S3 [Ambystoma mexicanum=Mexican axolotls,
                   embryos, Peptide, 253 aa] [Ambystoma mexicanum]
                   313298
Seq. No.
                   xyt700342384.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3717978
BLAST score
                   294
                   7.0e-27
E value
Match length
                   70
% identity
                   (Y12431) 5S ribosomal protein [Mus musculus]
NCBI Description
                   313299
Seq. No.
                   xyt700342396.hl
Seq. ID
Method
                   BLASTN
NCBI GI
                   g4099507
BLAST score
                   70
E value
                   1.0e-31
Match length
                   82
% identity
                   96
                   Zea mays proliferating cell nuclear antigen (ZmPCNA2) mRNA,
NCBI Description
                   complete cds
                   313300
Seq. No.
                   xyt700342427.h1
Seq. ID
Method
                   BLASTX
```

g1076678

274

NCBI GI

BLAST score



```
E value
                   2.0e-24
Match length
                  55
% identity
                   100
                  ubiquitin / ribosomal protein S27a - potato (fragment)
NCBI Description
                  313301
Seq. No.
                  xyt700342445.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                   g4101627
BLAST score
                  51
E value
                  7.0e-20
Match length
                  83
                   90
% identity
NCBI Description
                  Canis familiaris desmoglein-1 (DSG-1) gene, complete cds
                   313302
Seq. No.
                  xyt700342458.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q4432816
BLAST score
                   151
E value
                   5.0e-10
                   79
Match length
                   46
% identity
NCBI Description
                   (AC006593) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   313303
                  xyt700342466.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q4505193
BLAST score
                   343
                   8.0e-33
E value
Match length
                   76
                   79
% identity
                  membrane fatty acid (lipid) desaturase >gi 2232174
NCBI Description
                   (AF002668) MLD [Homo sapiens]
Seq. No.
                   313304
Seq. ID
                   xyt700342488.h1
Method
                  BLASTX
NCBI GI
                   g2511533
BLAST score
                   147
E value
                   1.0e-09
Match length
                   91
                   44
% identity
                  (AF008121) alpha-tubulin 2 [Eleusine indica]
NCBI Description
Seq. No.
                   313305
                  xyt700342495.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                   g4507780
BLAST score
                   43
                   4.0e-15
E value
Match length
                   59
                   93
% identity
                  Homo sapiens ubiquitin-conjugating enzyme E2G 2 (homologous
NCBI Description
```

to yeast UBC7) (UBE2G2) mRNA, and translated products >gi_3004908_gb_AF032456_AF032456 Homo sapiens ubiquitin

Seq. No.

Seq. ID

313311

xyt700342681.h1



conjugating enzyme G2 (UBE2G2) mRNA, complete cds

```
313306
Seq. No.
                    xyt700342511.h1
Seq. ID
Method
                    BLASTX
NCBI GI
                    g4063743
                    220
BLAST score
                    4.0e-18
E value
                    92
Match length
                    49
% identity
                    (AC005851) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                    313307
Seq. No.
                    xyt700342531.h1
Seq. ID
Method
                    BLASTX
                    g1335862
NCBI GI
BLAST score
                    360
                    2.0e-40
E value
                    92
Match length
                    91
% identity
                    (U42608) clathrin heavy chain [Glycine max]
NCBI Description
                    313308
Seq. No.
                    xyt700342591.h1
Seq. ID
                    BLASTN
Method
NCBI GI
                    g56322
BLAST score
                    75
                    3.0e - 34
E value
Match length
                    79
                    99
% identity
                    Rat gene for growth hormone (presomatotropin)
NCBI Description
                    313309
Seq. No.
                    xyt700342610.h1
Seq. ID
Method
                    BLASTX
NCBI GI
                    g1181331
BLAST score
                    236
                    8.0e-21
E value
Match length
                    62
% identity
                    87
                    (X77569) calnexin [Zea mays]
NCBI Description
                    313310
Seq. No.
                    xyt700342651.h1
Seq. ID
Method
                    BLASTX
                    g3913437
NCBI GI
BLAST score
                    240
                    9.0e-21
E value
                    50
Match length
% identity
                    88
                    PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA
NCBI Description
                    \label{eq:helicase} $$ HELICASE > gi_1402875 = mb_CAA66825 (X98130) RNA helicase $$ [Arabidopsis thaliana] > gi_1495271 = mb_CAA66613 (X97970) $$
                    RNA helicase [Arabidopsis thaliana]
```

NCBI GI

BLAST score

```
BLASTN
Method
                  g4140643
NCBI GI
BLAST score
                  51
                  7.0e-20
E value
Match length
                  95
                  88
% identity
                  Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster,
NCBI Description
                  complete sequence
                                                  - 3 _
                  313312
Seq. No.
                  xyt700342735.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4104975
BLAST score
                  176
                  2.0e-94
E value
                  227
Match length
                  93
% identity
                  Homo sapiens ubiquitin-fusion degradation protein 2 (UFD2)
NCBI Description
                  mRNA, complete cds
                  313313
Seq. No.
                  xyt700342751.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g322752
BLAST score
                  140
E value
                   5.0e-09
Match length
                  33
                  73
% identity
                  auxin-independent growth promoter - Nicotiana tabacum
NCBI Description
                  >gi 559921 emb CAA56570 (X80301) axi 1 [Nicotiana tabacum]
                   313314
Seq. No.
                  xyt700342769.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3319741
BLAST score
                   196
E value
                   2.0e-15
Match length
                   96
                   50
% identity
NCBI Description
                   (AL031035) hypothetical protein SC6A9.22c [Streptomyces
                   coelicolor]
                   313315
Seq. No.
                   xyt700342802.h1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g1304103
BLAST score
                   167
E value
                   3.0e-89
Match length
                   179
                   98
% identity
NCBI Description Human mRNA for basigin, complete cds
Seq. No.
                   313316
Seq. ID
                   xyt700342820.h1
Method
                   BLASTX
```

44783

g4539660

```
E value
                  1.0e-09
Match length
                  60
% identity
                  47
                  (AF061282) polyprotein [Sorghum bicolor]
NCBI Description
                  313317
Seq. No.
                  xyt700342874.h1
Seq. ID
Method
                  BLASTX
                  g3702342
NCBI GI
BLAST score
                  211
                  4.0e-17
E value
                  85
Match length
                  53
% identity
                  (AC005397) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  313318
                  xyt700342882.h1
Seq. ID
Method
                  BLASTX
                  g2130073
NCBI GI
BLAST score
                  138
                  8.0e-09
E value
Match length
                  27
                  96
% identity
                  fructose-bisphosphate aldolase (EC 4.1.2.13) isoenzyme C-1,
NCBI Description
                  cytosolic - rice >gi_786178 dbj BAA08845 (D50307) aldolase
                  C-1 [Oryza sativa] >gi 790970_dbj_BAA08830_ (D50301)
                  aldolase C-1 [Oryza sativa]
Seq. No.
                  313319
                  xyt700342883.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3337361
BLAST score
                  209
                  8.0e-20
E value
Match length
                  81
                  59
% identity
NCBI Description (AC004481) ankyrin-like protein [Arabidopsis thaliana]
                  313320
Seq. No.
Seq. ID
                  xyt700342886.h1
Method
                  BLASTX
NCBI GI
                  q1237102
BLAST score
                  285
E value
                  8.0e-26
Match length
                  79
% identity
                  72
NCBI Description
                  (L40358) calmodulin-binding protein [Arabidopsis thaliana]
                  >gi_1589171_prf__2210340A calmodulin-binding protein
                   [Arabidopsis thaliana]
```

Seq. No. 313321

Seq. ID xyt700342987.h1 Method BLASTN

NCBI GI g4502944
BLAST score 185
E value 1.0e-100
Match length 268

% identity 92

% identity 92
NCBI Description Homo sapiens collagen, type I, alpha 1 (COL1A1) mRNA
>gi_1418927_emb_Z74615_HSPPA1ICO H.sapiens mRNA for

prepro-alpha1(I) collagen

Seq. No. 313322

Seq. ID xyt700343055.h1

Method BLASTN
NCBI GI g2239259
BLAST score 139
E value 1.0e-72
Match length 147
% identity 99

NCBI Description Zea mays mRNA for cinnamoyl CoA reductase

Seq. No. 313323

Seq. ID xyt700343115.h1

Method BLASTX
NCBI GI g1172754
BLAST score 226
E value 5.0e-19
Match length 52
% identity 83

NCBI Description PHOSPHORIBOSYLFORMYLGLYCINAMIDINE CYCLO-LIGASE PRECURSOR

(AIRS) (PHOSPHORIBOSYL-AMINOIMIDAZOLE SYNTHETASE) (AIR

SYNTHASE) >gi_541885_pir__JQ2256

phosphoribosylformylglycinamidine cyclo-ligase (EC 6.3.3.1)

precursor - Arabidopsis thaliana >gi 289188 (L12457)

5'-phosphoribosyl-5-aminoimidazole synthetase [Arabidopsis

thaliana]

Seq. No. 313324

Seq. ID xyt700343138.h1

Method BLASTX
NCBI GI g1064931
BLAST score 316
E value 1.0e-29
Match length 73
% identity 82

NCBI Description (X92965) cyclin A-like protein [Nicotiana tabacum]

Seq. No. 313325

Seq. ID xyt700343156.h1

Method BLASTX
NCBI GI g4505135
BLAST score 259
E value 1.0e-22
Match length 86
% identity 57

NCBI Description midkine (neurite growth-promoting factor 2)

>gi_127116_sp_P21741_MK_HUMAN MIDKINE PRECURSOR (NEURITE
OUTGROWTH-PROMOTING PROTEIN) (MK) (MIDGESTATION AND KIDNEY
PROTEIN) (AMPHIREGULIN-ASSOCIATED PROTEIN) (ARAP) (NEURITE
OUTGROWTH-PROMOTING FACTOR 2) >gi_88156_pir__JH0385 midkine
precursor - human >gi_35087_emb_CAA38908_ (X55110) neurite
outgrowth-promoting protein [Homo sapiens] >gi_182651

(M69148) midkine [Homo sapiens] >gi_188571 (M94250)

retinoic acid inducible factor [Homo sapiens] >gi_219929_dbj_BAA01457_ (D10604) midkine [Homo sapiens]

313326 Seq. No. Seq. ID xyt700343159.h1

Method BLASTX NCBI GI g2781345 BLAST score 247 E value 2.0e-21 Match length 59

% identity NCBI Description (AC003113) F2401.2 [Arabidopsis thaliana]

Seq. No. 313327

Seq. ID xyt700343160.h1

80

Method BLASTX NCBI GI g1143864 BLAST score 329 E value 3.0e-31 Match length 66 % identity 91

NCBI Description (U28047) beta glucosidase [Oryza sativa]

Seq. No. 313328

xyt700343163.h1 Seq. ID

Method BLASTX NCBI GI q2673911 BLAST score 219 E value 3.0e-18 Match length 56 % identity 70

NCBI Description (AC002561) putative squamosa-promoter binding protein

[Arabidopsis thaliana]

Seq. No. 313329

Seq. ID xyt700343175.h1

Method BLASTX NCBI GI g2244996 BLAST score 182 E value 8.0e-14 Match length 81 % identity 43

(Z97341) similarity to a membrane-associated salt-inducible NCBI Description

protein [Arabidopsis thaliana]

Seq. No. 313330

Seq. ID xyt700343178.h1

Method BLASTX NCBI GI q4455302 BLAST score 314 E value 2.0e-29 Match length 74 77 % identity

NCBI Description (AL035528) putative protein [Arabidopsis thaliana]

Seq. No. 313331

xyt700343205.h1 Seq. ID



Method BLASTN
NCBI GI g2088550
BLAST score 157
E value 4.0e-83
Match length 259
% identity 91

NCBI Description Human hereditary haemochromatosis region, histone 2A-like

protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene,

complete cds

Seq. No. 313332

Seq. ID xyt700343207.h1

Method BLASTX
NCBI GI g3522937
BLAST score 169
E value 3.0e-12
Match length 44
% identity 64

NCBI Description (AC004411) unknown protein [Arabidopsis thaliana]

Seq. No. 313333

Seq. ID xyt700343209.h1

Method BLASTX
NCBI GI g3914083
BLAST score 205
E value 2.0e-16
Match length 86
% identity 51

NCBI Description MUTS2 PROTEIN >gi_1652751_dbj_BAA17670_ (D90908) DNA

mismatch repair protein MutS [Synechocystis sp.]

Seq. No. 313334

Seq. ID xyt700343212.h1

Method BLASTN
NCBI GI g1633547
BLAST score 246
E value 1.0e-136
Match length 269
% identity 98

NCBI Description Human chromosome 12p13 sequence, complete sequence [Homo

sapiens]

Seq. No. 313335

Seq. ID xyt700343214.h1

Method BLASTX
NCBI GI g4467124
BLAST score 152
E value 3.0e-10
Match length 75
% identity 36

NCBI Description (AL035538) hypothetical protein [Arabidopsis thaliana]

Seq. No. 313336

Seq. ID xyt700343295.h1

Method BLASTX NCBI GI g3885336



```
BLAST score
E value
                  3.0e-18
Match length
                  96
                  27
% identity
NCBI Description
                  (AC005623) receptor-like protein kinase [Arabidopsis
                  thaliana]
                  313337
Seq. No.
                  xyt700343308.h1
Seq. ID
Method
                  BLASTX
                  g498643
NCBI GI
BLAST score
                  211
E value
                  4.0e-17
Match length
                  46
% identity
                  100
                  (U10270) G-box binding factor 1 [Zea mays]
NCBI Description
                  313338
Seq. No.
Seq. ID
                  xyt700343312.h1
Method
                  BLASTX
NCBI GI
                  g1572719
BLAST score
                  303
E value
                  6.0e-28
Match length
                  74
% identity
                  74
NCBI Description
                  (U70135) PAST-1 [Drosophila melanogaster]
                  313339
Seq. No.
                  xyt700343322.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g22171
BLAST score
                  51
                  7.0e-20
E value
Match length
                  59
                  97
% identity
NCBI Description Maize nuclear ARS3 DNA autonomously replicating in yeast
Seq. No.
                  313340
                  xyt700343350.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  a577818
BLAST score
                  280
E value
                  1.0e-156
Match length
                  288
% identity
                  100
NCBI Description Z.mays gene for H2B histone (gH2B4)
                  313341
Seq. No.
Seq. ID
                  xyt700343356.hl
Method
                  BLASTX
NCBI GI
                  q1184774
```

Method BLASTX
NCBI GI g1184774
BLAST score 434
E value 3.0e-43
Match length 98
% identity 87

NCBI Description (U45856) cytosolic glyceroldehyde-3-phosphate dehydrogenase

GAPC3 [Zea mays]

Method

BLASTX

```
Seq. No.
                  313342
Seq. ID
                  xyt700343407.h1
Method
                  BLASTX
NCBI GI
                  q4544445
BLAST score
                  372
E value
                  5.0e-36
Match length
                  84
                  87
% identity
                   (AC006592) putative pyrophosphate--fructose 6-phosphate
NCBI Description
                  1-phosphotransferase [Arabidopsis thaliana]
Seq. No.
                  313343
Seq. ID
                  xyt700343429.h1
Method
                  BLASTX
                  g3779024
NCBI GI
                  200
BLAST score
                  8.0e-18
E value
Match length
                  94
% identity
                  51
NCBI Description
                  (AC005171) unknown protein [Arabidopsis thaliana]
Seq. No.
                  313344
Seq. ID
                  xyt700343446.h1
Method
                  BLASTX
                  g2352427
NCBI GI
BLAST score
                  167
E value
                  5.0e-12
Match length
                  87
% identity
                  43
                   (AF004161) peroxisomal Ca-dependent solute carrier
NCBI Description
                   [Oryctolagus cuniculus]
Seq. No.
                  313345
                  xyt700343495.hl
Seq. ID
Method
                  BLASTN
NCBI GI
                  q998429
BLAST score
                  142
E value
                   2.0e-74
Match length
                  196
                   99
% identity
                  GRF1=general regulatory factor [Zea mays, XL80, Genomic,
NCBI Description
                  5348 nt]
Seq. No.
                  313346
Seq. ID
                  xyt700343511.h1
Method
                  BLASTX
NCBI GI
                  q4508069
BLAST score
                  288
E value
                   4.0e-26
Match length
                  92
% identity
                  54
NCBI Description
                  (AC005882) 12246 [Arabidopsis thaliana]
Seq. No.
                  313347
Seq. ID
                  xyt700343526.h1
```

```
g1514643
NCBI GI
BLAST score
                  240
                  1.0e-20
E value
Match length
                  79
% identity
                  54
NCBI Description (Z70524) PDR5-like ABC transporter [Spirodela polyrrhiza]
Seq. No.
                  313348
Seq. ID
                  xyt700343535.h1
Method
                  BLASTX
NCBI GI
                  g2642156
BLAST score
                  191
                  9.0e-15
E value
Match length
                  85
% identity
                  45
                  (AC003000) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  313349
Seq. No.
Seq. ID
                  xyt700343548.hl
Method
                  BLASTN
NCBI GI
                  g2138090
BLAST score
                  39
E value
                  1.0e-12
Match length
                  39
% identity
                  100
NCBI Description
                  Gymnosiphon suaveolens 18S ribosomal RNA gene, partial
                  sequence
Seq. No.
                  313350
                  xyt700343550.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3915826
BLAST score
                  193
E value
                  2.0e-15
Match length
                  52
% identity
                  88
NCBI Description 60S RIBOSOMAL PROTEIN L5
Seq. No.
                  313351
Seq. ID
                  xyt700343594.hl
Method
                  BLASTN
NCBI GI
                  q1216497
BLAST score
                  105
E value
                  1.0e-52
Match length
                  109
```

% identity 99

NCBI Description Rattus norvegicus heat stable antigen CD24 mRNA, complete

Seq. No. 313352

Seq. ID xyt700343602.h1

Method BLASTN g4140643 NCBI GI BLAST score 129 E value 1.0e-66 Match length 143 % identity 49



Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster, NCBI Description complete sequence

313353 Seq. No.

xyt700343621.h1 Seq. ID

Method BLASTX NCBI GI q4567304 BLAST score 392 E value 3.0e-38 Match length 98 76 % identity

(AC005956) unknown protein [Arabidopsis thaliana] NCBI Description

Seq. No. 313354

Seq. ID xyt700343641.h1

Method BLASTN NCBI GI q3511235 BLAST score 76 E value 9.0e-35 Match length 148 % identity 88

NCBI Description Zea mays starch branching enzyme IIb (ae) gene, complete

cds

Seq. No. 313355

xyt700343672.h1 Seq. ID

Method BLASTN NCBI GI g2832242 BLAST score 88 E value 6.0e-42 108 Match length 95 % identity

NCBI Description Zea mays 22-kDa alpha zein gene cluster, complete sequence

Seq. No.

313356 Seq. ID xyt700343693.h1

Method BLASTX NCBI GI q4220527 BLAST score 166 E value 8.0e-12 Match length 58

57 % identity

NCBI Description (AL035356) putative protein [Arabidopsis thaliana]

Seq. No.

313357

Seq. ID xyt700343702.h1

Method BLASTX NCBI GI g1170606 BLAST score 307 E value 2.0e-28 Match length 97 % identity 61

ADENYLATE KINASE, CHLOROPLAST (ATP-AMP TRANSPHOSPHORYLASE) NCBI Description

>gi 629863 pir S45634 adenylate kinase (EC 2.7.4.3),

chloroplast - maize >gi_3114421_pdb_1ZAK_A Chain A, Adenylate Kinase From Maize In Complex With The Inhibitor

P1, P5-Bis (Adenosine-5'-) pentaphosphate (Ap5a)



>gi_3114422 pdb_1ZAK_B Chain B, Adenylate Kinase From Maize In Complex With The Inhibitor

P1, P5-Bis (Adenosine-5'-) pentaphosphate (Ap5a)

Seq. No. 313358

Seq. ID xyt700343717.h1

Method BLASTX
NCBI GI g2668744
BLAST score 453
E value 2.0e-45
Match length 89
% identity 91

NCBI Description (AF034946) ubiquitin conjugating enzyme [Zea mays]

Seq. No. 313359

Seq. ID xyt700343740.h1

Method BLASTX
NCBI GI g3935150
BLAST score 397
E value 6.0e-39
Match length 93
% identity 74

NCBI Description (AC005106) T25N20.14 [Arabidopsis thaliana]

Seq. No. 313360

Seq. ID xyt700343746.h1

Method BLASTX
NCBI GI g3882311
BLAST score 149
E value 7.0e-10
Match length 93
% identity 38

NCBI Description (AB018338) KIAA0795 protein [Homo sapiens]

Seq. No. 313361

Seq. ID xyt700343805.h1

Method BLASTX
NCBI GI g3859560
BLAST score 162
E value 2.0e-11
Match length 75
% identity 43

NCBI Description (AF098668) acyl-protein thioesterase [Homo sapiens]

>gi 4581413 emb CAB40158.1 (AL031295) dJ886K2.4

(acyl-protein thioesterase) [Homo sapiens]

Seq. No. 313362

Seq. ID xyt700343853.h1

Method BLASTN
NCBI GI g3090700
BLAST score 155
E value 4.0e-82
Match length 159
% identity 99

NCBI Description Homo sapiens chromosome 5, PAC clone 170m10 (LBNL H89),

complete sequence [Homo sapiens]

```
313363
Seq. No.
Seq. ID
                  xyt700343858.hl
Method
                  BLASTX
NCBI GI
                  g479357
BLAST score
                  267
E value
                  1.0e-23
Match length
                  95
% identity
                  51
NCBI Description hypothetical protein 612 - maize transposon MuA2
                  >gi_22375_emb_CAA44165_ (X62251) ORF [Zea mays]
                  313364
Seq. No.
Seq. ID
                  xyt700343992.h1
Method
                  BLASTX
NCBI GI
                  g729671
BLAST score
                  176
                  2.0e-13
E value
Match length
                  41
% identity
                  83
NCBI Description HISTONE H2A >gi 473603 (U08225) histone H2A [Zea mays]
                  313365
Seq. No.
                  xyt700344009.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4581164
BLAST score
                  246
                  3.0e-21
E value
Match length
                  82
% identity
                  60
NCBI Description (AC006220) putative polyprotein [Arabidopsis thaliana]
                  313366
Seq. No.
Seq. ID
                  xyt700344018.h1
Method
                  BLASTN
NCBI GI
                  g4506628
BLAST score
                  150
E value
                  4.0e-79
Match length
                  162
% identity
                  98
NCBI Description
                  Homo sapiens ribosomal protein L29 (RPL29) mRNA
                  >gi 984280 gb U10248 HSU10248 Human ribosomal protein L29
                   (humrpl29) mRNA, complete cds
Seq. No.
                  313367
Seq. ID
                  xyt700344029.h1
Method
                  BLASTX
```

NCBI GI g3914056 BLAST score 165

E value 5.0e-12 Match length 56 % identity 55

NCBI Description DNA MISMATCH REPAIR PROTEIN MSH2 >gi_2522362 (AF002706)

MutS homolog 2 [Arabidopsis thaliana] >gi_2522364 (AF003005) MutS homolog 2 [Arabidopsis thaliana]

>gi_2547236 (AF026549) DNA mismatch repair protein MSH2

[Arabidopsis thaliana]

% identity

```
Seq. No.
                  313368
Seq. ID
                  xyt700344038.h1
Method
                  BLASTX
NCBI GI
                  g3885519
BLAST score
                  164
                  1.0e-11
E value
Match length
                  35
% identity
                  94
                  (AF084204) similar to ribosomal protein L32 [Medicago
NCBI Description
                  sativa]
Seq. No.
                  313369
Seq. ID
                  xyt700344041.h1
Method
                  BLASTX
                  g3128168
NCBI GI
BLAST score
                  302
E value
                  8.0e-28
Match length
                  93
% identity
                  54
NCBI Description
                   (AC004521) putative carboxyl-terminal peptidase
                   [Arabidopsis thaliana]
                  313370
Seq. No.
Seq. ID
                  xyt700344055.hl
Method
                  BLASTN
                  g1032183
NCBI GI
BLAST score
                  113
E value
                  5.0e-57
Match length
                  143
% identity
                  94
NCBI Description
                  H.sapiens CpG island DNA genomic Msel fragment, clone
                  198d1, forward read cpg198d1.ft1a
Seq. No.
                  313371
                  xyt700344065.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4503117
BLAST score
                  240
                  8.0e-21
E value
Match length
                  50
% identity
                   94
                  cystatin B (stefin B) >gi 1706278 sp P04080 CYTB HUMAN
NCBI Description
                  CYSTATIN B (LIVER THIOL PROTEINASE INHIBITOR) (CPI-B)
                   (STEFIN B) >gi 291927 (L03558) cystatin B [Homo sapiens]
                  >gi_1235678 (U\overline{4}6692) cystatin B [Homo sapiens]
Seq. No.
                  313372
                  xyt700344066.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4505193
BLAST score
                  168
E value
                  2.0e-12
Match length
                  41
                  73
```

NCBI Description membrane fatty acid (lipid) desaturase >gi_2232174 (AF002668) MLD [Homo sapiens]



```
Seq. No.
                   313373
Seq. ID
                   xyt700344076.h1
Method
                   BLASTX
NCBI GI
                   q4454567
BLAST score
                   171
                   2.0e-12
E value
Match length
                   98
% identity
                   40
                  (AF128407) lipase homolog [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   313374
Seq. ID
                   xyt700344148.h1
Method
                   BLASTN
                   g2564044
NCBI GI
BLAST score
                   34
                   1.0e-09
E value
                   50
Match length
% identity
                   92
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                   K19P17, complete sequence [Arabidopsis thaliana]
Seq. No.
                   313375
Seq. ID
                   xyt700344162.h1
Method
                   BLASTX
NCBI GI
                   g2511533
                   198
BLAST score
E value
                   1.0e-15
Match length
                   47
% identity
                   79
                   (AF008121) alpha-tubulin 2 [Eleusine indica]
NCBI Description
                   313376
Seq. No.
                   xyt700344177.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2827715 ·
BLAST score
                   193
E value
                   5.0e-15
Match length
                   91
                   23
% identity
NCBI Description
                   (AL021684) receptor protein kinase - like protein
                   [Arabidopsis thaliana]
Seq. No.
                   313377
Seq. ID
                   xyt700344251.h1
Method
                   BLASTX
NCBI GI
                   q2252844
BLAST score
                   258
E value
                   1.0e-22
Match length
                   83
                   64
% identity
                   (AF013293) belongs to the cytochrome p450 family
NCBI Description
```

Seq. No. 313378

Seq. ID xyt700344259.h1

Method BLASTX NCBI GI g3193291

[Arabidopsis thaliana]

```
BLAST score
E value
                  2.0e-33
Match length
                  91
                   69
% identity
                   (AF069298) Similar to DNA mismatch repair protein; T14P8.6
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  313379
Seq. ID
                  xyt700344323.h1
Method
                  BLASTN
NCBI GI
                  g22324
BLAST score
                  96
E value
                  1.0e-46
Match length
                  194
                  88
% identity
NCBI Description Z.mays mRNA for H2B histone (clone cH2B221)
Seq. No.
                  313380
Seq. ID
                  xyt700344350.h1
Method
                  BLASTN
NCBI GI
                  g507770
BLAST score
                  40
                  2.0e-13
E value
Match length
                  48
                  96
% identity
NCBI Description
                  Zea mays D3L H(+)-transporting ATPase (Mha1) gene, complete
                  cds
Seq. No.
                  313381
Seq. ID
                  xyt700344436.h1
Method
                  BLASTX
NCBI GI
                  g4539660
BLAST score
                  189
E value
                  3.0e-21
Match length
                  72
% identity
                  69
NCBI Description
                  (AF061282) polyprotein [Sorghum bicolor]
Seq. No.
                  313382
Seq. ID
                  xyt700344504.h1
Method
                  BLASTX
NCBI GI
                  q2668744
BLAST score
                  345
E value
                  8.0e-33
Match length
                  64
                  97
% identity
NCBI Description (AF034946) ubiquitin conjugating enzyme [Zea mays]
```

Seq. No.

313383

Seq. ID

xyt700344542.h1

Method BLASTX
NCBI GI g1550660
BLAST score 184
E value 5.0e-14
Match length 88
% identity 47

NCBI Description (Z80226) ptrBa [Mycobacterium tuberculosis]

```
Seq. No.
                   313384
Seq. ID
                   xyt700344611.h1
Method
                   BLASTX
NCBI GI
                   q4159682
                   239
BLAST score
E value
                   3.0e-28
Match length
                   95
% identity
                   69
NCBI Description
                   (AB016930) Phosphatidylglycerophosphate synthase
                   [Cricetulus griseus]
Seq. No.
                   313385
Seq. ID
                   xyt700344615.h1
Method
                   BLASTN
                   g7109504
NCBI GI
BLAST score
                   56
E value
                   3.0e-23
Match length
                   116
                   88
% identity
NCBI Description
                  , complete sequence [Homo sapiens]
Seq. No.
                   313386
Seq. ID
                  xyt700344619.h1
                   BLASTX
Method
                   g418134
NCBI GI
BLAST score
                   140
E value
                   9.0e-09
Match length
                   49
% identity
                   57
                  ANTHRANILATE SYNTHASE COMPONENT I-2 PRECURSOR
NCBI Description
                   >gi 282854 pir S27752 anthranilate synthase (EC 4.1.3.27)
                   alpha chain - Arabidopsis thaliana >gi 166606 (M92354)
                   anthranilate synthase alpha subunit [Arabidopsis thaliana]
                   >gi_3582331 (AC005496) anthranilate synthase [Arabidopsis
                   thaliana]
Seq. No.
                   313387
Seq. ID
                  xyt700344662.h1
Method
                  BLASTX
NCBI GI
                  g2129709
BLAST score
                 .152
E value
                   3.0e-10
Match length
                   93
% identity
                   39
NCBI Description
                  reverse transcriptase - Arabidopsis thaliana
                   retrotransposon Tall-1 >gi_976278 (L47193) reverse
                   transcriptase [Arabidopsis thaliana]
Seq. No. Seq. ID
                   313388
                  xyt700344683.h1
Method
                  BLASTX
NCBI GI
                  q2961383
BLAST score
                  194
E value
                  2.0e-15
Match length
                  41
% identity
                  85
```



```
(AL022141) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  313389
                  xyt700344745.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4056502
BLAST score
                  281
                  3.0e-25
E value
Match length
                  74
                  73
% identity
                  (AC005896) 40S ribosomal protein S5 [Arabidopsis thaliana]
NCBI Description
                  313390
Seq. No.
Seq. ID
                  xyt700344757.h1
Method
                  BLASTX
                  g306812
NCBI GI
BLAST score
                  301
                  1.0e-27
E value
Match length
                  91
% identity
                  74
                  (J03817) glutathione transferase M1 [Homo sapiens]
NCBI Description
                  313391
Seq. No.
                  xyt700344794.h1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g397395
BLAST score
                  86
                  9.0e-41
E value
Match length
                  246
                   98
% identity
                  Z.mays MNB1b mRNA for DNA-binding protein
NCBI Description
                  313392
Seq. No.
                  xyt700344818.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                   g3638948
BLAST score
                   284
E value
                  1.0e-159
Match length
                   292
                  99
% identity
                  Homo sapiens PAC clone DJ1194E14 from 7p21, complete
NCBI Description
                   sequence [Homo sapiens]
                   313393
Seq. No.
                  xyt700344838.h1
Seq. ID
Method
                  BLASTN
                   g3694843
NCBI GI
BLAST score
                   224
E value
                   1.0e-123
Match length
                   270
% identity
                   96
                  Zea mays centromeric sequence similar to
NCBI Description
                   retrotransposon-like repeat CentA
```

313394

BLASTN

xyt700344851.h1

Seq. No. Seq. ID

Method

```
g21800
NCBI GI
BLAST score
                  102
                  3.0e-50
E value
Match length
                  225
% identity
                  78
                  T.aestivum L mRNA for histone H2B
NCBI Description
                  313395
Seq. No.
                  xyt700344856.hl
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4314400
BLAST score
                  239
                  2.0e-20
E value
Match length
                  92
% identity
                  49
                   (AC006232) putative selenium-binding protein [Arabidopsis
NCBI Description
                  thaliana]
                  313396
Seq. No.
                  xyt700344876.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4510348
BLAST score
                  231
                  2.0e-19
E value
Match length
                  75
% identity
                   60
                  (AC006921) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  313397
                   xyt700344893.h1
Seq. ID
                  BLASTX
Method
                   g1778374
NCBI GI
BLAST score
                   232
                   2.0e-19
E value
Match length
                  79
% identity
                   53
                  (U81287) glycine-rich RNA-binding protein PsGRBP [Pisum
NCBI Description
                   sativum]
                   313398
Seq. No.
                   xyt700344956.h1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2114242
                   158
BLAST score
                   1.0e-83
E value
Match length
                   206
% identity
                   94
NCBI Description Human (lambda) DNA for immunoglobulin light chain
```

 Seq. No.
 313399

 Seq. ID
 xyt700344960.h1

 Method
 BLASTX

Method BLASTX
NCBI GI g70774
BLAST score 336
E value 9.0e-32
Match length 68
% identity 100



NCBI Description histone H4 (TH091) - wheat >gi_170747 (M12277) histone H4 [Triticum aestivum]

Seq. No. 313400

Seq. ID xyt700344979.h1

Method BLASTX
NCBI GI g710549
BLAST score 141
E value 6.0e-09
Match length 62
% identity 52

NCBI Description (L40632) ankyrin 3 [Mus musculus]

Seq. No. 313401

Seq. ID xyt700345019.h1

Method BLASTX
NCBI GI g1172836
BLAST score 362
E value 8.0e-35
Match length 70
% identity 94

NCBI Description GTP-BINDING NUCLEAR PROTEIN RAN-B1 >qi 496272 (L16787)

small ras-related protein [Nicotiana tabacum]

Seq. No. 313402

Seq. ID xyt700345043.h1

Method BLASTX
NCBI GI g3236240
BLAST score 274
E value 1.0e-24
Match length 85
% identity 62

NCBI Description (AC004684) unknown protein [Arabidopsis thaliana]

Seq. No.

Seq. ID xyt700345044.h1

Method BLASTN
NCBI GI g902524
BLAST score 98
E value 3.0e-48
Match length 122
% identity 95

NCBI Description Zea mays clone MubG10 ubiquitin fusion protein gene,

complete cds

313403

Seq. No. 313404

Seq. ID xyt700345053.h1

Method BLASTX
NCBI GI g4263718
BLAST score 406
E value 7.0e-40
Match length 104
% identity 66

NCBI Description (AC006223) putative DNA topoisomerase III beta [Arabidopsis

thaliana]

Seq. No. 313405

```
Seq. ID
                  xyt700345064.h1
Method
                  BLASTN
                  g22469
NCBI GI
BLAST score
                  46
                  4.0e-17
E value
Match length
                  105
% identity
                  85
                  Maize mRNA for cytoplasmic ribosomal protein S11
NCBI Description
Seq. No.
                  313406
                  xyt700345117.h1
Seq. ID
Method
                  BLASTN
                  g2995603
NCBI GI
BLAST score
                  100
E value
                  2.0e-49
Match length
                  120
% identity
                  96
NCBI Description
                  Homo sapiens chromosome 17, clone hRPC.1110 E 20, complete
                  sequence [Homo sapiens]
Seq. No.
                  313407
Seq. ID
                  xyt700345188.h1
Method
                  BLASTX
NCBI GI
                  g1770190
BLAST score
                  237
E value
                  3.0e-20
Match length
                  80
% identity
                  65
NCBI Description
                  (Y10162) cyclin-D like protein [Chenopodium rubrum]
Seq. No.
                  313408
                  xyt700345189.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2129579
BLAST score
                  150
E value
                  5.0e-10
Match length
                  59
% identity
                  53
NCBI Description
                  Dwarfl protein - Arabidopsis thaliana >gi 516043 (U12400)
                  Dwarf1 [Arabidopsis thaliana]
Seq. No.
                  313409
Seq. ID
                  xyt700345212.h1
Method
                  BLASTX
NCBI GI
                  g112994
BLAST score
                  154
E value
                  4.0e-22
Match length
                  65
% identity
                  89
NCBI Description
                  GLYCINE-RICH RNA-BINDING, ABSCISIC ACID-INDUCIBLE PROTEIN
                  >gi_82685_pir__S04536 embryonic abundant protein,
                  glycine-rich - maize >gi_22313_emb_CAA31077_ (X12564)
                  ABA-inducible gene protein [Zea mays]
```

Seq. No. 313410

mays]

>gi_226091_prf__1410284A abscisic acid inducible gene [Zea

```
Seq. ID xyt700345218.h1
Method BLASTX
NCBI GI g3953478
BLAST score 145
E value 4.0e-12
```

% identity 47
NCBI Description (AC002328) F2202.23 [Arabidopsis thaliana]

Seq. No. 313411 Seq. ID xyt700

Match length

Seq. ID xyt700345257.h1

89

Method BLASTX
NCBI GI g4588906
BLAST score 243
E value 5.0e-21
Match length 79
% identity 62

NCBI Description (AF118149) ribosomal protein S7 [Secale cereale]

Seq. No. 313412

Seq. ID xyt700345424.h1

Method BLASTN
NCBI GI g168436
BLAST score 107
E value 3.0e-53
Match length 143
% identity 94

NCBI Description Zea mays catalase (Cat3) gene, complete cds

Seq. No. 313413

Seq. ID xyt700345447.h1

Method BLASTX
NCBI GI g4467110
BLAST score 463
E value 1.0e-46
Match length 94

% identity 89

NCBI Description (AL035538) putative protein [Arabidopsis thaliana]

Seq. No. 313414

Seq. ID xyt700345515.h1

Method BLASTX
NCBI GI g3600054
BLAST score 298
E value 3.0e-27
Match length 83
% identity 59

NCBI Description (AF080120) No definition line found [Arabidopsis thaliana]

Seq. No. 313415

Seq. ID xyt700345537.h1

Method BLASTX
NCBI GI g3335375
BLAST score 391
E value 3.0e-38
Match length 80
% identity 85

NCBI Description

thaliana]





```
NCBI Description
                  (AC003028) putative amidase [Arabidopsis thaliana]
                  313416
Seq. No.
                  xyt700345709.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g421929
BLAST score
                  502
E value
                  4.0e-51
Match length
                  102
                  14
% identity
                  ubiquitin - tomato >gi_312160_emb_CAA51679_ (X73156)
NCBI Description
                  ubiquitin [Lycopersicon esculentum]
Seq. No.
                  313417
                  xyt700345760.h1
Seq. ID
Method
                  BLASTN
                  g2618602
NCBI GI
BLAST score
                  33
E value
                  2.0e-09
Match length
                  77
                  86
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MSJ1, complete sequence [Arabidopsis thaliana]
Seq. No.
                  313418
Seq. ID
                  xyt700345843.h1
                  BLASTX
Method
                   g2244915
NCBI GI
BLAST score
                   147
                  1.0e-09
E value
Match length
                  84
% identity
                   38
                   (Z97339) strong homology to reverse transcriptase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   313419
Seq. ID
                  xyt700345853.h1
Method
                  BLASTX
NCBI GI
                   q3297816
BLAST score
                   276
E value
                   1.0e-24
Match length
                   92
% identity
                   57
NCBI Description
                  (AL031032) putative protein [Arabidopsis thaliana]
Seq. No.
                   313420
Seq. ID
                   xyt700345866.h1
Method
                  BLASTX
NCBI GI
                   g3738302
BLAST score
                   179
                   2.0e-13
E value
Match length
                   51
% identity
                   69
```

(AC005309) tubby-like protein [Arabidopsis thaliana]

>gi_4249398 (AC006072) putative tubby protein [Arabidopsis



```
313421
Seq. No.
                  xyt700345889.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2996096
BLAST score
                  407
                  3.0e-40
E value
Match length
                  81
% identity
                   98
                   (AF030517) translation elongation factor-1 alpha; EF-1
NCBI Description
                  alpha [Oryza sativa]
                   313422
Seq. No.
                  xyt700345926.h1
Seq. ID
                  BLASTX
Method
NCBI GI
                   g452593
BLAST score
                   221
                   3.0e-18
E value
Match length
                   96
% identity
                   42
                   (D21814) ORF [Lilium longiflorum]
NCBI Description
Seq. No.
                   313423
Seq. ID
                   xyt700345928.h1
Method
                   BLASTN
NCBI GI
                   g4218027
BLAST score
                   179
E value
                   2.0e-96
Match length
                   223
% identity
                   95
                   Homo sapiens BAC clone RG442F18 from 2, complete sequence
NCBI Description
                   [Homo sapiens]
Seq. No.
                   313424
                   xyt700345939.h1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g6978315
                   58
BLAST score
                   5.0e-24
E value
Match length
                   122
                   87
% identity
NCBI Description Mus musculus histone deacetylase mHDA2 mRNA, complete cds
                   313425
Seq. No.
                   xyt700345990.h1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3927830
BLAST score
                   213
                   2.0e-17
E value
                   90
Match length
                   56
% identity
                   (AC005727) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   313426
Seq. No.
```

Seq. ID xyt700346012.h1

Method BLASTX
NCBI GI g3292849
BLAST score 236

```
E value
                   4.0e-20
Match length
                   49
% identity
                   90
                  (AJ007582) arginine methyltransferase [Arabidopsis
NCBI Description
                  thaliana]
                  313427
Seq. No.
                  xyt700346018.hl
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4514559
BLAST score
                  490
                  7.0e-50
E value
Match length
                  92
% identity
                  9
NCBI Description
                  (AB024004) KRAB-containing zinc-finger protein KRAZ1 [Mus
                  musculus]
Seq. No.
                  313428
                  xyt700346063.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q395071
BLAST score
                  37
                  1.0e-11
E value
Match length
                  77
% identity
                  87
NCBI Description
                  V.faba guanine nucleotide regulatory protein mRNA, complete
                  CDS
Seq. No.
                  313429
                  xyt700346102.h1
Seq. ID
Method
                  BLASTN
                  g2826899
NCBI GI
BLAST score
                  78
                  5.0e-36
E value
Match length
                  230
% identity
                  84
NCBI Description Oryza sativa mRNA for DNA polymerase alpha catalytic
                  subunit, complete cds
Seq. No.
                  313430
Seq. ID
                  xyt700346178.h1
Method
                  BLASTX
NCBI GI
                  g3461817
BLAST score
                  169
E value
                  2.0e-12
Match length
                  43
% identity
NCBI Description (AC004138) unknown protein [Arabidopsis thaliana]
Seq. No.
                  313431
```

xyt700346243.h1 Seq. ID

Method BLASTX NCBI GI q585124 BLAST score 388 E value 1.0e-39 Match length 86 % identity 49



NCBI Description FIBULIN-1, ISOFORM D PRECURSOR >gi_1621019 (U01244) fibulin D [Homo sapiens]

Seq. No. 313432

Seq. ID xyt700346262.h1

Method BLASTN
NCBI GI g57138
BLAST score 71
E value 3.0e-32
Match length 99
% identity 93

NCBI Description Rat mRNA for ribosomal protein S8

Seq. No. 313433

Seq. ID xyt700346284.h1

Method BLASTX
NCBI GI g3024018
BLAST score 221
E value 5.0e-29
Match length 66
% identity 94

NCBI Description INITIATION FACTOR 5A (EIF-5A) (EIF-4D)

>gi_1546919_emb_CAA69225_ (Y07920) translation initiation factor 5A [Zea mays] >gi_2668738 (AF034943) translation

initiation factor 5A [Zea mays]

Seq. No. 313434

Seq. ID xyt700346293.h1

Method BLASTN
NCBI GI g3925228
BLAST score 40
E value 3.0e-13
Match length 72
% identity 89

NCBI Description Zea mays peroxidase J gene, partial cds

Seq. No. 313435

Seq. ID xyt700346306.h1

Method BLASTX
NCBI GI g4539463
BLAST score 185
E value 4.0e-14
Match length 83
% identity 48

NCBI Description (AL049500) putative protein [Arabidopsis thaliana]

Seq. No. 313436

Seq. ID xyt700346327.h1

Method BLASTN NCBI GI g3006211

BLAST score 77
E value 2.0e-35
Match length 109
% identity 93

NCBI Description Drosophila melanogaster (P1 DS02368 (D205)) DNA sequence,

complete sequence [Drosophila melanogaster]

Seq. ID

Method

NCBI GI



```
Seq. No.
                   313437
Seq. ID
                  xyt700346332.h1
Method
                  BLASTX
NCBI GI
                   g4512696
BLAST score
                   199
                   1.0e-15
E value
Match length
                   80
% identity
                   53
NCBI Description
                  (AC006569) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   313438
Seq. ID
                  xyt700346377.h1
Method
                  BLASTX
NCBI GI
                   g3184291
BLAST score
                   331
E value
                   3.0e-31
Match length
                   92
                   72
% identity
NCBI Description
                   (AC004136) putative DNA polymerase III gamma subunit
                   [Arabidopsis thaliana]
Seq. No.
                   313439
Seq. ID
                  xyt700346388.h1
Method
                  BLASTN
NCBI GI
                   g1185553
BLAST score
                  39
E value
                  1.0e-12
Match length
                  71
% identity
                  51
                  Zea mays glyceraldehyde-3-phosphate dehydrogenase (gpc2)
NCBI Description
                  gene, complete cds
Seq. No.
                  313440
Seq. ID
                  xyt700346422.h1
Method
                  BLASTX
NCBI GI
                  q1076777
BLAST score
                   193
                   5.0e-15
E value
Match length
                   51
% identity
                  84
                  protein H2A - wheat >gi 536890 dbj BAA07277 (D38088)
NCBI Description
                  protein H2A [Triticum aestivum]
Seq. No.
                  313441
Seq. ID
                  xyt700346430.h1
Method
                  BLASTN
NCBI GI
                  g312178
BLAST score
                  51
E value
                  7.0e-20
Match length
                  115
% identity
                  59
NCBI Description
                  Z.mays GapC2 gene
Seq. No.
                  313442
```

44807

xyt700346456.h1

BLASTN

g169818

Match length

% identity

82

79



```
BLAST score
                   7.0e-20
E value
Match length
                  86
                   91
% identity
NCBI Description Rice 25S ribosomal RNA gene
Seq. No.
                  313443
                  xyt700346477.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3337361
BLAST score
                   217
                   6.0e-18
E value
Match length
                   52
% identity
                  77
                  (AC004481) ankyrin-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  313444
Seq. ID
                  xyt700346559.h1
Method
                  BLASTX
                   g3695385
NCBI GI
BLAST score
                   162
                   2.0e-11
E value
Match length
                   87
                   41
% identity
                   (AF096370) similar to Medicago truncatula MtN21
NCBI Description
                   (GB:Y15293) [Arabidopsis thaliana]
Seq. No.
                   313445
Seq. ID
                   xyt700346561.h1
Method
                   BLASTX
                   g4107099
NCBI GI
BLAST score
                   148
                   1.0e-09
E value
                   50
Match length
% identity
                   60
                   (AB015141) AHP1 [Arabidopsis thaliana]
NCBI Description
                   >gi_4156245_dbj_BAA37112_ (AB012570) ATHP3 [Arabidopsis
                   thaliana]
Seq. No.
                   313446
                   xyt700346577.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3135264
BLAST score
                   171
E value
                   2.0e-12
Match length
                   46
% identity
                   78
                   (AC003058) unknown protein [Arabidopsis thaliana]
NCBI Description
                   313447
Seq. No.
Seq. ID
                   xyt700346584.h1
Method
                   BLASTX
NCBI GI
                   g1209756
BLAST score
                   258
E value
                   2.0e-29
```

```
NCBI Description (U43629) integral membrane protein [Beta vulgaris]
                  313448
Seq. No.
                  xyt700346660.h1
Seq. ID
Method
                  BLASTX
                  q4539423
NCBI GI
BLAST score
                  163
                  1.0e-11
E value
                  62
Match length
                  55
% identity
                  (AL049171) pyrophosphate-dependent phosphofructo-1-kinase
NCBI Description
                   [Arabidopsis thaliana]
                  313449
Seq. No.
Seq. ID
                  xyt700346708.h1
Method
                  BLASTX
                  g123378
NCBI GI
BLAST score
                  292
                  1.0e-26
E value
                  82
Match length
% identity
                  76
                  DNA-BINDING PROTEIN MNB1B (HMG1-LIKE PROTEIN)
NCBI Description
                  >gi_100886_pir__S16670 high mobility group protein - maize
                  >gi_539062_pir__B47150 DNA-binding protein MNB1b - maize
                  >gi_22329_emb_CAA41220_ (X58282) high mobility group
                  protein [Zea mays]
Seq. No.
                  313450
                  xyt700346720.hl
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4510395
BLAST score
                   437
                   1.0e-43
E value
                  101
Match length
% identity
                   71
                   (AC006587) putative beta-galactosidase precursor
NCBI Description
                   [Arabidopsis thaliana]
                   313451
Seq. No.
                   xyt700346873.hl
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2252843
BLAST score
                   235
E value
                   5.0e-20
                   87
Match length
% identity
                   51
                  (AF013293) No definition line found [Arabidopsis thaliana]
NCBI Description
                   313452
Seq. No.
                   xyt700346880.hl
Seq. ID
Method
                   BLASTX
                   q1431870
NCBI GI
BLAST score
                   168
                   4.0e-12
E value
Match length
                   63
                   48
% identity
                  (U43904) ent-kaurene synthase B [Cucurbita maxima]
NCBI Description
```

```
Seq. No.
                  313453
                  xyt700346917.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2760323
BLAST score
                   228
                   4.0e-19
E value
Match length
                   45
% identity
                   80
                   (AC002130) F1N21.8 [Arabidopsis thaliana]
NCBI Description
                   313454
Seq. No.
                  xyt700346994.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4309698
BLAST score
                   344
                   1.0e-32
E value
Match length
                   66
                   97
% identity
                   (AC006266) putative glucosyltransferase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   313455
                   xyt700347010.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4249404
BLAST score
                   193
E value
                   3.0e-15
Match length
                   53
% identity
                   66
                   (AC006072) putative nuclear protein SA-1 [Arabidopsis
NCBI Description
                   thaliana]
                   313456
Seq. No.
                   xyt700347045.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g548774
BLAST score
                   269
                   4.0e-24
E value
Match length
                   50
                   98
% identity
                   60S RIBOSOMAL PROTEIN L7A >gi 542158 pir__S38360 ribosomal
NCBI Description
                   protein L7a - rice >gi_303855_dbj_BAA02156_ (D12631)
                   ribosomal protein L7A [Oryza sativa]
Seq. No.
                   313457
Seq. ID
                   xyt700347170.h1
Method
                   BLASTX
NCBI GI
                   g3218544
BLAST score
                   223
E value
                   3.0e-39
Match length
                   87
                   98
% identity
NCBI Description
                   (AB004813) alternative oxidase [Oryza sativa]
                   >gi_3218546_dbj_BAA28773_ (AB004864) alternative oxidase
                   [Oryza sativa]
```

```
Seq. No.
                   313458
Seq. ID
                   xyt700347186.h1
Method
                   BLASTX
NCBI GI
                   g585771
BLAST score
                   395
                   8.0e-39
E value
Match length
                   84
% identity
                   89
NCBI Description
                  MEIOTIC RECOMBINATION PROTEIN DMC1 HOMOLOG
                   >gi_629874_pir__JC2214 hypothetical 38.3K protein, LIM15 -
                   Trumpet lily >gi_431168_dbj_BAA04845_ (D21821) RAD51-like
                   protein [Lilium Tongiflorum]
                   313459
Seq. No.
                   xyt700347190.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3047118
BLAST score
                   206
E value
                   1.0e-16
Match length
                   87
% identity
                   49
NCBI Description
                  (AF058919) No definition line found [Arabidopsis thaliana]
Seq. No.
                   313460
Seq. ID
                   xyt700347191.h1
Method
                   BLASTX
NCBI GI
                   g2494625
BLAST score
                   152
                   3.0e-10
E value
Match length
                   62
% identity
                   47
                  HYPOTHETICAL PROTEIN KIAA0107 >gi_285951_dbj_BAA03497_
NCBI Description
                   (D14663) KIAA0107 [Homo sapiens]
Seq. No.
                   313461
Seq. ID
                   xyt700347220.h1
Method
                   BLASTX
                   g4056488
NCBI GI
BLAST score
                   176
E value
                   4.0e-13
Match length
                   31
% identity
                   90
NCBI Description
                  (AC005896) unknown protein [Arabidopsis thaliana]
Seq. No.
                   313462
Seq. ID
                   xyt700347223.h1
Method
                   BLASTX
NCBI GI
                   g2660670
```

Method BLASTX
NCBI GI g2660670
BLAST score 236
E value 2.0e-20
Match length 64
% identity 77

NCBI Description (AC002342) putative Cu2+-transporting ATPase [Arabidopsis

thaliana]

Seq. No. 313463

Seq. ID yd1700405355.h1

Match length



```
100°
Method
                   BLASTN
NCBI GI
                   g22322
BLAST score
                   225
E value
                   1.0e-123
Match length
                   236
                   99
% identity
NCBI Description
                   Z.mays mRNA for H2B histone (clone cH2B214)
Seq. No.
                   313464
Seq. ID
                   yd1700405422.h1
Method
                   BLASTX
NCBI GI
                   g1172836
BLAST score
                   408
                   4.0e-40
E value
Match length
                   78
% identity
                   96
NCBI Description
                   GTP-BINDING NUCLEAR PROTEIN RAN-B1 >gi 496272 (L16787)
                   small ras-related protein [Nicotiana tabacum]
                   313465
Seq. No.
Seq. ID
                   ymt700218517.h1
Method
                   BLASTX
NCBI GI
                   g1477428
BLAST score
                   224
                   9.0e-19
E value
Match length
                   81
% identity
                   62
NCBI Description
                   (X99623) alpha-tubulin 1 [Hordeum vulgare]
Seq. No.
                   313466
Seq. ID
                   ymt700218523.h1
Method
                   BLASTX
NCBI GI
                   g4581156
BLAST score
                   155
E value
                   5.0e-17
Match length
                   63
% identity
                   75
NCBI Description
                   (AC006919) putative pyruvate kinase [Arabidopsis thaliana]
Seq. No.
                   313467
Seq. ID
                   ymt700218626.h1
Method
                   BLASTN
NCBI GI
                   g1245938
BLAST score
                   35
E value
                   2.0e-10
Match length
                   35
% identity
                   100
NCBI Description
                   rabClC-2 beta=chloride channel ClC-2G isoform [rabbits,
                   heart atrium, mRNA, 2998 nt]
Seq. No.
                   313468
Seq. ID
                   ymt700218678.h1
Method
                   BLASTX
NCBI GI
                   g2911052
BLAST score
                   404
E value
                   7.0e-40
```

% identity

```
% identity
NCBI Description (AL021961) putative protein [Arabidopsis thaliana]
Seq. No.
                   313469
                   ymt700218691.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g548774
BLAST score
                   341
E value
                   2.0e-32
Match length
                   65
% identity
                   98
                   60S RIBOSOMAL PROTEIN L7A >gi_542158_pir__S38360 ribosomal protein L7a - rice >gi_303855_dbj_BAA02156_ (D12631)
NCBI Description
                   ribosomal protein L7A [Oryza sativa]
Seq. No.
                   313470
Seq. ID
                   ymt700218729.h1
Method
                   BLASTN
                   g22356
NCBI GI
BLAST score
                   107
E value
                   2.0e-53
Match length
                   153
% identity
                   93
                   Maize mRNA for light-harvesting chlorophyll a/b binding
NCBI Description
                   protein LHCP
Seq. No.
                   313471
Seq. ID
                   ymt700218750.h1
Method
                   BLASTX
NCBI GI
                   q3142289
BLAST score
                   383
E value
                   3.0e-37
Match length
                   93
% identity
                   76
NCBI Description
                   (AC002411) Strong similarity to beta-keto-Coa synthase
                   gb_U37088 from Simmondsia chinensis. [Arabidopsis thaliana]
Seq. No.
                   313472
Seq. ID
                   ymt700218796.h1
Method
                   BLASTX
NCBI GI
                   q544076
BLAST score
                   226
E value
                   6.0e-19
Match length
                   83
% identity
                   49
NCBI Description
                   COATOMER BETA' SUBUNIT (BETA'-COAT PROTEIN) (BETA'-COP)
                   (P102) >gi_298097_emb_CAA49900_ (X70476) subunit of
                   coatomer complex [Homo sapiens]
Seq. No.
                   313473
Seq. ID
                   ymt700218817.h1
Method
                   BLASTX
NCBI GI
                   g2160692
BLAST score
                   250
E value
                   9.0e-22
Match length
                   62
```

```
(U73527) B' regulatory subunit of PP2A [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  313474
Seq. ID
                  ymt700218830.h1
Method
                  BLASTX
                  q3810676
NCBI GI
BLAST score
                  375
E value
                  2.0e-36
Match length
                  85
% identity
                  (AJ223357) SKOR [Arabidopsis thaliana]
NCBI Description
                  313475
Seq. No.
Seq. ID
                  ymt700218843.h1
Method
                  BLASTX
                  q120670
NCBI GI
BLAST score
                  329
                   4.0e-31
E value
Match length
                  62
                   100
% identity
NCBI Description
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
                  >qi 100879 pir S06879 qlyceraldehyde-3-phosphate
                   dehydrogenase (EC 1.2.1.12) C - maize
                   >gi 295853 emb CAA33620_ (X15596) GAPDH [Zea mays]
Seq. No.
                   313476
Seq. ID
                   ymt700218888.h1
Method
                  BLASTX
NCBI GI
                   q421809
BLAST score
                   193
E value
                   4.0e-15
Match length
                   82
% identity
                   46
NCBI Description dnaJ protein homolog DnaJ-1 - cucumber
Seq. No.
                   313477
                   ymt700218890.h1
Seq. ID
Method
                   BLASTX
                   g2935342
                   167
                   5.0e-12
                   81
                   41
                   (AF044216) steroid 22-alpha-hydroxylase; DWF4; CYP90B1
NCBI Description
```

NCBI GI BLAST score E value Match length % identity

[Arabidopsis thaliana]

313478 Seq. No.

ymt700218936.hl Seq. ID

Method BLASTX NCBI GI g4263721 BLAST score 163 1.0e-11 E value 79 Match length % identity 48

(AC006223) putative DNA repair protein RAD50 [Arabidopsis NCBI Description

thaliana]

Method

NCBI GI

BLAST score

BLASTX

265

g3236237

```
313479
Seq. No.
Seq. ID
                  ymt700218960.h1
                  BLASTX
Method
                  g729671
NCBI GI
                  202
BLAST score
                   4.0e-16
E value
Match length
                   42
% identity
                   98
                  HISTONE H2A >gi 473603 (U08225) histone H2A [Zea mays]
NCBI Description
                   313480
Seq. No.
                   ymt700218962.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                   g22324
BLAST score
                   112
                   3.0e-56
E value
Match length
                   204
% identity
                   89
NCBI Description
                  Z.mays mRNA for H2B histone (clone cH2B221)
Seq. No.
                   313481
                   ymt700219040.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3252856
BLAST score
                   185
E value
                   3.0e-14
Match length
                   60
% identity
                   62
                   (AF020425) glutamate decarboxylase isozyme 1 [Nicotiana
NCBI Description
                   tabacum]
                   313482
Seq. No.
                   ymt700219042.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4512263
BLAST score
                   367
                   2.0e-35
E value
Match length
                   87
                   84
% identity
                  (AB018526) H+/Ca2+ exchanger 2 [Ipomoea nil]
NCBI Description
                   313483
Seq. No.
                   ymt700219068.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4544390
BLAST score
                   162
E value
                   2.0e-11
Match length
                   84
% identity
                   42
NCBI Description
                  (AC007047) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   313484
                   ymt700219107.h1
Seq. ID
```

```
E value
                   2.0e-23
                   83
Match length
% identity
                   61
                   (AC004684) putative ribotol dehydrogenase [Arabidopsis
NCBI Description
                   thaliana]
                   313485
Seq. No.
Seq. ID
                   ymt700219108.h1
Method
                   BLASTX
NCBI GI
                   g1723953
BLAST score
                   239
                   2.0e-20
E value
                   77
Match length
                   56
% identity
NCBI Description
                  MINICHROMOSOME MAINTENANCE PROTEIN 6
                   >gi_2131619_pir__S64219 hypothetical protein YGL201c -
                   yeast (Saccharomyces cerevisiae) >gi 1322832 emb CAA96913
                   (Z72723) ORF YGL201c [Saccharomyces cerevisiae]
Seq. No.
                   313486
Seq. ID
                   ymt700219137.h1
Method
                   BLASTX
NCBI GI
                   g2257756
BLAST score
                   227
                   5.0e-19
E value
Match length
                   66
% identity
                   70
NCBI Description
                   (U82815) nucleolar histone deacetylase HD2-p39 [Zea mays]
                   >gi 3650466 (AF026917) histone deacetylase HD2-p39 [Zea
Seq. No.
                   313487
Seq. ID
                   ymt700219144.h1
Method
                   BLASTX
                   g3402697
                   341
                   2.0e-32
Match length
                   87
% identity
                   69
NCBI Description
                   (AC004261) putative phosphatidylinositol-4-phosphate
```

NCBI GI BLAST score E value

5-kinase [Arabidopsis thaliana]

Seq. No. 313488

Seq. ID ymt700219170.h1

Method BLASTX NCBI GI g3152608 BLAST score 371 E value 7.0e-36 Match length 72 93 % identity

(AC004482) putative BEL1-like homeotic protein [Arabidopsis ... NCBI Description

thaliana]

313489 Seq. No.

Seq. ID ymt700219207.h1

Method BLASTX NCBI GI g4102600

```
BLAST score
E value
                  1.0e-46
Match length
                  92
% identity
                  92
NCBI Description
                  (AF013467) ARF6 [Arabidopsis thaliana]
Seq. No.
                  313490
Seq. ID
                  ymt700219252.h1
Method
                  BLASTX
NCBI GI
                  q2961375
BLAST score
                  210
E value
                  5.0e-17
Match length
                  50
% identity
                  74
NCBI Description
                  (AL022141) NAM like protein [Arabidopsis thaliana]
                  313491
Seq. No.
Seq. ID
                  ymt700219258.hl
Method
                  BLASTX
NCBI GI
                  g479357
BLAST score
                  267
E value
                  1.0e-23
Match length
                  82
% identity
                  62
NCBI Description
                  hypothetical protein 612 - maize transposon MuA2
                  >gi_22375_emb_CAA44165_ (X62251) ORF [Zea mays]
Seq. No.
                  313492
Seq. ID
                  ymt700219317.h1
Method
                  BLASTN
                  g3821780
NCBI GI
BLAST score
                  35
E value
                  1.0e-10
Match length
                  35
% identity
                  100
NCBI Description
                  Xenopus laevis cDNA clone 27A6-1
Seq. No.
                  313493
Seq. ID
                  ymt700219344.h1
Method
                  BLASTX
NCBI GI
                  g2047324
BLAST score
                  270
E value
                  4.0e-24
Match length
                  73
% identity
                  68
NCBI Description
                  (U80192) HAL3 homolog [Arabidopsis thaliana]
Seq. No.
                  313494
Seq. ID
                  ymt700219379.h1
Method
                  BLASTX
NCBI GI
                  q2244910
BLAST score
                  152
E value
                  3.0e-10
Match length
                  72
% identity
                  (Z97339) unnamed protein product [Arabidopsis thaliana]
NCBI Description
```

```
Seq. No.
                   313495
Seq. ID
                   vmt700219426.h1
Method
                   BLASTN
NCBI GI
                   g2062705
BLAST score
                   36
E value
                   5.0e-11
Match length
                   36
                   100
% identity
NCBI Description
                   Human butyrophilin (BTF5) mRNA, complete cds
Seq. No.
                   313496
Seq. ID
                   ymt700219430.h1
Method
                   BLASTX
NCBI GI
                   g121695
BLAST score
                   317
                   1.0e-29
E value
Match length
                   64
% identity
                   95
NCBI Description
                   GLUTATHIONE S-TRANSFERASE I (GST-I) (GST-29) (CLASS-PHI)
                   >gi 22315 emb CAA29928 (X06754) GST I (AA 1-214) [Zea
                   mays]
Seq. No.
                   313497
Seq. ID
                   ymt700219435.h1
Method
                   BLASTX
                   g3786009
NCBI GI
                   303
BLAST score
E value
                   4.0e-28
Match length
                   78
% identity
                   72
NCBI Description
                  (AC005499) unknown protein [Arabidopsis thaliana]
Seq. No.
                   313498
Seq. ID
                   ymt700219436.h1
Method
                   BLASTX
NCBI GI
                   g4589961
BLAST score
                   195
                   2.0e-15
E value
                   77
Match length
% identity
                   49
NCBI Description
                  (AC007169) unknown protein [Arabidopsis thaliana]
Seq. No.
                   313499
Seq. ID
                   ymt700219464.h1
Method
                   BLASTX
NCBI GI
                   g2674203
BLAST score
                   281
E value
                   3.0e-25
Match length
                   75
% identity
                   71
NCBI Description
                   (AF036328) CLP protease regulatory subunit CLPX
                   [Arabidopsis thaliana]
Seq. No.
                   313500
Seq. ID
                   ymt700219503.h1
Method
                   BLASTX
NCBI GI
                   g2507281
```



```
BLAST score
                  5.0e-24
E value
Match length
                  52
                  98
% identity
                  GTP-BINDING NUCLEAR PROTEIN RAN-2 >gi 1668706_emb_CAA66048_
NCBI Description
                  (X97380) atran2 [Arabidopsis thaliana]
Seq. No.
                  313501
                  ymt700219538.h1
Seq. ID
Method
                  BLASTX
                  g3776027
NCBI GI
BLAST score
                  216
E value
                  5.0e-18
Match length
                  61
% identity
                  72
                  (AJ010475) RNA helicase [Arabidopsis thaliana]
NCBI Description
                  313502
Seq. No.
                  ymt700219553.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4538947
BLAST score
                  242
                  5.0e-21
E value
Match length
                  74
% identity
                  59
                  (AL049483) putative mitochondrial carrier protein
NCBI Description
                   [Arabidopsis thaliana]
                  313503
Seq. No.
                  ymt700219595.h1
Seq. ID
Method
                  BLASTX
                  g116923
NCBI GI
BLAST score
                  174
E value
                  5.0e-13
Match length
                  61
% identity
                  61
                  COATOMER BETA SUBUNIT (BETA-COAT PROTEIN) (BETA-COP)
NCBI Description
                  >gi_111414 pir S13520 beta-COP protein - rat
                  >gi 55819 emb CAA40505 (X57228) beta COP [Rattus
                  norvegicus]
Seq. No.
                  313504
Seq. ID
                  ymt700219601.h1
Method
                  BLASTX
NCBI GI
                  g1498229
BLAST score
                  266
                  1.0e-23
E value
Match length
                  87
% identity
                  62
NCBI Description
                  (X98743) RNA helicase [Homo sapiens]
```

Seq. No. 313505

Seq. ID ymt700219625.h1

Method BLASTX NCBI GI g1172836 BLAST score 359 2.0e-34 E value



```
Match length
                   96
% identity
                  GTP-BINDING NUCLEAR PROTEIN RAN-B1 >gi_496272 (L16787)
NCBI Description
                   small ras-related protein [Nicotiana tabacum]
                   313506
Seq. No.
                   ymt700219660.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2147484
                   310
BLAST score
                   8.0e-29
E value
                   80
Match length
                   74
% identity
                  homeotic protein - Phalaenopsis sp >gi_1173622 (U34743)
NCBI Description
                   homeobox protein [Phalaenopsis sp. 'hybrid SM9108']
                   313507
Seq. No.
                   ymt700219691.h1
Seq. ID
Method
                   BLASTX
                   q741983
NCBI GI
BLAST score
                   350
                   1.0e-33
E value
Match length
                   68
                   100
% identity
                   sucrose synthase:ISOTYPE=2 [Zea mays]
NCBI Description
Seq. No.
                   313508
                   ymt700219713.h1
Seq. ID
Method
                   BLASTX
                   g2708624
NCBI GI
BLAST score
                   268
                   7.0e-24
E value
                   70
Match length
% identity
                   66
                  (AF036618) acetyl-CoA synthetase [Arabidopsis thaliana]
NCBI Description
                   313509
Seq. No.
                   ymt700219717.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1346251
BLAST score
                   194
                   3.0e-15
E value
Match length
                   61
                   67
% identity
                   HISTONE H2B.4 >gi 577819 emb CAA49585 (X69961) H2B histone
NCBI Description
                   [Zea mays]
                   313510
Seq. No.
```

Seq. ID

ymt700219728.h1

Method BLASTX NCBI GI g3687224 BLAST score 337 E value 6.0e-32 Match length 86 73 % identity

NCBI Description (AC005169) putative N-acetyl-gamma-glutamyl-phosphate

reductase [Arabidopsis thaliana]

```
Seq. No.
                  313511
Seq. ID
                  ymt700219745.h1
Method
                  BLASTX
NCBI GI
                  q1945283
                  260
BLAST score
E value
                  6.0e-23
Match length
                  85
% identity
                  59
NCBI Description (Y11351) myb factor [Oryza sativa]
Seq. No.
                  313512
                  ymt700219760.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3522942
BLAST score
                  244
                  5.0e-21
E value
Match length
                  59
% identity
                  73
NCBI Description
                   (AC004411) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  313513
Seq. ID
                  ymt700219767.h1
Method
                  BLASTX
NCBI GI
                  g3914019
BLAST score
                  309
E value
                  1.0e-28
Match length
                  61
% identity
                  93
NCBI Description
                  S-ADENOSYLMETHIONINE SYNTHETASE (METHIONINE
                  ADENOSYLTRANSFERASE) (ADOMET SYNTHETASE) >qi 2305014
                   (AF004317) S-adenosyl-L-methionine synthetase homolog [Musa
                  acuminata]
Seq. No.
                  313514
Seq. ID
                  ymt700219818.h1
Method
                  BLASTN
NCBI GI
                  g166548
BLAST score
                  124
E value
                  2.0e-63
Match length
                  192
% identity
                  91
NCBI Description Avena sativa vacuolar H+-ATPase 16 kDa proteolipid subunit
                  (vatp-P1) mRNA, complete cds
Seq. No.
                  313515
Seq. ID
                  ymt700219825.h1
Method
                  BLASTX
NCBI GI
                  g1731324
BLAST score
                  230
E value
                  2.0e-19
Match length
                  62
% identity
                  74
NCBI Description HYPOTHETICAL PROTEIN >qi 166306 (M23451) steroid receptor
```

Seq. No. 313516

[Achlya ambisexualis]

Seq. ID

Method

NCBI GI



```
Seq. ID
                  ymt700219870.h1
Method
                  BLASTX
                  g2738248
NCBI GI
BLAST score
                  347
                  3.0e - 33
E value
Match length
                  87
                  83
% identity
NCBI Description
                   (U97200) cobalamin-independent methionine synthase
                   [Arabidopsis thaliana]
Seq. No.
                  313517
Seq. ID
                  ymt700219926.h1
Method
                  BLASTX
NCBI GI
                  g4033424
BLAST score
                  334
                  1.0e-31
E value
Match length
                  66
% identity
                  100
NCBI Description
                  SOLUBLE INORGANIC PYROPHOSPHATASE (PYROPHOSPHATE
                  PHOSPHO-HYDROLASE) (PPASE) >qi 2668746 (AF034947) inorganic
                  pyrophosphatase [Zea mays]
                  313518
Seq. No.
Seq. ID
                  ymt700219932.h1
Method
                  BLASTX
NCBI GI
                  g2589162
BLAST score
                  203
E value
                  3.0e-16
Match length
                  86
% identity
                  43
NCBI Description
                  (D88451) aldehyde oxidase [Zea mays]
Seq. No.
                  313519
                  ymt700219986.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4049342
BLAST score
                  184
                   5.0e-14
E value
Match length
                  79
% identity
                   46
NCBI Description
                   (AL034567) adenylate translocator (brittle-1)-like protein
                   [Arabidopsis thaliana]
Seq. No.
                  313520
Seq. ID
                  ymt700220025.h1
Method
                  BLASTX
NCBI GI
                  g2213594
BLAST score
                  320
                  5.0e-30
E value
Match length
                  86
% identity
                  66
                  (AC000348) T7N9.14 [Arabidopsis thaliana]
NCBI Description
                  313521
Seq. No.
```

ymt700220033.h1

BLASTX

g1172833

```
BLAST score
E value
                  5.0e-47
Match length
                  85
                  98
% identity
                  GTP-BINDING NUCLEAR PROTEIN RAN-1 >qi 495729 (L16789) small
NCBI Description
                  ras-related protein [Arabidopsis thaliana]
                  >gi 2058278 emb CAA66047 (X97379) atran1 [Arabidopsis
                  thaliana]
                  313522
Seq. No.
                  ymt700220077.h1
Seq. ID
Method
                  BLASTX
                  g95995
NCBI GI
BLAST score
                  196
E value
                  2.0e-15
Match length
                  59
                  64
% identity
                  mrp protein - Escherichia coli >gi 42017_emb_CAA39316
NCBI Description
                   (X55791) put. ATPase [Escherichia coli]
                  313523
Seq. No.
                  ymt700220078.h1
Seq. ID
Method
                  BLASTN
                  g1256711
NCBI GI
BLAST score
                  95
                   3.0e-46
E value
Match length
                  152
                   97
% identity
                  Zea mays O-methyltransferase (OMT) gene, complete cds
NCBI Description
Seq. No.
                   313524
                   ymt700220093.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3738257
BLAST score
                   145
                   9.0e-18
E value
Match length
                   61
                   77
% identity
                   (AB018410) cytosolic phosphoglycerate kinase 1 [Populus
NCBI Description
                  nigra]
                   313525
Seq. No.
                   ymt700220117.h1
Seq. ID
Method
                   BLASTN
                  g3821780
NCBI GI
BLAST score
                   36
                   6.0e-11
E value
Match length
                   45
                   65
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                   313526
                   ymt700220128.h1
Seq. ID
```

Method BLASTX g3786005 NCBI GI BLAST score 311 E value 7.0e-29



```
Match length
                  66
                  43
% identity
NCBI Description
                  (AC005499) putative phosphoethanolamine
                  cytidylyltransferase [Arabidopsis thaliana]
                  313527
Seq. No.
                  ymt700220130.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3914056
BLAST score
                  437
E value
                  1.0e-43
Match length
                  90
% identity
                  90
NCBI Description
                  DNA MISMATCH REPAIR PROTEIN MSH2 >qi 2522362 (AF002706)
                  MutS homolog 2 [Arabidopsis thaliana] >gi 2522364
                   (AF003005) MutS homolog 2 [Arabidopsis thaliana]
                  >gi 2547236 (AF026549) DNA mismatch repair protein MSH2
                   [Arabidopsis thaliana]
Seq. No.
                  313528
Seq. ID
                  ymt700220131.h1
Method
                  BLASTX
NCBI GI
                  g4406781
BLAST score
                  189
E value
                  1.0e-14
Match length
                  71
% identity
NCBI Description
                  (AC006532) putative Na+/H+ antiporter [Arabidopsis
                  thaliana]
Seq. No.
                  313529
Seq. ID
                  ymt700220137.h1
Method
                  BLASTX
NCBI GI
                  g606811
BLAST score
                  273
E value
                  2.0e-24
Match length
                  57
                  45
% identity
NCBI Description
                  (U08401) carbonic anhydrase [Zea mays]
                  313530
Seq. No.
Seq. ID
                  ymt700220140.h1
                  BLASTX
Method
NCBI GI
                  q4589965
BLAST score
                  173
E value
                  1.0e-12
Match length
                  43
                  72
% identity
NCBI Description
                  (AC007169) putative glyoxalase II [Arabidopsis thaliana]
Seq. No.
                  313531
```

Seq. ID ymt700220150.h1

Method BLASTX
NCBI GI g3702352
BLAST score 174
E value 5.0e-15
Match length 71



```
% identity
                   (AC005397) putative mitochondrial carrier protein
NCBI Description
                   [Arabidopsis thaliana]
                  313532
Seq. No.
Seq. ID
                  ymt700220159.h1
Method
                  BLASTX
NCBI GI
                  g1652678
                  188
BLAST score
                  1.0e-14
E value
Match length
                  55
% identity
                   64
                  (D90907) amidase [Synechocystis sp.]
NCBI Description
                  313533
Seq. No.
Seq. ID
                  ymt700220203.h1
Method
                  BLASTN
NCBI GI
                  g3821780
BLAST score
                  36
                   6.0e-11
E value
                  55
Match length
                   53
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                   313534
Seq. No.
Seq. ID
                   ymt700220218.h1
Method
                  BLASTX
NCBI GI
                   g4454466
BLAST score
                   193
E value
                   4.0e-15
Match length
                   48
% identity
                   71
NCBI Description
                  (AC006234) unknown protein [Arabidopsis thaliana]
                   313535
Seq. No.
Seq. ID
                   ymt700220236.h1
Method
                   BLASTX
NCBI GI
                   g2117937
BLAST score
                   327
E value
                   8.0e-31
Match length
                   70
% identity
                   UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) -
NCBI Description
                   barley >gi 1212996 emb CAA62689 (X91347) UDP-glucose
                  pyrophosphorylase [Hordeum vulgare]
Seq. No.
                   313536
Seq. ID
                   ymt700220249.h1
Method
                   BLASTX
NCBI GI
                   g3445201
BLAST score
                   230
E value
                   1.0e-19
Match length
                   60
% identity
                   73
```

Seq. No. 313537

NCBI Description

(AC004786) unknown protein [Arabidopsis thaliana]

Seq. ID

Method

NCBI GI

```
ymt700220261.h1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g22312
BLAST score
                   71
E value
                   3.0e-32
Match length
                   111
% identity
                   91
                  Maize ABA-inducible gene for glycine-rich protein ( ABA =
NCBI Description
                   abscisic acid)
Seq. No.
                   313538
                   ymt700220314.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4584527
BLAST score
                   144
                   3.0e-09
E value
Match length
                   88
                   38
% identity
NCBI Description (AL049607) putative protein [Arabidopsis thaliana]
Seq. No.
                   313539
Seq. ID
                   ymt700220319.h1
Method
                   BLASTX
NCBI GI
                   g2392895
BLAST score
                   267
                   1.0e-23
E value
                   78
Match length
                   63
% identity
                   (AF017056) brassinosteroid insensitive 1 [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   313540
Seq. ID
                   ymt700220321.h1
Method
                   BLASTX
NCBI GI
                   g4587533
                   159
BLAST score
                   2.0e-11
E value
Match length
                   63
                   52
% identity
                   (AC007060) EST gb AA721821 comes from this gene.
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   313541
Seq. ID
                   ymt700220357.h1
Method
                   BLASTX
NCBI GI
                   g3413511
BLAST score
                   313
E value
                   4.0e-29
Match length
                   70
% identity
NCBI Description
                   (AJ000265) glucose-6-phosphate isomerase [Spinacia
                   oleracea]
Seq. No.
                   313542
```

44826

ymt700220433.h1

BLASTX

g1184774

```
BLAST score
E value
                   6.0e-26
Match length
                   60
                   92
% identity
NCBI Description
                   (U45856) cytosolic glyceroldehyde-3-phosphate dehydrogenase
                   GAPC3 [Zea mays]
                   313543
Seq. No.
Seq. ID
                   ymt700220449.h1
Method
                   BLASTX
NCBI GI
                   q4325342
BLAST score
                   194
                   5.0e-15
E value
Match length
                   101
% identity
                   47
NCBI Description
                   (AF128393) No definition line found [Arabidopsis thaliana]
Seq. No.
                   313544
Seq. ID
                   ymt700220463.h1
Method
                   BLASTX
NCBI GI
                   q2494260
BLAST score
                   260
E value
                   9.0e-23
Match length
                   75
                   69
% identity
                  ELONGATION FACTOR TU (EF-TU) >gi_1653407_dbj_BAA18321_
NCBI Description
                   (D90913) protein synthesis elongation factor Tu
                   [Synechocystis sp.]
Seq. No.
                   313545
Seq. ID
                   ymt700220479.h1
Method
                   BLASTX
NCBI GI
                   q2959767
BLAST score
                   318
E value
                   5.0e-31
Match length
                   92
% identity
                   75
NCBI Description
                   (AJ002584) AtMRP4 [Arabidopsis thaliana] >gi 3738292
                   (AC005309) glutathione-conjugate transporter AtMRP4
                   [Arabidopsis thaliana]
Seq. No.
                   313546
Seq. ID
                   ymt700220505.h1
Method
                   BLASTX
NCBI GI
                   g1143069
BLAST score
                   158
                   9.0e-15
E value
Match length
                   56
% identity
                   75
```

NCBI Description

(U30600) 3-ketoacyl carrier protein synthase III [Allium

porrum]

Seq. No.

313547

Seq. ID

ymt700220507.h1

Method NCBI GI BLASTX g3522943

260

BLAST score

```
E value
                   4.0e-23
Match length
                   60
% identity
                   44
NCBI Description
                   (AC004411) putative p-glycoprotein [Arabidopsis thaliana]
Seq. No.
                   313548
                   ymt700220556.h1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g4105124
BLAST score
                   202
                   1.0e-110
E value
Match length
                   256
% identity
                   96
NCBI Description
                   Zea mays cell wall invertase (incw4) gene, complete cds
Seq. No.
                   313549
Seq. ID
                   ymt700220560.h1
Method
                   BLASTN
NCBI GI
                   q4138731
BLAST score
                   137
E value
                   3.0e-71
Match length
                   189
% identity
                   96
NCBI Description
                   Zea mays mRNA for proline-rich protein
Seq. No.
                   313550
Seq. ID
                   ymt700220583.h1
Method
                   BLASTX
NCBI GI
                   q1658193
BLAST score
                   166
E value
                   4.0e-12
Match length
                   62
% identity
                   56
NCBI Description
                   (U74319) obtusifoliol 14-alpha demethylase CYP51 [Sorghum
                   bicolor]
Seq. No.
                   313551
Seq. ID
                   ymt700220622.h1
Method
                   BLASTX
                   g1854378
```

1,5

NCBI GI BLAST score 213 E value 2.0e-30 Match length 91 % identity 82

NCBI Description (AB001338) Sucrose-Phosphate Synthase [Saccharum

officinarum]

Seq. No. 313552

Seq. ID ymt700220633.h1

Method BLASTX NCBI GI q4538993 BLAST score 203 E value 3.0e-16 Match length 74 % identity 46

NCBI Description (AL049481) putative host response protein [Arabidopsis

thaliana]

```
Seq. No.
                   313553
Seq. ID
                   ymt700220657.h1
Method
                   BLASTX
NCBI GI
                   g2342685
BLAST score
                   170
E value
                   2.0e-12
Match length
                   63
% identity
                   52
NCBI Description
                   (AC000106) Contains similarity to Rhodococcus amidase
                   (gb D16207). ESTs gb T20504, qb H36650, qb N97423, qb H36595
                   come from this gene. [Arabidopsis thaliana]
Seq. No.
                   313554
Seq. ID
                   ymt700220682.h1
Method
                   BLASTN
NCBI GI
                   q862309
BLAST score
                   45
E value
                   3.0e-16
Match length
                   85
% identity
                   88
NCBI Description Rice G protein alpha-subunit (RGA1) mRNA, complete cds
Seq. No.
                   313555
Seq. ID
                   ymt700220728.h1
Method
                   BLASTN
NCBI GI
                   q2431768
BLAST score
                   37
E value
                   2.0e-11
Match length
                   111
% identity
NCBI Description
                   Zea mays acidic ribosomal protein Pla (rppla) mRNA,
                   complete cds
Seq. No.
                   313556
Seq. ID
                   ymt700220730.h1
Method
                   BLASTX
NCBI GI
                   g4538911
BLAST score
                   157
E value
                   9.0e-11
Match length
                   80
% identity
                   44
NCBI Description
                  (AL049482) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   313557
Seq. ID
                   ymt700220746.h1
Method
                   BLASTX
NCBI GI
                   g2598227
BLAST score
                   333
E value
                   2.0e-31
Match length
                   88
% identity
                   76
NCBI Description (AJ222585) AT-hook protein 1 [Arabidopsis thaliana]
```

Seq. No. 313558

Seq. ID ymt700220832.h1

Method BLASTX



```
NCBI GI
                  q3929396
BLAST score
                  158
E value
                  6.0e-11
Match length
                  90
% identity
                  41
                  HYPOTHETICAL 47.8 KD PROTEIN F57B9.5 IN CHROMOSOME III
NCBI Description
                  >qi 532824 (U13876) F57B9.5 gene product [Caenorhabditis
                  elegans]
Seq. No.
                  313559
Seq. ID
                  ymt700220857.h1
Method
                  BLASTX
NCBI GI
                  g2244915
BLAST score
                  144
E value
                  3.0e-09
Match length
                  87
% identity
NCBI Description
                  (Z97339) strong homology to reverse transcriptase
                  [Arabidopsis thaliana]
Seq. No.
                  313560
Seq. ID
                  vmt700220866.h1
Method
                  BLASTX
NCBI GI
                  g2499114
BLAST score
                  351
E value
                  2.0e-33
                                                              -
Match length
                  86
                  77
% identity
NCBI Description
                  VACUOLAR ASSEMBLY PROTEIN VPS41 HOMOLOG >gi 1839240
                   (U86663) aVps41p [Arabidopsis thaliana]
Seq. No.
                  313561
                  ymt700220888.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3600048
BLAST score
                  162
E value
                  2.0e-11
Match length
                  69
% identity
                  52
                   (AF080120) similar to hypothetical proteins in
NCBI Description
                  Schizosaccharomyces pombe (GB:Z98533) and C. elegans
                   (GB:Z48334 and Z78419) [Arabidopsis thaliana]
Seq. No.
                  313562
                  ymt700220894.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4006859
BLAST score
                  155
E value
                  1.0e-10
Match length
                  56
% identity
NCBI Description
                  (Z99707) putative protein [Arabidopsis thaliana]
```

Seq. No.

313563

ymt700220939.h1 Seq. ID

Method BLASTX NCBI GI g4468812

Method

NCBI GI

BLASTX

g1708059

```
BLAST score
                  245
E value
                  4.0e-21
Match length
                  78
% identity
                  67
NCBI Description
                  (AL035601) putative protein [Arabidopsis thaliana]
                  313564
Seq. No.
                  ymt700220952.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3462349
BLAST score
                  143
                  4.0e-09
E value
Match length
                  41
                  71
% identity
NCBI Description
                  (U56257) intronic protein 259 [Drosophila melanogaster]
Seq. No.
                  313565
                  ymt700220964.hl
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1168654
BLAST score
                  280
                  3.0e-25
E value
Match length
                  84
% identity
                  56
                  BETA-GALACTOSIDASE PRECURSOR (LACTASE)
NCBI Description
                  >gi 542198 pir S41889 beta-galactosidase (EC 3.2.1.23) - `
                  garden asparagus >gi 452712 emb CAA54525 (X77319)
                  beta-galactosidase [Asparagus officinalis]
Seq. No.
                  313566
                  ymt700220971.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3913437
BLAST score
                  231
E value
                  2.0e-19
                  77
Match length
                  61
% identity
                  PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA
NCBI Description
                  HELICASE >gi 1402875 emb CAA66825 (X98130) RNA helicase
                   [Arabidopsis thaliana] >gi_1495271_emb_CAA66613_ (X97970)
                  RNA helicase [Arabidopsis thaliana]
Seq. No.
                  313567
Seq. ID
                  ymt700221045.h1
Method
                  BLASTX
NCBI GI
                  g3360289
BLAST score
                  194
E value
                  3.0e-15
Match length
                  50
% identity
                  76
NCBI Description
                  (AF023164) leucine-rich repeat transmembrane protein kinase
                  1 [Zea mays]
Seq. No.
                  313568
Seq. ID
                  ymt700221077.h1
```

```
BLAST score
                  192
E value
                  3.0e-15
Match length
                  77
                  55
% identity
                  GLUTATHIONE REDUCTASE, CHLOROPLAST PRECURSOR (GR) (GRASE)
NCBI Description
                  >gi 481593 pir S38908 glutathione reductase (NADPH) (EC
                  1.6.4.2) - common tobacco (fragment)
                  >qi 431955 emb CAA53925 (X76293) glutathione reductase
                   (NADPH) [Nicotiana tabacum]
                  313569
Seq. No.
                  ymt700221095.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2182267
BLAST score
                  244
                  2.0e-24
E value
Match length
                  85
                  61
% identity
                  (L37359) lipoxygenase [Hordeum vulgare]
NCBI Description
Seq. No.
                  313570
                  ymt700221137.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3395436
BLAST score
                  162
E value
                  2.0e-11
Match length
                  84
% identity
                  38
NCBI Description
                  (AC004683) unknown protein [Arabidopsis thaliana]
Seq. No.
                  313571
                  ymt700221143.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3435196
BLAST score
                  401
                  2.0e-39
E value
Match length
                  87
                  76
% identity
                  (AF067773) glutamyl-tRNA synthetase [Arabidopsis thaliana]
NCBI Description
                  313572
Seq. No.
                  ymt700221155.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4467152
BLAST score
                  297
E value
                  1.0e-28
Match length
                  89
                   65
% identity
                  (AL035540) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  313573
```

 Seq. No.
 313573

 Seq. ID
 ymt700221210.h1

 Method
 BLASTX

 NCBI GI
 g4538961

BLAST score 244 E value 3.0e-23 Match length 81

Match length

% identity

37

100

```
% identity
NCBI Description
                  (ALO49488) isoleucine-tRNA ligase-like protein [Arabidopsis
                  thaliana]
                  313574
Seq. No.
                  ymt700221258.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3123165
BLAST score
                  204
                  2.0e-16
E value
Match length
                  54
                  59
% identity
                  ZINC FINGER PROTEIN 183 >gi 2274982 emb CAA66907 (X98253)
NCBI Description
                  ZNF183 [Homo sapiens] >gi 2341022 (AC002477) zinc-finger
                  protein [Homo sapiens]
Seq. No.
                  313575
Seq. ID
                  ymt700221343.h1
Method
                  BLASTX
NCBI GI
                  g1890577
BLAST score
                  194
                  3.0e-15
E value
Match length
                  55
% identity
                  71
NCBI Description
                  (X93175) xyloglucan endotransglycosylase (XET) [Hordeum
Seq. No.
                  313576
Seq. ID
                  ymt700221385.h1
Method
                  BLASTX
NCBI GI
                  q4567304
BLAST score
                  189
                  1.0e-14
E value
Match length
                  90
% identity
                  44
NCBI Description (AC005956) unknown protein [Arabidopsis thaliana]
Seq. No.
                  313577
Seq. ID
                  ymt700221443.h1
Method
                  BLASTN
NCBI GI
                  g435678
BLAST score
                  43
E value
                  4.0e-15
Match length
                  87
% identity
                  87
NCBI Description
                  L.esculentum Mill (cv. Rutgers) mRNA for ribosomal protein
Seq. No.
                  313578
Seq. ID
                  ymt700221479.h1
Method
                  BLASTN
                  g2062705
NCBI GI
BLAST score
                  37
                  2.0e-11
E value
```

44833

NCBI Description Human butyrophilin (BTF5) mRNA, complete cds

Seq. ID

Method

```
Seq. No.
                   313579
Seq. ID
                   ymt700221596.h2
Method
                   BLASTX
                   g168489
NCBI GI
BLAST score
                   407
E value
                   4.0e-40
Match length
                   77
                   100
% identity
NCBI Description
                   (M16902) glutathione S-transferase I [Zea mays] >gi_168491
                   (M16901) glutathione S-transferase I [Zea mays]
                   >gi_225458_prf 1303351A transferase,glutathione S [Zea
                   mays]
                   313580
Seq. No.
Seq. ID
                   ymt700221616.h1
Method
                   BLASTX
NCBI GI
                   g4006921
BLAST score
                   382
                   3.0e-37
E value
Match length
                   92
% identity
                   77
NCBI Description
                   (Z99708) putative protein [Arabidopsis thaliana]
Seq. No.
                   313581
Seq. ID
                   ymt700221624.h1
Method
                   BLASTX
NCBI GI
                   g3540184
BLAST score
                   204
E value
                   2.0e-16
Match length
                   89
% identity
                   51
NCBI Description
                  (AC004122) Similar to endoxylanases [Arabidopsis thaliana]
Seq. No.
                   313582
Seq. ID
                   ymt700221670.h1
Method
                   BLASTX
NCBI GI
                   q4538911
BLAST score
                   229
E value
                   3.0e-19
-Match length
                   59
% identity
                   73
NCBI Description
                   (AL049482) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   313583
Seq. ID
                   ymt700221681.h1
Method
                   BLASTN
NCBI GI
                   g22320
BLAST score
                   32
E value
                   5.0e-09
Match length
                   40
                   95
% identity
NCBI Description Maize H1 mRNA for H1 histone
Seq. No.
                   313584
```

ymt700221726.h1

BLASTX

```
NCBI GI
                   q4559353
BLAST score
                   385
E value
                  1.0e-37
Match length
                   88
% identity
                   85
                   (AC006585) putative extragenic suppressor protein
NCBI Description
                   [Arabidopsis thaliana]
                  313585
Seq. No.
Seq. ID
                  ymt700221765.h1
Method
                  BLASTX
NCBI GI
                  g4263717
BLAST score
                   343
                  1.0e-32
E value
Match length
                  93
% identity
                  71
                   (ACO06223) putative inositol polyphosphate 5-phosphatase
NCBI Description
                   [Arabidopsis thaliana]
                   313586
Seq. No.
                  ymt700221766.hl
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2253278
BLAST score
                  144
E value
                  3.0e-09
Match length
                   44
                  70
% identity
NCBI Description
                  (AF005492) RF2a [Oryza sativa]
Seq. No.
                  313587
                  ymt700221784.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4586053
BLAST score
                   275
E value
                  1.0e-24
Match length
                  86
% identity
                   66
NCBI Description
                  (AC007020) putative lacasse [Arabidopsis thaliana]
Seq. No.
                   313588
Seq. ID
                   ymt700221790.h1
Method
                  BLASTX
NCBI GI
                  q3786017
BLAST score
                   191
E value
                   8.0e-15
Match length
                   84
```

% identity 44

NCBI Description (AC005499) putative non-green plastid inner envelope membrane protein [Arabidopsis thaliana]

Seq. No. 313589

Seq. ID ymt700221819.h1

Method BLASTN NCBI GI g3821780 BLAST score 36 E value 6.0e-11 Match length 48

NCBI GI

E value

BLAST score

Match length

g2493131

4.0e-20

236

50

```
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                   313590
                   ymt700221847.h1
Seq. ID
Method
                   BLASTX
                   g1703129
NCBI GI
                   333
BLAST score
                   2.0e-31
E value
Match length
                   63
% identity
                   100
NCBI Description
                   ACTIN 11 >gi_2129522_pir__S68109 actin 11 - Arabidopsis
                   thaliana >gi 1002533 (U27981) actin-11 [Arabidopsis
                   thaliana]
                   313591
Seq. No.
                   ymt700221866.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4406812
BLAST score
                   277
E value
                   5.0e-25
Match length
                   59
% identity
                   81
NCBI Description
                   (AC006201) putative DNA binding protein [Arabidopsis
                   thaliana]
                   313592
Seq. No.
                   ymt700221913.h1
Seq. ID
Method
                   BLASTX
                   g3128168
NCBI GI
BLAST score
                   233
                   5.0e-20
E value
Match length
                   54
% identity
                   74
                   (AC004521) putative carboxyl-terminal peptidase
NCBI Description
                    [Arabidopsis thaliana]
Seq. No.
                   313593
Seq. ID
                   ymt700221930.h1
Method
                   BLASTX
NCBI GI
                   g129916
BLAST score
                   312
E value
                   7.0e-29
Match length
                   72
% identity
                   86
                   PHOSPHOGLYCERATE KINASE, CYTOSOLIC >gi_66911_pir__TVWTGY phosphoglycerate kinase (EC 2.7.2.3), cytosolic - wheat
NCBI Description
                   >gi_21835_emb_CAA33302_ (X15232) phosphoglycerate kinase
                    (AA 1 - 401) [Triticum aestivum]
Seq. No.
                   313594
Seq. ID
                   ymt700221950.h1
Method
                   BLASTX
```



Method BLASTX
NCBI GI g2583135
BLAST score 140
E value 6.0e-09
Match length 32
% identity 84

NCBI Description (AC002387) hypothetical protein [Arabidopsis thaliana]

>gi 3822216 (AF074948) FIL [Arabidopsis thaliana]

>gi 4322477 gb AAD16053 (AF087015) abnormal floral organs

protein [Arabidopsis thaliana]

Seq. No. 313596

Seq. ID ymt700221995.h1

Method BLASTX
NCBI GI g3522937
BLAST score 197
E value 3.0e-23
Match length 68
% identity 72

NCBI Description (AC004411) unknown protein [Arabidopsis thaliana]

Seq. No. 313597

Seq. ID ymt700222016.h1

Method BLASTX
NCBI GI g4559333
BLAST score 144
E value 3.0e-09
Match length 71

% identity 42

NCBI Description (AC007087) unknown protein [Arabidopsis thaliana]

Seq. No. 313598

Seq. ID ymt700222036.h1

Method BLASTX
NCBI GI g2191187
BLAST score 252
E value 5.0e-22
Match length 80
% identity 59

NCBI Description (AF007271) contains similarity to a DNAJ-like domain

[Arabidopsis thaliana]

Seq. No. 313599

Seq. ID ymt700222086.h1

Method BLASTX
NCBI GI g2649806
BLAST score 151
E value 4.0e-10
Match length 75
% identity 43

```
NCBI Description
                   (AE001049) diaminopimelate decarboxylase (lysA)
                   [Archaeoglobus fulgidus]
                  313600
Seq. No.
                  ymt700222121.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3367522
                  230
BLAST score
                  6.0e-22
E value
Match length
                  85
% identity
                  60
NCBI Description
                  (AC004392) EST gb_T04691 comes from this gene. [Arabidopsis
                  thaliana]
Seq. No.
                  313601
Seq. ID
                  ymt700222154.h1
Method
                  BLASTX
NCBI GI
                  g3193306
BLAST score
                  174
                  8.0e-13
E value
Match length
                  89
% identity
                  39
NCBI Description
                  (AF069300) contains similarity to Arabidopsis
                  membrane-associated salt-inducible-like protein
                  (GB:AL021637) [Arabidopsis thaliana]
Seq. No.
                  313602
Seq. ID
                  ymt700222159.h1
Method
                  BLASTX
NCBI GI
                  g4584527
BLAST score
                  185
E value
                  3.0e-14
Match length
                  71
% identity
                  54
NCBI Description
                  (AL049607) putative protein [Arabidopsis thaliana]
Seq. No.
                  313603
Seq. ID
                  ymt700222166.h1
Method
                  BLASTX
NCBI GI
                  q477819
BLAST score
                  194
E value
                  3.0e-15
Match length
                  62
% identity
                  63
NCBI Description
                  mitochondrial processing peptidase (EC 3.4.99.41) beta
                  chain precursor - potato >gi_410634_bbs_136741 cytochrome c
                  reductase-processing peptidase subunit II, MPP subunit II,
                  P53 [potatoes, var. Marfona, tuber, Peptide Mitochondrial,
                  530 aa]
```

Seq. No. 313604 Seq. ID ymt700222169.h1

Method BLASTX
NCBI GI g4204303
BLAST score 215
E value 8.0e-18

Match length 43

NCBI Description

[Zea mays]



```
% identity
NCBI Description
                   (AC003027) lcl prt seq No definition line found
                   [Arabidopsis thaliana]
                  313605
Seq. No.
Seq. ID
                  ymt700222173.h1
Method
                  BLASTX
NCBI GI
                  g4539394
BLAST score
                  195
E value
                  3.0e-15
Match length
                  88
                  43
% identity
NCBI Description
                  (AL035526) putative protein [Arabidopsis thaliana]
Seq. No.
                  313606
                  ymt700222176.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4585976
BLAST score
                  310
E value
                  5.0e-29
Match length
                  73
% identity
                  75
NCBI Description
                  (AC005287) Unknown protein [Arabidopsis thaliana]
Seq. No.
                  313607
Seq. ID
                  ymt700222180.h1
Method
                  BLASTX
                  g2492511
NCBI GI
BLAST score
                  208
E value
                  4.0e-17
Match length
                  61
% identity
                  67
NCBI Description CELL DIVISION PROTEIN FTSH HOMOLOG 2
                  >gi_1652282_dbj_BAA17205_ (D90904) cell division protein
                  FtsH [Synechocystis sp.]
Seq. No.
                  313608
Seq. ID
                  ymt700222207.h1
Method
                  BLASTX
NCBI GI
                  q2460251
BLAST score
                  342
                  1.0e-32
E value
Match length
                  84
% identity
                  76
NCBI Description (AF020791) ferrochelatase [Hordeum vulgare]
Seq. No.
                  313609
Seq. ID
                  ymt700222232.h1
Method
                  BLASTX
NCBI GI
                  q3851003
BLAST score
                  246
E value
                  3.0e-21
Match length
                  48
% identity
                  96
```

(AF069910) pyruvate dehydrogenase E1 beta subunit isoform 3

```
313610
Seq. No.
Seq. ID
                  ymt700222287.h1
Method
                  BLASTN
NCBI GI
                  g2589161
BLAST score
                   64
E value
                  1.0e-27
Match length
                  76
% identity
                  96
NCBI Description Zea mays mRNA for aldehyde oxidase, complete cds
Seq. No.
                  313611
Seq. ID
                  ymt700222331.h1
Method
                  BLASTN
                  g1220422
NCBI GI
BLAST score
                  193
E value
                  1.0e-104
Match length
                  216
% identity
                  98
NCBI Description Zea mays ubiquitin (MUB14) mRNA, 3' end
Seq. No.
                  313612
Seq. ID
                  ymt700222343.h1
Method
                  BLASTX
NCBI GI
                  g3776005
BLAST score
                  271
E value
                  2.0e-24
Match length
                  51
% identity
                  100
NCBI Description (AJ010466) RNA helicase [Arabidopsis thaliana]
Seq. No.
                  313613
Seq. ID
                  ymt700222346.h1
Method
                  BLASTX
NCBI GI
                  g400983
BLAST score
                  263
E value
                  3.0e-23
Match length
                  64
% identity
                  78
NCBI Description
                  50S RIBOSOMAL PROTEIN L11, CHLOROPLAST PRECURSOR (CL11)
                  >gi_279648_pir__R5SP11 ribosomal protein L11 precursor -
                  spinach >gi_21313 emb CAA39950 (X56615) ribosomal protein
                  L11 [Spinacia oleracea]
Seq. No.
                  313614
Seq. ID
                  ymt700222373.h1
Method
                  BLASTX
NCBI GI
                  g1084481
BLAST score
                  327
E value
                  9.0e-31
Match length
                  91
% identity
                  74
NCBI Description heat shock protein 70 - Maize
Seq. No.
                  313615
Seq. ID
                  ymt700222404.h1
Method
```

44840

BLASTN

g168406

NCBI GI

E value

Match length

% identity

4.0e-21

47

```
BLAST score
E value
                  7.0e-26
Match length
                  125
% identity
                  87
                  Z.mays alcohol dehydrogenase (ADH-1 C-m allele) gene,
NCBI Description
                  complete cds
Seq. No.
                  313616
                  ymt700222581.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3747049
BLAST score
                  68
E value
                  3.0e-30
Match length
                  128
% identity
                  88
NCBI Description
                  Zea mays ribosomal protein L26 mRNA, partial cds
                  313617
Seq. No.
                  ymt700222593.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2443329
BLAST score
                  246
                  3.0e-21
E value
Match length
                  67
% identity
                  70
NCBI Description
                  (D86122) Mei2-like protein [Arabidopsis thaliana]
                  313618
Seq. No.
Seq. ID
                  ymt700222618.h1
Method
                  BLASTX
NCBI GI
                  g3250695
BLAST score
                  216
E value
                  9.0e-18
Match length
                  83
% identity
                  53
NCBI Description
                  (AL024486) putative protein [Arabidopsis thaliana]
Seq. No.
                  313619
Seq. ID
                  ymt700222647.h1
Method
                  BLASTX
                  g3757523
NCBI GI
BLAST score
                  198
E value
                  7.0e-16
Match length
                  60
% identity
                  63
NCBI Description
                  (AC005167) putative transportin [Arabidopsis thaliana]
Seq. No.
                  313620
Seq. ID
                  ymt700222668.h1
Method
                  BLASTX
NCBI GI
                  g2341031
BLAST score
                  245
```

44841

NCBI Description (AC000104) F19P19.10 [Arabidopsis thaliana]

Seq. No.

Seq. ID

Method

NCBI GI

313626

BLASTX

g1076813

ymt700222952.h1

```
313621
Seq. No.
                  ymt700222692.h1
Seq. ID
Method :
                  BLASTX
NCBI GI
                   g629792
BLAST score
                   170
                  1.0e-12
E value
Match length
                   39
                  77
% identity
                  cysteine proteinase - rice >gi 530335 emb CAA56844
NCBI Description
                   (X80876) cysteine protease [Oryza sativa]
Seq. No.
                   313622
                   ymt700222722.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4432828
BLAST score
                   248
                   1.0e-21
E value
Match length
                   83
                   55
% identity
                  (AC006593) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   313623
                   ymt700222741.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g516553
BLAST score
                ·· 130
E value
                   5.0e-67
                  239
Match length
% identity
                   89
NCBI Description
                  Zea mays B73 cyclin IaZm mRNA, partial cds
                   313624
Seq. No.
                   ymt700222763.h1
Seq. ID
Method
                   BLASTX
                   g554565
NCBI GI
BLAST score
                   459
E value
                   3.0e-46
Match length
                   87
% identity
                   100
NCBI Description
                  (M24889) glutathione S-transferase [Artificial gene]
Seq. No.
                   313625
                   ymt700222827.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1053047
BLAST score
                   441
                   4.0e-44
E value
Match length
                   90
% identity
                   99
NCBI Description
                   (U38425) histone H3 [Glycine max] >gi 1053049 (U38426)
                   histone H3 [Glycine max] >gi 1053051 (U38427) histone H3
                   [Glycine max]
```

BLAST score

Match length

E value

36

72

2.0e-11



```
BLAST score
E value
                   3.0e-46
Match length
                   90
                   99
% identity
NCBI Description initiator-binding protein - maize
                  313627
Seq. No.
                  ymt700222964.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4249382
BLAST score
                   325
E value
                   2.0e-30
Match length
                   91
% identity
                   71
                  (AC005966) Strong similarity to gi_3337350 F13P17.3
NCBI Description
                   putative permease from Arabidopsis thaliana BAC
                   gb AC004481. [Arabidopsis thaliana]
Seq. No.
                   313628
Seq. ID
                   ymt700223014.hl
Method
                   BLASTX
                  g3643598
NCBI GI
BLAST score
                   149
E value
                   6.0e-10
Match length
                   42
% identity
                   60
                   (AC005395) putative poly(A) polymerase [Arabidopsis
NCBI Description
                   thaliana]
                   313629
Seq. No.
                   ymt700223029.h1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g4321977
BLAST score
                   167
E value
                   4.0e-89
Match length
                   199
% identity
                   96
NCBI Description
                  Zea mays beta-amylase (Amy2) gene, complete cds
Seq. No.
                   313630
Seq. ID
                   ymt700223053.h1
Method
                   BLASTX
NCBI GI
                   q4580394
BLAST score
                   195
E value
                   3.0e-15
Match length
                   88
% identity
                   49
NCBI Description
                   (AC007171) putative fatty acid elongase [Arabidopsis
                   thaliana]
Seq. No.
                   313631
Seq. ID
                   ymt700223088.h1
Method
                   BLASTN
                   g22292
NCBI GI
```



% identity

NCBI Description Z.mays mRNA for glycine-rich protein

Seq. No.

313632

Seq. ID

ymt700223103.h1

Method NCBI GI BLASTX q400989

BLAST score

177

E value

3.0e-13

Match length % identity

60 55

NCBI Description

50S RIBOSOMAL PROTEIN L24, CHLOROPLAST PRECURSOR (CL24)

>gi_322771_pir__A45113 ribosomal protein L24 precursor common tobacco >gi_170273 (M87838) ribosomal protein L24 [Nicotiana tabacum] >gi 170324 (M87839) ribosomal protein

L24 [Nicotiana tabacum]

Seq. No.

313633

Seq. ID

ymt700223122.h1

Method NCBI GI BLAST score BLASTX g1706103

E value

220 3.0e-18

Match length % identity

81 54

NCBI Description

CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD

SUBUNIT (CPSF 100 KD SUBUNIT) >gi_1363022_pir__A56351 cleavage and polyadenylation specificity factor 100K chain - bovine >gi_599683_emb_CAA53535_ (X75931) Cleavage and Polyadenylation specificity factor (CPSF) 100kD subunit

[Bos taurus]

Seq. No.

313634

Seq. ID

ymt700223141.h1

Method NCBI GI BLAST score BLASTX q2244793 229

E value Match length 2.0e-19

% identity

81 51

NCBI Description

(Z97336) TMV resistance protein homolog [Arabidopsis

thaliana]

Seq. No.

313635

Seq. ID

ymt700223164.h1

Method BLASTN NCBI GI g2826899 BLAST score 123 8.0e-63 E value

Match length % identity

275

NCBI Description

Oryza sativa mRNA for DNA polymerase alpha catalytic

subunit, complete cds

Seq. No.

313636

Seq. ID

ymt700223178.h1

Method

BLASTX



```
g4646206
NCBI GI
                  172
BLAST score
E value
                  1.0e-12
                  51
Match length
% identity
                  (AC007230) Contains similarity to gb_D13630 KIAA0005 gene
NCBI Description
                  from Homo sapiens. ESTs gb_T45345, gb_T21086, gb_R90360,
                  gb T20468, gb T45191 and gb AI100459 come from this gene.
                  [Arabidopsis thaliana]
                  313637
Seq. No.
                  ymt700223181.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g477819
                  270
BLAST score
                  4.0e-24
E value
Match length
                  87
                  59
% identity
NCBI Description mitochondrial processing peptidase (EC 3.4.99.41) beta
                  chain precursor - potato >gi 410634 bbs 136741 cytochrome c
                  reductase-processing peptidase subunit II, MPP subunit II,
                  P53 [potatoes, var. Marfona, tuber, Peptide Mitochondrial,
                  530 aa]
Seq. No.
                  313638
                  ymt700223209.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3513727
BLAST score
                  216
E value
                  8.0e-18
Match length
                  63
% identity
                  68
                  (AF080118) contains similarity to TPR domains (Pfam:
NCBI Description
                  TPR.hmm: score: 11.15) and kinesin motor domains (Pfam:
                  kinesin2.hmm, score: 17.49, 20.52 and 10.94) [Arabidopsis
                  thaliana] >gi_4539358_emb_CAB40052.1_ (AL049525) putative
                  protein [Arabidopsis thaliana]
Seq. No.
                  313639
                  ymt700223211.h1
Seq. ID
Method
                  BLASTX
                  g3386620
NCBI GI
BLAST score
                  389
E value
                  4.0e-38
Match length
                  81
% identity
                  85
```

(AC004665) hypothetical protein [Arabidopsis thaliana] NCBI Description

Seq. No. 313640 Seq. ID ymt700223225.h1 Method BLASTX NCBI GI q2130137 BLAST score 304

E value 4.0e-28 Match length 85 % identity 73

NCBI Description homeotic protein Hox2b - maize >gi_1143707_emb_CAA61910_

% identity



(X89761) Hox2b [Zea mays]

```
Seq. No.
                   313641
                   ymt700223236.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4455326
BLAST score
                   320
                   5.0e-30
E value
Match length
                  75
% identity
                  72
NCBI Description
                  (AL035525) putative protein [Arabidopsis thaliana]
Seq. No.
                  313642
Seq. ID
                  ymt700223246.h1
Method
                  BLASTX
NCBI GI
                  g2833460
BLAST score
                   167
E value
                   5.0e-12
Match length
                  54
% identity
                   59
NCBI Description RIBOFLAVIN-SPECIFIC DEAMINASE >gi 1001153 dbj BAA10295
                   (D64001) riboflavin biosynthesis protein [Synechocystis
                   sp.]
Seq. No.
                  313643
Seq. ID
                   ymt700223252.h1
Method
                  BLASTX
                  g3319355
NCBI GI
BLAST score
                   264
                   4.0e-28
E value
Match length
                  85
% identity
                   74
NCBI Description
                  (AF077407) similar to chaperonin containing TCP-1 complex
                   gamma chain [Arabidopsis thaliana]
Seq. No.
                   313644
Seq. ID
                   ymt700223264.h1
Method
                  BLASTX
NCBI GI
                  g131770
BLAST score
                   204
E value
                   2.0e-16
Match length
                   54
% identity
                   70
NCBI Description
                  40S RIBOSOMAL PROTEIN S9 (40S RIBOSOMAL PROTEIN 1024)
                   (VEGETATIVE SPECIFIC PROTEIN V12) >gi_70880_pir__R3D024
                   ribosomal protein S9.e - slime mold (Dictyostelium
                   discoideum) >gi_7353_emb_CAA29844_ (X06636) rp1024 protein
                   [Dictyostelium discoideum]
Seq. No.
                  313645
Seq. ID
                  ymt700223302.h1
Method
                  BLASTX
NCBI GI
                  g1335862
BLAST score
                  438
E value
                  8.0e-44
Match length
                  89
                  97
```





```
NCBI Description (U42608) clathrin heavy chain [Glycine max]
Seq. No.
                  313646
Seq. ID
                  ymt700223319.h1
Method
                  BLASTX
NCBI GI
                  g4455251
BLAST score
                  255
E value
                  2.0e-22
                  85
Match length
```

% identity NCBI Description (AL035523) magnesium-protoporphyrin IX

methyltransferase-like protein [Arabidopsis thaliana]

Seq. No. 313647 Seq. ID ymt700223366.h1 Method BLASTX NCBI GI q2827666

66

BLAST score 216 E value 1.0e-17 Match length 83 % identity 47

NCBI Description (AL021637) hypothetical protein [Arabidopsis thaliana]

>gi_2982429_emb_CAA18237_ (AL022224) hypothetical protein

[Arabidopsis thaliana]

Seq. No. 313648

Seq. ID ymt700223384.h1

Method BLASTX NCBI GI g1350680 BLAST score 326 E value 1.0e-30 Match length 69 % identity 87

NCBI Description 60S RIBOSOMAL PROTEIN L1

Seq. No. 313649

Seq. ID ymt700223386.h1

Method BLASTX NCBI GI g122007 BLAST score 145 2.0e-09 E value Match length 35 % identity 83

NCBI Description

<code>HISTONE H2A > gi_100161_pir__ S11498 histone H2A - parsley > gi_20448_emb_CAA37828_ (X53831) H2A histone protein (AA 1</code>

- 149) [Petroselinum crispum]

Seq. No. 313650

Seq. ID ymt700223420.h1

Method BLASTX NCBI GI q417570 BLAST score 327 E value 9.0e-31 Match length 87 70 % identity

DIHYDROOROTATE DEHYDROGENASE PRECURSOR (DIHYDROOROTATE NCBI Description

OXIDASE) (DHODEHASE) >gi_478676 pir \$23762 dihydroorotate

oxidase (EC 1.3.3.1) - Arabidopsis thaliana >gi_16449_emb_CAA44695_ (X62909) dihydroorotate dehydrogenase [Arabidopsis thaliana]

Seq. No. 313651

Seq. ID ymt700223439.h1

Method BLASTX
NCBI GI g2708532
BLAST score 149
E value 6.0e-10
Match length 48
% identity 54

NCBI Description (AF029351) putative RNA binding protein [Nicotiana tabacum]

Seq. No. 313652

Seq. ID ymt700223441.h1

Method BLASTX
NCBI GI g2500548
BLAST score 154
E value 1.0e-10
Match length 57
% identity 54

NCBI Description DIS3 PROTEIN HOMOLOG >gi_3873904_emb_CAA94677_ (Z70718)

predicted using Genefinder; Similarity to S.pombe mitotic control protein DIS3 (SW:DIS3_SCHPO); cDNA EST EMBL:D34017 comes from this gene; cDNA EST EMBL:D37007 comes from this

gene; cDNA EST EMBL: D67423 comes from this

Seq. No. 313653

Seq. ID ymt700223535.h1

Method BLASTX
NCBI GI g1127575
BLAST score 375
E value 2.0e-36
Match length 84
% identity 80

NCBI Description (U33817) dhurrinase [Sorghum bicolor]

Seq. No. 313654

Seq. ID ymt700223582.h1

Method BLASTX
NCBI GI g2459441
BLAST score 149
E value 1.0e-15
Match length 86
% identity 46

NCBI Description (AC002332) putative SWI/SNF complex subunit BAF170

[Arabidopsis thaliana]

Seq. No. 313655

Seq. ID ymt700223593.h1

Method BLASTN
NCBI GI g3821780
BLAST score 37
E value 2.0e-11
Match length 37

% identity 100



```
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                   313656
Seq. ID
                   ymt700223615.h1
Method
                   BLASTX
NCBI GI
                   g4454051
BLAST score
                   203
E value
                   3.0e-16
Match length
                   53
% identity
                   60
NCBI Description
                   (AL035394) putative polygalacturonase [Arabidopsis
                   313657
Seq. No.
Seq. ID
                   ymt700223706.h1
Method
                   BLASTX
NCBI GI
                   g4204304
BLAST score
                   421
E value
                   8.0e-42
Match length
                   78
% identity
                   90
NCBI Description
                   (AC003027) lcl_prt_seq No definition line found
                   [Arabidopsis thaliana]
Seq. No.
                   313658
Seq. ID
                   ymt700223759.h1
Method
                  BLASTX
NCBI GI
                   q4006900
BLAST score
                   180
E value
                   1.0e-13
Match length
                   67
% identity
                   51
NCBI Description
                  (Z99708) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  313659
Seq. ID
                  ymt700223771.h1
Method -
                  BLASTX
NCBI GI
                  q4206209
BLAST score
                  223
E value
                  1.0e-18
Match length
                  69
                  65
% identity
NCBI Description
                   (AF071527) putative glucan synthase component [Arabidopsis
                  thaliana] >gi 4263042 gb AAD15311 (AC005142) putative
                  glucan synthase component [Arabidopsis thaliana]
                  313660
Seq. No.
Seq. ID
                  ymt700223783.h1
Method
                  BLASTX
NCBI GI
                  g3819699
BLAST score
                  327
```

E value 8.0e-31 Match length 86 % identity 74

NCBI Description (AJ009609) BnMAP4K alpha2 [Brassica napus]

Seq. No. 313661



```
ymt700223842.h1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1703012
                   186
BLAST score
E value
                   3.0e-14
Match length
                   81
                   48
% identity
NCBI Description
                  CYTOSOLIC PURINE 5'-NUCLEOTIDASE >gi 1079484 pir JC2436
                   5'-nucleotidase (EC 3.1.3.5) - human
                  >gi 633071_dbj_BAA07529_ (D38524) 5'-nucleotidase [Homo
                   sapiens]
                   313662
Seq. No.
Seq. ID
                   ymt700223867.h1
Method
                  BLASTX
                   q4218120
NCBI GI
BLAST score
                   246
                   3.0e-21
E value
                   73
Match length
% identity
                   63
NCBI Description
                   (AL035353) Proline-rich APG-like protein [Arabidopsis
                   thaliana]
Seq. No.
                   313663
                   ymt700223895.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3163946
BLAST score
                   478
E value
                   2.0e-48
Match length
                   89
% identity
                   100
NCBI Description
                  (AJ005599) alpha-tubulin 1 [Eleusine indica]
Seq. No.
                   313664
Seq. ID
                   ymt700223906.h1
Method
                  BLASTX
NCBI GI
                  q3075398
BLAST score
                   286
E value
                   6.0e-26
                  71
Match length
                  70
% identity
NCBI Description
                   (AC004484) unknown protein [Arabidopsis thaliana]
                   313665
Seq. No.
Seq. ID
                  ymt700223944.h1
Method
                  BLASTX
NCBI GI
                  g3935168
BLAST score
                  181
E value
                  1.0e-13
                  73
Match length
% identity
                  52
NCBI Description
                  (AC004557) F17L21.11 [Arabidopsis thaliana]
Seq. No.
                  313666
Seq. ID
                  ymt700223951.h1
```

44850

BLASTX

g3377851

Method NCBI GI

```
BLAST score
                  6.0e-15
E value
Match length
                  80
% identity
                  44
                   (AF076274) contains similarity to ATPases associated with
NCBI Description
                  various cellular activities (Pfam: AAA.hmm, score: 155.05)
                   [Arabidopsis thaliana]
                  313667
Seq. No.
Seq. ID
                  ymt700223967.h1
Method
                  BLASTX
NCBI GI
                  q3360291
BLAST score
                  184
E value
                  5.0e-14
Match length
                  90
                  50
% identity
                   (AF023165) leucine-rich repeat transmembrane protein kinase
NCBI Description
                  2 [Zea mays]
                  313668
Seq. No.
                  ymt700223974.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2326946
BLAST score
                   233
                   1.0e-128
E value
                   247
Match length
% identity
NCBI Description Z.mays mRNA for chlorophyll a/b-binding protein CP29
                   313669
Seq. No.
Seq. ID
                   ymt700223977.h1
Method
                   BLASTX
NCBI GI
                  q2934902
BLAST score
                   441
E value
                   4.0e-44
Match length
                   92
% identity
                   99
NCBI Description
                   (AF039304) cpSecY [Zea mays]
Seq. No.
                   313670
Seq. ID
                   ymt700224008.h1
Method
                   BLASTX
NCBI GI
                   g729671
BLAST score
                   215
E value
                   4.0e-25
Match length
                   87
% identity
NCBI Description HISTONE H2A >qi 473603 (U08225) histone H2A [Zea mays]
Seq. No.
                   313671
                   ymt700224014.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1653395
BLAST score
                   344
E value
                   9.0e-33
                   88
Match length
```

76

% identity

Seq. ID

```
NCBI Description (D90913) PET112 [Synechocystis sp.]
                    313672
Seq. No.
Seq. ID
                    ymt700224084.hl
Method
                    BLASTX
                    g3132477
NCBI GI
BLAST score
                    321
                    4.0e-30
E value
Match length
                    85
                    73
% identity
                    (AC003096) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                    313673
                    ymt700224128.h1
Seq. ID
Method
                    BLASTX
                    g2506793
NCBI GI
                    200
BLAST score
                    5.0e-16
E value
Match length
                    78
                    59
% identity
                    KINESIN-LIKE PROTEIN OSM-3 >gi_1362570_pir__S54351 kinesin osm-3 - Caenorhabditis elegans >gi_1490195_dbj_BAA07612_
NCBI Description
                    (D38632) OSM-3 (kinesin protein) [Caenorhabditis elegans]
Seq. No.
                    313674
                    ymt700224151.h1
 Seq. ID
Method
                    BLASTX
                    g4585998
 NCBI GI
                    174
 BLAST score
E value
                    9.0e-13
                    49
Match length
                    69
 % identity
                    (AC005287) Hypothetical protein [Arabidopsis thaliana]
 NCBI Description
                    313675
Seq. No.
                    ymt700224178.h1
 Seq. ID
 Method
                    BLASTX
                    q2827143
 NCBI GI
 BLAST score
                     195
 E value
                     3.0e-15
                     56
 Match length
 % identity
                     64
                     (AF027174) cellulose synthase catalytic subunit
 NCBI Description
                     [Arabidopsis thaliana]
 Seq. No.
                     313676
 Seq. ID
                     ymt700224188.h1
 Method
                    BLASTN
 NCBI GI
                     g3821780
 BLAST score
                     35
 E value
                     2.0e-10
 Match length
                     35
 % identity
                     100
 NCBI Description Xenopus laevis cDNA clone 27A6-1
                     313677
 Seq. No.
```

44852

ymt700224189.h1

```
BLASTX
Method
NCBI GI
                   q3426039
                   251
BLAST score
                   7.0e-22
E value
Match length
                   78
                   58
% identity
                   (AC005168) unknown protein [Arabidopsis thaliana]
NCBI Description
                   313678
Seq. No.
                   ymt700224194.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g548774
BLAST score
                   198
E value
                   1.0e-19
                   55
Match length
                   98
% identity
                   60S RIBOSOMAL PROTEIN L7A >gi_542158_pir__S38360 ribosomal protein L7a - rice >gi_303855_dbj_BAA02156_ (D12631)
NCBI Description
                   ribosomal protein L7A [Oryza sativa]
                   313679
Seq. No.
                   ymt700224202.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3061308
BLAST score
                   233
E value
                   9.0e-20
Match length
                   86
                   56
% identity
                   (AB006074) topoisomerase III [Mus musculus]
NCBI Description
                   313680
Seq. No.
                    ymt700224213.h1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g747914
BLAST score
                    117
E value
                    3.0e-59
Match length
                   237
% identity
                    98
NCBI Description Z.mays CaM1 mRNA for calmodulin
                    313681
Seq. No.
                    ymt700224254.h1
Seq. ID
Method
                    BLASTX
NCBI GI
                    g3157949
BLAST score
                    248
                    6.0e-22
E value
                    85
Match length
                    67
% identity
                    (AC002131) Similar to glucan endo-1,3-beta-D-glucosidase
NCBI Description
                    precursor gb_Z28697 from Nicotiana tabacum. ESTs gb Z18185
                    and gb AA605362 come from this gene. [Arabidopsis thaliana]
```

Seq. No. 313682 Seq. ID ymt700224334.h1

Method BLASTX
NCBI GI g2191152
BLAST score 194

```
4.0e-15
E value
Match length
                   67
% identity
                   57
                   (AF007269) A IG002N01.31 gene product [Arabidopsis
NCBI Description
                   thaliana]
                   313683
Seq. No.
Seq. ID
                   ymt700224336.h1
Method
                   BLASTN
                   g3821780
NCBI GI
BLAST score
                   37
                   2.0e-11
E value
Match length
                   37
% identity
                   100
NCBI Description Xenopus laevis cDNA clone 27A6-1
```

 Seq. No.
 313684

 Seq. ID
 ymt700224356.h1

 Method
 BLASTX

 NCBI GI
 g113621

 BLAST score
 451

 E value
 3.0e-45

Match length 90 % identity 98

NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME

>gi_68196_pir__ADZM fructose-bisphosphate aldolase (EC
4.1.2.13), cytosolic - maize >gi_168420 (M16220) aldolase
[Zea mays] >gi_295850_emb_CAA31366_ (X12872) fructose
bisphosphate aldolase [Zea mays] >gi_225624_prf__1307278A

cytoplasmic aldolase [Zea mays]

Seq. No. 313685

Seq. ID ymt700224371.h1

Method BLASTX
NCBI GI g2149640
BLAST score 196
E value 2.0e-15
Match length 57
% identity 65

NCBI Description (U91995) Argonaute protein [Arabidopsis thaliana]

Seq. No. 313686

Seq. ID ymt700224376.h1

Method BLASTX
NCBI GI g548770
BLAST score 389
E value 4.0e-38
Match length 80
% identity 91

NCBI Description 60S RIBOSOMAL PROTEIN L3 >gi_481228_pir__S38359 ribosomal

protein L3 - rice >gi 303853 dbj_BAA02155_ (D12630)

ribosomal protein L3 [Oryza sativa]

Seq. No. 313687

Seq. ID ymt700224387.h1

Method BLASTX NCBI GI g3559805

```
BLAST score
                   3.0e-13
E value
                   33
Match length
                   85
% identity
                   (AJ006787) putative phytochelatin synthetase [Arabidopsis
NCBI Description
                   thaliana]
                   313688
Seq. No.
                   ymt700224419.h1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g1857254
BLAST score
                   37
                   7.0e-12
E value
Match length
                   37
% identity
                   100
                   Zea mays transposon MuDRzc MURAZC (mudrAzc) and MURBZC
NCBI Description
                   (mudrBzc) genes, complete cds
Seq. No.
                   313689
Seq. ID
                   ymt700224514.h1
Method
                   BLASTX
NCBI GI
                   q3377810
BLAST score
                   261
E value
                   5.0e-23
Match length
                   91
                   58
% identity
                   (AF076275) contains similarity to glutaredoxins
NCBI Description
                   [Arabidopsis thaliana]
                   313690
Seq. No.
Seq. ID
                   ymt700224526.h1
Method
                   BLASTX
NCBI GI
                   g2344904
BLAST score
                   192
                   6.0e-15
E value
Match length
                   87
% identity
                   46
                   (AC002388) giberellin beta-hydroxylase isolog, 5' partial
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   313691
Seq. ID
                   ymt700224537.h1
Method
                   BLASTX
                   g70774
NCBI GI
BLAST score
                   372
E value
                   6.0e-36
Match length
                   84
% identity
                   93
```

Seq. No. 313692

NCBI Description

Seq. ID ymt700224549.h1

[Triticum aestivum]

Method BLASTX
NCBI GI g2829910
BLAST score 390
E value 4.0e-38

histone H4 (TH091) - wheat >gi 170747 (M12277) histone H4

NCBI Description



```
96
Match length
                   68
% identity
                   (AC002291) Unknown protein, contains regulator of
NCBI Description
                   chromosome condensation motifs [Arabidopsis thaliana]
                   313693
Seq. No.
Seq. ID
                   ymt700224559.h1
                   BLASTX
Method
NCBI GI
                   q3355717
BLAST score
                   317
                   6.0e-43
E value
Match length
                   94
% identity
                   94
                  (Y13053) seryl-tRNA synthetase [Zea mays]
NCBI Description
                   313694
Seq. No.
Seq. ID
                   ymt700224574.h1
Method
                   BLASTX
                   g4376203
NCBI GI
BLAST score
                   167
                   5.0e-12
E value
Match length
                   66
% identity
                   55
                   (U35226) putative cytochrome P-450 [Nicotiana
NCBI Description
                   plumbaginifolia]
Seq. No.
                   313695
Seq. ID
                   ymt700224591.h1
Method
                   BLASTX
NCBI GI
                   g3551219
BLAST score
                   401
                   2.0e-39
E value
Match length
                   90
                   73
% identity
                   (AB012627) blue-light photoreceptor [Adiantum
NCBI Description
                   capillus-veneris] >gi 3551225 dbj BAA32811 (AB012630)
                   blue-light photoreceptor [Adiantum capillus-veneris]
                   313696
Seq. No.
                   ymt700224619.h1
Seq. ID
Method
                   BLASTX
                   g2213632
NCBI GI
BLAST score
                   160
                   3.0e-11
E value
                   50
Match length
                   60
% identity
                   (AC000103) F21J9.24 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   313697
                   ymt700224681.h1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4586246
BLAST score
                   151
E value
                   2.0e-21
Match length
                   75
                   62
% identity
```

(AL049640) putative protein [Arabidopsis thaliana]

```
Seq. No.
                   313698
                   ymt700224703.h1
Seq. ID
Method
                  BLASTX
                   g3292816
NCBI GI
                   218
BLAST score
E value
                   5.0e-26
                   81
Match length
% identity
                   (AL031018) putative fizzy-related protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   313699
```

Seq. ID ymt700224716.h1
Method BLASTX
NCBI GI g122106
BLAST score 251
E value 8.0e-22
Match length 53
% identity 96

NCBI Description HISTONE H4 >gi_70771_pir__HSZM4 histone H4 - maize >gi_81642_pir__S06904 histone H4 - Arabidopsis thaliana

>gi_2119028_pir__S60475 histone H4 - garden pea

>gi_21795_emb_CAA24924_ (X00043) histone H4 [Triticum aestivum] >gi_166740 (M17132) histone H4 [Arabidopsis thaliana] >gi_166742 (M17133) histone H4 [Arabidopsis thaliana] >gi_168499 (M36659) histone H4 (H4C13) [Zea mays]

>gi_168501 (M13370) histone H4 [Zea mays] >gi_168503

(M13377) histone H4 [Zea mays] >gi 498898 (U10042) histone

H4 homolog [Pisum sativum] >gi_1806285 emb_CAB01914_ (Z79638) histone H4 homologue [Sesbania rostrata] >gi_3927823 (AC005727) histone H4 [Arabidopsis thaliana] >gi_4580385 gb_AAD24364.1_AC007184_4 (AC007184) histone H4 [Arabidopsis thaliana] >gi_225838_prf__1314298A histone H4

[Arabidopsis thaliana]

Seq. No. 313700

Seq. ID ymt700224717.h1

Method BLASTX
NCBI GI g479413
BLAST score 138
E value 8.0e-09
Match length 31
% identity 84

NCBI Description myosin-like protein - Arabidopsis thaliana

Seq. No. 313701

Seq. ID ymt700224721.h1

Method BLASTX
NCBI GI g3337350
BLAST score 241
E value 1.0e-20

Match length 48 % identity 90

NCBI Description (AC004481) putative permease [Arabidopsis thaliana]

Seq. No. 313702

```
vmt700224793.h1
Seq. ID
                  BLASTX
Method
                  q3914996
NCBI GI
BLAST score
                  243
                  5.0e-21
E value
                  72
Match length
% identity
                  PHOSPHOSERINE AMINOTRANSFERASE PRECURSOR (PSAT)
NCBI Description
                  >gi_1665831_dbj_BAA13640_ (D88541) phosphoserine
                  aminotransferase [Arabidopsis thaliana]
                  >gi_2804260_dbj_BAA24441_ (AB010408) phosphoserine
                  aminotransferase [Arabidopsis thaliana]
                  >gi 3367581_emb_CAA20033_ (AL031135) phosphoserine
                  aminotransferase [Arabidopsis thaliana]
                  313703
Seq. No.
                  ymt700224804.h1
Seq. ID
Method
                  BLASTX
                  q3283026
NCBI GI
                  158
BLAST score
                  7.0e-11
E value
                  57
Match length
% identity
                  (AF051562) putative transposase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  313704
                  ymt700224851.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2244740
                  340
BLAST score
                  3.0e-32
E value
                  86
Match length
% identity
NCBI Description (D88417) endo-1,4-beta-glucanase [Gossypium hirsutum]
Seq. No.
                  313705
Seq. ID
                  ymt700224868.h1
Method
                  BLASTX
NCBI GI
                  g1617219
BLAST score
                  251
                  7.0e-22
E value
Match length
                  87
% identity
                  54
                   (X99301) CPD photolyase [Arabidopsis thaliana] >gi_2984707
NCBI Description
                   (AF053365) type II CPD photolyase PHR1 [Arabidopsis
                   thaliana]
Seq. No.
                  313706
                   ymy700282428.h2
Seq. ID
Method
                  BLASTX
                  g4204312
NCBI GI
                  150
BLAST score
                  3.0e-10
E value
```

44858

[Arabidopsis thaliana]

(AC003027) lcl prt seq No definition line found

37

81

Match length % identity

NCBI Description

```
Seq. No.
                   313707
Seq. ID
                   ymy700282461.h2
Method
                   BLASTX
NCBI GI
                   g3820531
BLAST score
                   205
E value
                   2.0e-16
Match length
                   58
```

% identity NCBI Description (AF072736) beta-glucosidase [Pinus contorta]

Seq. No. 313708 Seq. ID ymy700282469.h2 Method BLASTX q548492 NCBI GI 373 BLAST score 6.0e-47 E value

Match length 103 % identity 89

EXOPOLYGALACTURONASE PRECURSOR (EXOPG) (PECTINASE) NCBI Description

(GALACTURAN 1,4-ALPHA-GALACTURONIDASE)

>gi_629853_pir__S30066 polygalacturonase - maize

>gi_288379_emb_CAA45751_ (X64408) polygalacturonase [Zea

mays]

313709 Seq. No.

ymy700282473.h2 Seq. ID

Method BLASTX NCBI GI q3820531 243 BLAST score 5.0e-21 E value 59 Match length 69 % identity

NCBI Description (AF072736) beta-glucosidase [Pinus contorta]

Seq. No. 313710

Seq. ID yne700378416.hl

Method BLASTX NCBI GI q1082633 BLAST score 189 E value 8.0e-15 Match length 38 97 % identity

NCBI Description Nascent polypeptide associated complex alpha chain - human

>gi_556642_emb_CAA56869_ (X80909) Nascent polypeptide
associated complex alpha subunit [Homo sapiens] >gi_4092060

(AF054187) alpha NAC [Homo sapiens]

Seq. No. 313711

Seq. ID yne700378474.h1

Method BLASTN NCBI GI g2738496 BLAST score 100 E value 1.0e-49 Match length 111 98 % identity

Homo sapiens putative oral tumor suppressor protein (doc-1) NCBI Description

Seq. ID Method



mRNA, complete cds

```
313712
Seq. No.
                  yne700378504.hl
Seq. ID
                  BLASTX
Method
                  g4558664
NCBI GI
                  140
BLAST score
                  8.0e-13
E value
                  92
Match length
                  11
% identity
NCBI Description (AC007063) hypothetical protein [Arabidopsis thaliana]
                  313713
Seq. No.
                  yne700378616.h1
Seq. ID
Method
                  BLASTN
                  g3646133
NCBI GI
BLAST score
                  106
                   9.0e-53
E value
                  162
Match length
                   92
% identity
NCBI Description Homo sapiens mRNA for putative Ca2+-transporting ATPase,
                  partial
                   313714
Seq. No.
                   yne700378654.h1
Seq. ID
                   BLASTX
Method
                   g3560557
NCBI GI
                   220
BLAST score
                   3.0e-18
E value
Match length
                   48
                   92
% identity
                  (AF053641) cellular apoptosis susceptibility protein [Homo
NCBI Description
                   sapiens]
                   313715
Seq. No.
                   yne700378678.h1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g2832242
BLAST score
                   44
                   1.0e-15
E value
Match length
                   209
                   85
% identity
NCBI Description Zea mays 22-kDa alpha zein gene cluster, complete sequence
                   313716
Seq. No.
                   yne700378689.h1
Seq. ID
                   BLASTN
Method
                   g183063
NCBI GI
BLAST score
                   64
                   1.0e-27
E value
Match length
                   84
                   94
% identity
NCBI Description Human glia-derived nexin (GDN) mRNA, 5' end
                   313717
Seq. No.
```

44860

.yne700378702.h1

BLASTX

```
NCBI GI
                   g1648931
BLAST score
                   260
E value
                   8.0e-23
Match length
                   79
                   66
% identity
NCBI Description
                  (X92428) HOX1B protein [Zea mays]
Seq. No.
                   313718
                   yne700378730.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                   g4105701
BLAST score
                   202
E value
                   1.0e-110
                   278
Match length
                   93
% identity
                  Homo sapiens clone F19374 APO E-C2 gene cluster, complete
NCBI Description
                   sequence [Homo sapiens]
Seq. No.
                   313719
                   yne700378752.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3193297
BLAST score
                   159
E value
                   4.0e-11
Match length
                   44
% identity
                   66
                   (AF069298) similar to epoxide hydrolases [Arabidopsis
NCBI Description
                   thaliana]
                   313720
Seq. No.
                   yne700378754.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4138265
BLAST score
                   434
E value
                   3.0e-43
Match length
                   92
% identity
                   77
NCBI Description
                   (AJ006228) Avr9 elicitor response protein [Nicotiana
                   tabacum]
Seq. No.
                   313721
                   yne700378775.h1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g32106
BLAST score
                   131
                   1.0e-67
E value
Match length
                   251
% identity
                   96
NCBI Description
                  Human gene for histone H1(0)
Seq. No.
                   313722
                   yne700378915.h1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g902585
BLAST score
                   35
                   2.0e-10
E value
Match length
                   43
```



% identity 95
NCBI Description Zea mays clone MubG9 ubiquitin gene, complete cds

 Seq. No.
 313723

 Seq. ID
 yne700378940.h1

 Method
 BLASTX

NCBI GI g4538926
BLAST score 309
E value 1.0e-28
Match length 75
% identity 79

NCBI Description (AL049483) putative phosphatidylserine decarboxylase

[Arabidopsis thaliana]

Seq. No. 313724

Seq. ID yne700379054.hl

Method BLASTX
NCBI GI g4454484
BLAST score 171
E value 1.0e-12
Match length 48
% identity 71

NCBI Description (AC006234) putative diacylglycerol kinase [Arabidopsis

thaliana]

Seq. No. 313725

Seq. ID yne700379096.hl

Method BLASTX
NCBI GI g3449282
BLAST score 389
E value 5.0e-38
Match length 92
% identity 79

NCBI Description (AB006139) phosphoribosylformimino-5-aminoimidazole

carboxamide ribotide isomerase [Arabidopsis thaliana]

٠.

>gi 3449284 dbj BAA32457 (AB008929)

N'-5'-phosphoribosyl-formimino-5-aminoimidazole-4-carboxamide ribonucleotide isomerase [Arabidopsis thaliana] >gi 4510353 gb AAD21442.1 (AC006921) phosphoribosylformimino-5-aminoimidazole carboxamide

ribotide isomerase [Arabidopsis thaliana]

Seq. No. 313726

Seq. ID yne700379157.h1

Method BLASTX
NCBI GI g2286153
BLAST score 221
E value 3.0e-18
Match length 41
% identity 98

NCBI Description (AF007581) cytoplasmic malate dehydrogenase [Zea mays]

Seq. No.

Seq. ID yne700379321.h1

313727

Method BLASTN NCBI GI g181179 BLAST score 229

NCBI GI

E value

BLAST score

Match length

% identity

q4140643

2.0e-19

50

119

80



```
1.0e-126
E value
Match length
                  272
% identity
NCBI Description Human cathepsin D mRNA, complete cds
                  313728
Seq. No.
                  yne700379482.h1
Seq. ID
Method
                  BLASTX
                  g118104
NCBI GI
                  303
BLAST score
                  7.0e-28
E value
                  94
Match length
                  68
% identity
                  PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE)
NCBI Description
                  (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN)
                  >gi_68408_pir__CSZM peptidylprolyl isomerase (EC 5.2.1.8) -
                  maize >gi 168461 (M55021) cyclophilin [Zea mays]
                  >gi 829148 emb CAA48638 (X68678) cyclophilin [Zea mays]
Seq. No.
                  313729
                  yne700379506.h1
Seq. ID
Method
                  BLASTN
                  g1648930
NCBI GI
BLAST score
                  51
E value
                  4.0e-20
Match length
                  55
                  98
% identity
NCBI Description Z.mays mRNA for Hox1b protein
Seq. No.
                  313730
                  yne700379508.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4467424
BLAST score
                  108
E value
                   3.0e-54
Match length
                  128
                   96
% identity
NCBI Description Homo sapiens PISSLRE gene, exons 8 to
                   313731
Seq. No.
                   yne700379549.hl
Seq. ID
Method
                   BLASTX
                   q4539660
NCBI GI
                   171
BLAST score
E value
                   2.0e-12
                   47
Match length
% identity
                   72
                  (AF061282) polyprotein [Sorghum bicolor]
NCBI Description
                   313732
Seq. No.
Seq. ID
                   yne700379559.h1
Method
                   BLASTN
```



```
NCBI Description
                  Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster,
                  complete sequence
Seq. No.
                  313733
                  yne700379583.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2642323
BLAST score
                  105
E value
                  3.0e-52
Match length
                  113
% identity
                  98
NCBI Description Zea mays profilin (PRO4) mRNA, complete cds
Seq. No.
                  313734
Seq. ID
                  yne700379596.h1
Method
                  BLASTN
NCBI GI
                  g1399085
BLAST score
                  45
                  1.0e-16
E value
Match length
                  101
% identity
                  86
NCBI Description Human ribosomal protein L23a mRNA, complete cds
Seq. No.
                  313735
                  ypc700798774.h1
Seq. ID
Method
                  BLASTX
                  g141605
NCBI GI
                  274
BLAST score
E value
                  1.0e-24
Match length
                  67
% identity
                  84
NCBI Description
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)
                  >gi_72312_pir__ZIZM92 19K zein precursor (clone cZ19C2) -
                  maize >gi_168680 (M12145) 19 kDa zein protein [Zea mays]
Seq. No.
                  313736
                  ypc700798794.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2832246
BLAST score
                  242
E value
                  6.0e-21
Match length
                  59
% identity
                  86
NCBI Description (AF031569) 22-kDa alpha zein 8 [Zea mays]
Seq. No.
                  313737
Seq. ID
                  ypc700798879.h1
Method
                  BLASTN
NCBI GI
                  g535019
BLAST score
                  95
E value
                  4.0e-46
Match length
                  199
% identity
                  46
NCBI Description Z.mays Zdl tandem genes for zein Zdl (19 kDa Zein)
```

Seq. No. 313738

Seq. ID ypc700798990.h1

```
Method
                   BLASTX
NCBI GI
                   g224513
BLAST score
                   263
```

3.0e-23 E value 85 Match length 68 % identity

NCBI Description zein M6 [Zea mays]

Seq. No.

313739

ypc700799131.hl Seq. ID

Method BLASTN NCBI GI g662367 BLAST score 79 E value 8.0e-37 Match length 79 100 % identity

Zea mays farnesyl pyrophosphate synthetase (fps) mRNA, NCBI Description

complete cds

Seq. No.

313740

ypc700799219.h1 Seq. ID

Method BLASTX g1931645 NCBI GI 241 BLAST score 9.0e-21 E value 55 Match length 85 % identity

(U95973) Fe(II) transporter isolog [Arabidopsis thaliana] NCBI Description

Seq. No.

313741

ypc700799235.h1 Seq. ID Method BLASTN

NCBI GI g3493042 BLAST score 45 9.0e-17 E value Match length 45 100 % identity

NCBI Description Zea luxurians granule-bound starch synthase (waxy) gene,

partial cds

313742 Seq. No.

ypc700799355.h1 Seq. ID

Method BLASTX NCBI GI g2826900 BLAST score 379 7.0e-37 E value Match length 85 % identity 86

NCBI Description (AB004461) DNA polymerase alpha catalytic subunit [Oryza

sativa]

Seq. No. 313743

ypc700799476.h1 Seq. ID

Method BLASTX NCBI GI g4126809 BLAST score 159 E value 4.0e-11

```
'Match length
                   71
% identity
                   (AB017042) glyoxalase I [Oryza sativa]
NCBI Description
                   313744
Seq. No.
                   ypc700799478.h1
Seq. ID
Method
                   BLASTN
                   g168700
NCBI GI
BLAST score
                   74
                   9.0e-34
E value
                   100
Match length
                    95
% identity
                   Z.mays zein mRNA, complete cds
NCBI Description
Seq. No.
                   313745
                   ypc700799668.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                    g260042
BLAST score
                    294
                    4.0e-27
E value
                    57
Match length
                    98
% identity
                    (S48563) endosperm ADP-glucose pyrophosphorylase subunit
NCBI Description
                    homolog=Sh2 [maize, Peptide Partial, 542 aa] [Zea mays]
                    313746
Seq. No.
                    ypc700799670.h1
Seq. ID
Method
                    BLASTN
                    g168681
NCBI GI
BLAST score
                    134
E value
                    2.0e-69
                    202
Match length
                    55
% identity
                   Maize 19 kDa zein mRNA, clone cZ19D1, complete cds.
NCBI Description
                    >gi 270686 gb I03333 Sequence 8 from Patent US
                    313747
Seq. No.
                    ypc700799672.h1
Seq. ID
                    BLASTX
Method
NCBI GI
                    q141608
BLAST score
                    250
E value
                    8.0e-22
                    52
Match length
                    94
 % identity
                    ZEIN-ALPHA PRECURSOR (19 KD) (PMS1) >gi 100943 pir S15655
NCBI Description
                    zein, 19K - maize >gi_22446_emb_CAA3765\overline{1}_ (X53\overline{5}82) \overline{1}9 kDa
                    zein [Zea mays]
Seq. No.
                    313748
 Seq. ID
                    ypc700799740.h1
```

Method BLASTN
NCBI GI g2370460
BLAST score 61
E value 6.0e-26
Match length 127
% identity 89

NCBI Description Sorghum bicolor mRNA for putative glycoprotein

```
Seq. No.
                   313749
                   ypc700799777.h1
Seq. ID
                   BLASTN
Method
                   q12158
NCBI GI
                   34
BLAST score
E value
                   8.0e-10
                   58
Match length
                   91
% identity
                   Pea gpal gene for subunit A of chloroplast
NCBI Description
                   glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.13)
Seq. No.
                   313750
                   ypc700799830.h1
Seq. ID
Method
                   BLASTX
                   q141605
NCBI GI
                   327
BLAST score
                   8.0e-31
E value
Match length
                   83
                   82
% identity
                   ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)
NCBI Description
                   >gi_72312_pir__ZIZM92 19K zein precursor (clone cZ19C2) -
                   maize >gi 168680 (M12145) 19 kDa zein protein [Zea mays]
Seq. No.
                   313751
                   ypc700799863.h1
Seq. ID
Method
                   BLASTX
                   q2829870
NCBI GI
BLAST score
                   314
                   3.0e-29
E value
                   81
Match length
                   69
% identity
                   (AC002396) Hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   313752
Seq. No.
                   ypc700800021.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3779024
BLAST score
                   341
E value
                   8.0e-34
                   89
Match length
                   79
% identity
                   (AC005171) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   313753
                   ypc700800047.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4539660
                   276
BLAST score
E value
                   7.0e-27
                   91
Match length
                   70
% identity
                   (AF061282) polyprotein [Sorghum bicolor]
NCBI Description
                   313754
Seq. No.
Seq. ID
                   ypc700800276.h1
Method
                   BLASTX
```

```
a1174778
NCBI GI
BLAST score
                  248
                  1.0e-21
E value
Match length
                  46
                  100
% identity
                  TRYPTOPHAN SYNTHASE BETA CHAIN 1 (ORANGE PERICARP 1)
NCBI Description
                  >gi 320136 pir PQ0449 tryptophan synthase (EC 4.2.1.20)
                  beta-1 chain - maize (fragment) >gi_168572 (M76684)
                  tryptophan synthase beta-subunit [Zea mays]
                  313755
Seq. No.
                  ypc700800318.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2498077
BLAST score
                  166
                  8.0e-12
E value
                  40
Match length
                  85
% identity
                  NUCLEOSIDE DIPHOSPHATE KINASE I (NDK I) (NDP KINASE I)
NCBI Description
                   (PP18) >gi_1777930 (U55019) nucleoside diphosphate kinase
                   [Saccharum officinarum]
                  313756
Seq. No.
                  ypc700800430.h1
Seq. ID
Method
                  BLASTN
                  g949979
NCBI GI
BLAST score
                   66
E value
                  8.0e-29
Match length
                  174
                   89
% identity
NCBI Description Z.mays Glossy2 locus DNA
                   313757
Seq. No.
                   ypc700800483.h1
Seq. ID
Method
                   BLASTX
                   g3892709
NCBI GI
BLAST score
                   196
                   2.0e-15
E value
                   90
Match length
% identity
                   48
                  (AL033545) putative protein [Arabidopsis thaliana]
NCBI Description
                   313758
Seq. No.
                   ypc700800659.h1
Seq. ID
Method
                   BLASTX
                   q135060
NCBI GI
BLAST score
                   194
                   3.0e-15
E value
Match length
                   79
% identity
                   86
                   SUCROSE SYNTHASE 1 (SUCROSE-UDP GLUCOSYLTRANSFERASE 1)
NCBI Description
                   (SHRUNKEN-1) >gi_66570_pir__YUZMS sucrose synthase (EC
                   2.4.1.13) - maize >gi_22486_emb_CAA26247_ (X02400) sucrose
                   synthase [Zea mays] >gi 22488 emb CAA26229 (X02382)
```

Seq. No. 313759

sucrose synthase [Zea mays]



```
Seq. ID ypc700800684.h1
Method BLASTN
NCBI GI g4185305
BLAST score 118
E value 4.0e-60
Match length 142
% identity 96
```

NCBI Description Zea mays cosmid IV.1E1 22-kDa alpha zein protein 21

(sz22-21) gene, complete cds; retrotransposon Opie-2 gag protein, polyprotein, and copia protein genes, complete

cds; and unknown genes

Seq. No. 313760

Seq. ID ypc700800724.h1

Method BLASTX
NCBI GI g16073
BLAST score 146
E value 6.0e-10
Match length 39
% identity 100

NCBI Description (X59526) zein protein [Acetabularia mediterranea]

Seq. No. 313761

Seq. ID ypc700801086.h1

Method BLASTN
NCBI GI g168673
BLAST score 138
E value 8.0e-72
Match length 138
% identity 100

NCBI Description Maize 19 kDa zein mRNA, clone cZ19B1, complete cds

Seq. No. 313762

Seq. ID ypc700801123.h1

Method BLASTX
NCBI GI g1707642
BLAST score 247
E value 2.0e-21
Match length 67
% identity 73

NCBI Description (Y07748) TMK [Oryza sativa]

Seq. No. 313763

Seq. ID ypc700801148.h1

Method BLASTN NCBI GI g4185305 BLAST score 53

E value 2.0e-21
Match length 104
% identity 90

NCBI Description Zea mays cosmid IV.1E1 22-kDa alpha zein protein 21

(sz22-21) gene, complete cds; retrotransposon Opie-2 gag protein, polyprotein, and copia protein genes, complete

cds; and unknown genes

Seq. No. 313764

Seq. ID ypc700801174.h1

```
Method
                   BLASTN
NCBI GI
                   g168694
BLAST score
                   234
                   1.0e-129
E value
                   256
Match length
                   98
% identity
NCBI Description Maize gamma zein mRNA, partial cds
                   313765
Seq. No.
                   ypc700801284.h1
Seq. ID
Method
                   BLASTN
NCBI GI
                   q498741
BLAST score
                   56
                   3.0e-23
E value
                   92
Match length
                   90
% identity
NCBI Description H.vulgare (pMaW25) mRNA for beta-ketoacyl-ACP synthase
                   313766
Seq. No.
                   ypc700801343.hl
Seq. ID
Method
                   BLASTN
                   q1657760
NCBI GI
BLAST score
                   75
E value
                   3.0e - 34
                   90
Match length
                   97
% identity
                   Zea mays retrotransposon Cinful 5' LTR and and primer
NCBI Description
                   binding site DNA sequence
Seq. No.
                   313767
                   ypc700801380.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q913865
BLAST score
                   196
E value
                   2.0e-15
Match length
                   34
                   100
% identity
                   branching enzyme II BEII [Zea mays, cultivar B73,
NCBI Description
                   endosperms, Peptide, 738 aa]
                   313768
Seq. No.
                   ypc700801480.hl
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3024018
                   336
BLAST score
                   8.0e-32
E value
Match length
                   63
                   100
% identity
                   INITIATION FACTOR 5A (EIF-5A) (EIF-4D)
NCBI Description
                   >gi_1546919_emb_CAA69225_ (Y07920) translation initiation
```

factor 5A [Zea mays] >gi 2668738 (AF034943) translation

initiation factor 5A [Zea mays]

313769 Seq. No.

ypc700801557.h1 Seq. ID

BLASTX Method g3645899 NCBI GI

NCBI Description



```
BLAST score
                  147
E value
                  1.0e-09
Match length
                  39
% identity
                  67
NCBI Description (U68408) 5' end not determined experimentally [Zea mays]
                  313770
Seq. No.
                  ypc700801630.h1
Seq. ID
                  BLASTX
Method
                  g2623295
NCBI GI
BLAST score
                  305
                  3.0e-28
E value
                  83
Match length
                  69
% identity
NCBI Description (AC002409) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  313771
Seq. ID
                  ypc700801748.h1
Method
                  BLASTX
NCBI GI
                  g4185308
BLAST score
                  186
E value
                  3.0e-14
Match length
                  50
                  76
% identity
NCBI Description (AF090446) 22-kDa alpha zein protein 21 [Zea mays]
Seq. No.
                  313772
                  ypc700801749.hl
Seq. ID
Method
                  BLASTN
                  g3819327
NCBI GI
BLAST score
                   49
                  9.0e-19
E value
Match length
                   100
% identity
                  88
NCBI Description Hordeum vulgare genomic DNA fragment; clone MWG0626.uni
                   313773
Seq. No.
Seq. ID
                   ypc700801896.hl
                  BLASTX
Method
NCBI GI
                  g3135254
BLAST score
                  185
                   3.0e-14
E value
Match length
                   60
% identity
NCBI Description (AC003058) hypothetical protein [Arabidopsis thaliana]
                   313774
Seq. No.
                  ypc700801954.hl
Seq. ID
Method
                  BLASTX
NCBI GI
                  g463152
BLAST score
                   214
E value
                   9.0e-18
                   39
Match length
% identity
                   100
```

seed storage protein [Zea mays]

(L29505) zein [Zea mays] >gi 1094858 prf 2106415A Met-rich

```
313775
`Seq. No.
                   ypc700802009.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g168699
BLAST score
                   216
                   9.0e-30
E value
                   101
Match length
                   75
% identity
                   (M60836) zein [Zea mays]
NCBI Description
                   313776
Seq. No.
                   ypc700802010.h1
Seq. ID
                   BLASTN
Method
                   g168673
NCBI GI
BLAST score
                   97
E value
                   2.0e-47
Match length
                   185
                   92
% identity
NCBI Description Maize 19 kDa zein mRNA, clone cZ19B1, complete cds
                   313777
Seq. No.
                   ypc700802062.h1
Seq. ID
                   BLASTN
Method
                   g22528
NCBI GI
BLAST score
                   139
                   2.0e-72
E value
                   193
Match length
                   95
% identity
                   Zea mays mRNA encoding a zein (clone A20)
NCBI Description
                   313778
Seq. No.
                   ypc700802273.h1
 Seq. ID
                   BLASTN
Method
                   g22485
NCBI GI
                    121
 BLAST score
                    5.0e-62
 E value
 Match length
                    125
                    99
 % identity
NCBI Description Maize mRNA for sucrose synthase (EC 2.4.1.13)
                    313779
 Seq. No.
                    ypc700802282.h1
 Seq. ID
                    BLASTX
 Method
```

Method BLASTX
NCBI GI g100846
BLAST score 208
E value 7.0e-17
Match length 43
% identity 98

NCBI Description 22K zein precursor (clone gZ22.8H3) - maize

>gi_22179_emb_CAA43399_ (X61085) 22 kD alpha-zein [Zea

mays]

313780

Seq. No.

Seq. ID ypc700802340.hl

Method BLASTN
NCBI GI g459267
BLAST score 120

44872

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```
E value
                  4.0e-61
Match length
                  136
                  98
% identity
NCBI Description Z.mays gene for HMG protein
                  313781
Seq. No.
                  ypc700802358.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q168681
BLAST score
                  212
E value
                  1.0e-116
Match length
                  246
                  54
% identity
NCBI Description Maize 19 kDa zein mRNA, clone cZ19D1, complete cds.
                  >gi 270686 gb I03333 Sequence 8 from Patent US
                  313782
Seq. No.
                  ypc700802565.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q141613
BLAST score
                  159
                  4.0e-11
E value
Match length
                  46
                  74
% identity
NCBI Description ZEIN-ALPHA PRECURSOR (22 KD) (CLONES PZ22.1 AND 22A1)
                  >gi_72305_pir__ZIZM21 22K zein precursor (clone pZ22.1) -
                  maize >gi 22532 emb CAA24725 (V01478) zein [Zea mays]
Seq. No.
                  313783
Seq. ID
                  ypc700802570.h1
Method
                  BLASTX
NCBI GI
                  g168701
BLAST score
                  150
E value
                  4.0e-10
Match length
                  58
                  57
% identity
NCBI Description (M60837) zein [Zea mays]
                  313784
Seq. No.
                  ypc700802636.h1
Seq. ID
Method
                  BLASTN
                  g168669
NCBI GI
BLAST score
                  60
E value
                  2.0e-25
Match length
                  72
% identity
                  96
NCBI Description Maize 19 kDa zein mRNA, clone cZ19A2, partial cds
                  313785
Seq. No.
Seq. ID
                  ypc700802688.h1
Method
                  BLASTX
                  g1174448
NCBI GI
```

Method BLASTX
NCBI GI g1174448
BLAST score 154
E value 1.0e-10
Match length 51
% identity 53

NCBI Description TRANSLOCON-ASSOCIATED PROTEIN, ALPHA SUBUNIT PRECURSOR



% identity

NCBI Description

(TRAP-ALPHA) (SIGNAL SEQUENCE RECEPTOR ALPHA SUBUNIT) (SSR-ALPHA) >gi_547391 (L32016) alpha-subunit; putative [Arabidopsis thaliana]

```
Seq. No.
                   313786
Seq. ID
                   ypc700802705.hl
Method
                   BLASTX
NCBI GI
                   q4056507
BLAST score
                   169
E value
                   3.0e-12
Match length
                   89
 % identity
                   45
                   (AC005896) putative RNA binding protein [Arabidopsis
NCBI Description
                   thaliana]
                   313787
 Seq. No.
                   ypc700802734.h1
 Seq. ID
Method
                   BLASTX
                   q4454464
NCBI GI
BLAST score
                   192
E value
                   6.0e-15
Match length
                   79
                   49
 % identity
NCBI Description (AC006234) unknown protein [Arabidopsis thaliana]
 Seq. No.
                   313788
                   ypc700802735.h1
 Seq. ID
Method
                   BLASTX
                   g3540195
NCBI GI
BLAST score
                   254
 E value
                   3.0e-22
Match length
                   58
 % identity
                   38
NCBI Description (AC004260) Unknown protein [Arabidopsis thaliana]
                   313789
 Seq. No.
 Seq. ID
                   ypc700802845.hl
                   BLASTN
 Method
 NCBI GI
                   g168681
 BLAST score
                   35
                   1.0e-10
 E value
 Match length
                   63
                   89
 % identity
 NCBI Description Maize 19 kDa zein mRNA, clone cZ19D1, complete cds.
                   >gi 270686 gb I03333 Sequence 8 from Patent US
 Seq. No.
                   313790
 Seq. ID
                   ypc700802849.hl
 Method
                   BLASTX
 NCBI GI
                   g2129932
 BLAST score
                   308
 E value
                   1.0e-28
Match length
                   67
```

[Lycopersicon esculentum]

myb-related transcription factor TMH1 - tomato

>gi_1167486_emb_CAA64615_ (X95297) transcription factor

```
313791
Seq. No.
                   ypc700802941.h1
Seq. ID
Method
                   BLASTX
                   g135060
NCBI GI
                    149
BLAST score
                    4.0e-10
E value
                    29
Match length
                    97
% identity
                    SUCROSE SYNTHASE 1 (SUCROSE-UDP GLUCOSYLTRANSFERASE 1)
NCBI Description
                    (SHRUNKEN-1) >gi_66570_pir__YUZMS sucrose synthase (EC 2.4.1.13) - maize >gi_22486_emb_CAA26247__(X02400) sucrose
                    synthase [Zea mays] >gi_22488_emb_CAA26229_ (X02382)
                    sucrose synthase [Zea mays]
Seq. No.
                    313792
                    ypc700802952.hl
Seq. ID
                    BLASTN
Method
                    g22514
NCBI GI
BLAST score
                    64
                    4.0e-28
E value
                    99
Match length
                    92
% identity
                    Maize Zc1 gene for Zein Zc1 (14 kD zein-2)
NCBI Description
                    313793
Seq. No.
                    ypc700802959.h1
Seq. ID
Method
                    BLASTN
                    g22537
NCBI GI
                    35
BLAST score
                    8.0e-11
E value
Match length
                    67
                    88
% identity
                    Maize mRNA for zein polypeptide (clone M6)
NCBI Description
                    313794
 Seq. No.
                    ypc700802971.hl
 Seq. ID
                    BLASTN
Method
                    g22387
 NCBI GI
                    108
 BLAST score
                     3.0e-54
 E value
```

121 Match length 97 % identity

NCBI Description Zea mays opaque-2 gene

313795 Seq. No.

ypc700802991.hl Seq. ID

BLASTX Method g3319340 NCBI GI 144 BLAST score 2.0e-09 E value Match length 32 81 % identity

(AF077407) contains similarity to E. coli cation transport NCBI Description

protein ChaC (GB:D90756) [Arabidopsis thaliana]

313796 Seq. No.

```
YF.
```

```
ypc700803071.hl
Seq. ID
                   BLASTN
Method
                   g22222
NCBI GI
                   240
BLAST score
                   1.0e-132
E value
                   305
Match length
                   95
% identity
                   Z.mays ZSF4C4 gene for zein
NCBI Description
                   313797
Seq. No.
                   ypc700803090.h1
Seq. ID
                   BLASTX
Method
                    g2642158
NCBI GI
                    320
BLAST score
                    7.0e-30
E value
                    97
Match length
% identity
                    61
                    (AC003000) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                    313798
Seq. No.
                    ypc700803118.h1
Seq. ID
                    BLASTX
Method
                    g232033
NCBI GI
                    265
BLAST score
                    1.0e-23
E value
                    58
Match length
                    88
% identity
                    ELONGATION FACTOR 1 BETA' >gi_479830_pir__S35501 translation elongation factor eEF-1 beta' chain - wheat
NCBI Description
                    >gi_218341_dbj_BAA02436_ (D13147) elongation factor 1 beta'
                    [Triticum aestivum]
                    313799
Seq. No.
                    ypc700803296.h1
Seq. ID
                    BLASTX
Method
                    g3193333
NCBI GI
                    155
BLAST score
                    1.0e-10
E value
                    74
Match length
                    50
% identity
                    (AF069299) contains similarity to breast cancer
NCBI Description
                    susceptibility (Brca2) [Arabidopsis thaliana]
                    313800
 Seq. No.
                    ypc700803361.h1
 Seq. ID
                    BLASTX
Method
                    q2081612
NCBI GI
                    331
BLAST score
                    3.0e - 31
E value
Match length
                    83
                    80
 % identity
                    (D49714) deltal-pyrroline-5-carboxylate synthetase [Oryza
 NCBI Description
                    sativa]
```

313801

BLASTN

ypc700803511.h1

Seq. No.

Seq. ID

Method

```
g168669
NCBI GI
BLAST score
                  93
                  5.0e-45
E value
                  206
Match length
                  94
% identity
NCBI Description Maize 19 kDa zein mRNA, clone cZ19A2, partial cds
                  313802
Seq. No.
                  ypc700803512.h1
Seq. ID
                  BLASTN
Method
                  g168681
NCBI GI
                  189
BLAST score
                  1.0e-102
E value
                   236
Match length
% identity
                   95
                  Maize 19 kDa zein mRNA, clone cZ19D1, complete cds.
NCBI Description
                   >qi 270686 gb I03333_ Sequence 8 from Patent US
                   313803
Seq. No.
                   ypc700803635.h1
Seq. ID
Method
                   BLASTN
                   g3851000
NCBI GI
BLAST score
                   66
                   7.0e-29
E value
                   66
Match length
                   100
% identity
                   Zea mays pyruvate dehydrogenase El beta subunit isoform 2
NCBI Description
                   mRNA, nuclear gene encoding mitochondrial protein, complete
                   cds
                   313804
Seq. No.
                   ypc700803789.h1
Seq. ID
                   BLASTX
Method
                   g3176714
NCBI GI
BLAST score
                   150
                   5.0e-12
E value
                   88
Match length
                   48
% identity
                   (AC002392) putative tRNA-splicing endonuclease positive
NCBI Description
                   effector [Arabidopsis thaliana]
                   313805
Seq. No.
                   ypc700803834.hl
Seq. ID
                   BLASTX
Method
                   g3163946
NCBI GI
                   275
BLAST score
                   1.0e-24
E value
                   54
Match length
% identity
                   93
                   (AJ005599) alpha-tubulin 1 [Eleusine indica]
NCBI Description
                   313806
Seq. No.
                   ypc700803839.hl
Seq. ID
                   BLASTX
Method
                   g16073
NCBI GI
 BLAST score
                   158
                   2.0e-23
E value
```



Match length 87 % identity 67

NCBI Description (X59526) zein protein [Acetabularia mediterranea]

Seq. No.

313807

Seq. ID Method ypc700803882.h1
BLASTX

NCBI GI BLAST score E value g1143515 173 5.0e-13

Match length 40 % identity 85

NCBI Description (Z47078) Ser/Thr protein phosphatase homologous to PP2A

[Malus domestica]

Seq. No.

313808

Seq. ID

ypc700803887.h1

Method BLASTX
NCBI GI g3292826
BLAST score 322
E value 2.0e-31
Match length 80

% identity 78

NCBI Description (AL031018) hypothetical protein [Arabidopsis thaliana]

Seq. No.

313809

Seq. ID

ypc700803966.hl

Method BLASTN
NCBI GI 9434333
BLAST score 37
E value 2.0e-11
Match length 37
% identity 100

NCBI Description Z.mays mRNA gs2 for glutamine synthatase

Seq. No.

313810

Seq. ID

ypc700803989.hl

Method BLASTX
NCBI GI 94140644
BLAST score 191
E value 8.0e-15
Match length 50
% identity 76

NCBI Description (AF090447) 22-kDa zein protein 12 [Zea mays]

Seq. No.

313811

Seq. ID

ypc700804011.h1

Method BLASTN
NCBI GI g2832242
BLAST score 33
E value 4.0e-09
Match length 37
% identity 97

NCBI Description Zea mays 22-kDa alpha zein gene cluster, complete sequence

Seq. No.

313812

Seq. ID

ypc700804027.hl



NCBI Description (D63581) EF-1 alpha [Oryza sativa]

% identity

```
BLASTX
Method
                   g141601
NCBI GI
                   212
BLAST score
                   3.0e-17
E value
Match length
                   67
                   66
% identity
                   ZEIN-ALPHA PRECURSOR (19 KD) (CLONE GZ19AB11)
NCBI Description
                   >gi_82657_pir__S03417 19K zein precursor (clone gZ19AB11) -
                   maize >gi_22543_emb_CAA29340_ (X05911) 19 kd alpha zein (AA
                   1 - 234) [Zea mays]
                   313813
Seq. No.
                   ypc700804034.h1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q322870
BLAST score
                   149
                   4.0e-13
E value
                   50
Match length
                   82
% identity
                   glucose-1-phosphate adenylyltransferase (EC 2.7.7.27) -
NCBI Description
                   maize (fragment)
                   313814
Seq. No.
                   ypc700804067.h1
Seq. ID
                   BLASTN
Method
NCBI GI
                    g22485
BLAST score
                    85
                    3.0e-40
E value
Match length
                    215
                    93
% identity
NCBI Description Maize mRNA for sucrose synthase (EC 2.4.1.13)
                    313815
Seq. No.
                    ypc700804137.hl
Seq. ID
                    BLASTX
Method
                    g113621
NCBI GI
                    238
BLAST score
                    2.0e-20
E value
                    53
Match length
                    92
 % identity
                    FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME
 NCBI Description
                    >gi_68196_pir__ADZM fructose-bisphosphate aldolase (EC
                    4.1.2.13), cytosolic - maize >gi_168420 (M16220) aldolase [Zea mays] >gi_295850_emb_CAA31366_ (X12872) fructose
                    bisphosphate aldolase [Zea mays] >gi_225624_prf__1307278A
                    cytoplasmic aldolase [Zea mays]
                    313816
 Seq. No.
                    ypc700804182.h1
 Seq. ID
                    BLASTX
 Method
 NCBI GI
                    g2662343
                    390
 BLAST score
                    3.0e-38
 E value
                    78
 Match length
```

```
313817
Seq. No.
                  ypc700804191.h1
Seq. ID
                   BLASTX
Method
                  g2832247
NCBI GI
                   327
BLAST score
                   6.0e-31
E value
                   84
Match length
                   83
% identity
                   (AF031569) 22-kDa alpha zein 10 [Zea mays]
NCBI Description
                   313818
Seq. No.
                   ypc700804193.h1
Seq. ID
                   BLASTX
Method
                   g168699
NCBI GI
BLAST score
                   332
                   2.0e-31
E value
                   78
Match length
                   88
% identity
                   (M60836) zein [Zea mays]
NCBI Description
Seq. No.
                   313819
                   ypc700804309.hl
Seq. ID
                   BLASTX
Method
                   g2444176
NCBI GI
                   137
BLAST score
                   1.0e-08
E value
                   44
Match length
                   64
% identity
                   (U94782) unconventional myosin [Helianthus annuus]
NCBI Description
                   313820
Seq. No.
                   ypc700804310.hl
Seq. ID
                   BLASTN
Method
                   g22542
NCBI GI
BLAST score
                   92
                   2.0e-44
E value
                  - 171
Match length
                   91
% identity
NCBI Description Maize gene for Mr 19000 alpha zein and 5'-flanking region
                   313821
 Seq. No.
                   ypc700804327.h1
 Seq. ID
                   BLASTX
Method
                   g2580499
NCBI GI
                   182
BLAST score
                   6.0e-14
E value
                   44
Match length
                    77
 % identity
                   (U67186) NADPH: ferrihemoprotein oxidoreductase
 NCBI Description
```

Seq. No.

vpc700804342.h1 Seq. ID

BLASTX Method g2589164 NCBI GI BLAST score 141 3.0e-09 E value

[Eschscholzia californica]

```
Match length
% identity
NCBI Description
                  (D88452) aldehyde oxidase-2 [Zea mays]
Seq. No.
                  313823
Seq. ID
                  ypc700804534.hl
Method
                  BLASTX
NCBI GI
                  q168701
BLAST score
                  249
E value
                  1.0e-21
Match length
                  69
% identity
                  75
NCBI Description
                  (M60837) zein [Zea mays]
Seq. No.
                  313824
Seq. ID
                  ypc700804565.h1
Method
                  BLASTX
NCBI GI
                  g16073
BLAST score
                  162
E value
                  2.0e-11
                  34
Match length
                  94
% identity
                  (X59526) zein protein [Acetabularia mediterranea]
NCBI Description
Seq. No.
                  313825
Seq. ID
                  ypc700804574.h1
Method
                  BLASTX
                  g468515
NCBI GI
BLAST score
                  192
                  5.0e-15
E value
Match length
                  53
                  75
% identity
NCBI Description (X55726) zein [Zea mays]
Seq. No.
                  313826
Seq. ID
                  ypc700804627.h1
Method
                  BLASTX
NCBI GI
                  g141608
                  149
BLAST score
                  2.0e-13
E value
                  51
Match length
                  76
% identity
                  ZEIN-ALPHA PRECURSOR (19 KD) (PMS1) >gi_100943_pir__S15655
NCBI Description
```

zein, 19K - maize >gi_22446_emb_CAA37651_ (X53582) 19 kDa

zein [Zea mays]

Seq. No. 313827

Seq. ID ypc700804651.h1

Method BLASTX NCBI GI g141603 BLAST score 221 2.0e-18 E value Match length 48 90 % identity

ZEIN-ALPHA PRECURSOR (19 KD) (CLONE A20) NCBI Description

>gi 72311_pir__ZIZM2 19K zein precursor (clone A20) - maize

>gi_22529_emb_CAA24723_ (V01476) zein [Zea mays]

```
313828
Seq. No.
                  ypc700804694.h1
Seq. ID
                  BLASTX
Method
                  g4204304
NCBI GI
                  275
BLAST score
                  1.0e-24
E value
                  49
Match length
                   98
% identity
                   (AC003027) lcl_prt_seq No definition line found
NCBI Description
                   [Arabidopsis thaliana]
                   313829
Seq. No.
                   ypc700804712.h1
Seq. ID
Method
                   BLASTX
                   g100846
NCBI GI
                   219
BLAST score
                   4.0e-18
E value
                   45
Match length
                   98
% identity
                   22K zein precursor (clone gZ22.8H3) - maize
NCBI Description
                   >gi_22179_emb_CAA43399_ (X61085) 22 kD alpha-zein [Zea
                   mays]
                   313830
Seq. No.
                   ypc700804722.h1
Seq. ID
                   BLASTX
Method
                   g224507
NCBI GI
BLAST score
                   147
                   1.0e-09
E value
                   42
Match length
                   79
% identity
                  zein A1 [Zea mays]
NCBI Description
                   313831
Seq. No.
                   ypc700804771.h1
Seq. ID
                   BLASTX
Method
                   g4325342
NCBI GI
                   187
BLAST score
                   1.0e-15
E value
Match length
                   68
                   68
% identity
                   (AF128393) No definition line found [Arabidopsis thaliana]
NCBI Description
                   313832
Seq. No.
                   ypc700804994.h1
Seq. ID
                   BLASTX
Method
                   q2827643
NCBI GI
BLAST score
                   272
                   2.0e-24
E value
Match length
                   72
                   67
 % identity
                   (AL021636) predicted protein [Arabidopsis thaliana]
NCBI Description
                   >gi 3549641_emb CAA06432_ (AJ005195) receiver-like protein
                   4 [Arabidopsis thaliana]
```

313833

Seq. No.

```
vpc700805157.hl
Seq. ID
Method
                  BLASTN
                  a22514
NCBI GI
                  157
BLAST score
                  4.0e-83
E value
                  221
Match length
% identity
                  Maize Zc1 gene for Zein Zc1 (14 kD zein-2)
NCBI Description
                  313834
Seq. No.
                  ypc700805215.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g141605
                  154
BLAST score
                  7.0e-15
E value
                   68
Match length
                  73
% identity
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)
NCBI Description
                  >gi_72312_pir_ ZIZM92 19K zein precursor (clone cZ19C2) -
                  maize >gi_168680 (M12145) 19 kDa zein protein [Zea mays]
                   313835
Seq. No.
                   ypc700805354.h1
Seq. ID
                  BLASTX
Method
                   g2662341
NCBI GI
BLAST score
                   346
                   4.0e-33
E value
                   68
Match length
                   99
% identity
                   (D63580) EF-1 alpha [Oryza sativa]
NCBI Description
                   >gi_2662345_dbj_BAA23659_ (D63582) EF-1 alpha [Oryza
                   satīva] >gi_2662347_dbj_BAA23660_ (D63583) EF-1 alpha
                   [Oryza sativa]
                   313836
Seq. No.
                   ypc700805371.h1
Seq. ID
Method
                   BLASTN
                   q4416300
NCBI GI
                   151
BLAST score
E value
                   9.0e-80
                   167
Match length
                   49
% identity
                   Zea mays chromosome 4 22 kDa zein-associated intercluster
NCBI Description
                   region, complete sequence
                   313837
Seq. No.
                   ypc700805404.h1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2213632
BLAST score
                   214
                   2.0e-17
E value
Match length
                   64
% identity
                   59
                   (AC000103) F21J9.24 [Arabidopsis thaliana]
NCBI Description
```

313838

ypc700805506.hl

Seq. No.

Seq. ID

E value

Match length

% identity

2.0e-22 99



```
BLASTN
Method
                  g2832242
NCBI GI
BLAST score
                  129
E value
                  1.0e-66
                  197
Match length
                  91
% identity
NCBI Description Zea mays 22-kDa alpha zein gene cluster, complete sequence
                  313839
Seq. No.
Seq. ID
                  ypc700805583.h1
                  BLASTN
Method
NCBI GI
                  g4539654
                  54
BLAST score
                  1.0e-21
E value
                  165
Match length
% identity
                  44
NCBI Description Sorghum bicolor 22 kDa kafirin cluster
Seq. No.
                  313840
Seq. ID
                  ypc700805654.h1
Method
                  BLASTX
NCBI GI
                  g2062172
BLAST score
                  212
                  3.0e-17
E value
Match length
                  58
                  71
% identity
NCBI Description (AC001645) unknown protein [Arabidopsis thaliana]
Seq. No.
                  313841
                  ypc700805836.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1200239
BLAST score
                  224
E value
                  9.0e-19
Match length
                  49
                  78
% identity
NCBI Description (X87690) GAMyb protein [Hordeum vulgare]
                  313842
Seq. No.
Seq. ID
                  ypc700805845.h1
                  BLASTN
Method
                  g3493574
NCBI GI
BLAST score
                  58
                  1.0e-24
E value
                  86
Match length
                  96
% identity
NCBI Description Homo sapiens lipoprotein receptor-related protein (LRP1),
                  exons 80 through 89 and complete cds
Seq. No.
                  313843
                  ypc700805919.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g22542
                  55
BLAST score
```



```
NCBI Description Maize gene for Mr 19000 alpha zein and 5'-flanking region
                    313844
 Seq. No.
                    ypc700805934.h1
 Seq. ID
                    BLASTX
 Method
                    g141601
 NCBI GI
                    207
 BLAST score
                    1.0e-16
 E value
                    90
 Match length
                    83
 % identity
                    ZEIN-ALPHA PRECURSOR (19 KD) (CLONE GZ19AB11)
 NCBI Description
                    >gi_82657_pir__S03417 19K zein precursor (clone gZ19AB11) -
                    maize >gi_22543_emb_CAA29340_ (X05911) 19 kd alpha zein (AA
                    1 - 234) [Zea mays]
                    313845
 Seq. No.
                    ypc700805935.h1
 Seq. ID
 Method
                    BLASTN
                    g2828011
 NCBI GI
BLAST score
                    38
                    4.0e-12
 E value
 Match length
                    46
                    96
 % identity
                    Zea mays starch synthase I precursor (Ss1) mRNA, nuclear
 NCBI Description
                    gene encoding plastid protein, complete cds
 Seq. No.
                    313846
                    ypc700805961.h1
 Seq. ID
                    BLASTX
 Method
                    g4164404
 NCBI GI
                    207
 BLAST score
 E value
                    1.0e-16
                    90
 Match length
                    49
 % identity
                    (AL035248) putative ubiquitin protein ligase
 NCBI Description
                    [Schizosaccharomyces pombe]
 Seq. No.
                    313847
                    ypc700805974.h1
 Seq. ID
 Method
                    BLASTN
                    q2832242
 NCBI GI
                    111
 BLAST score
                    7.0e-56
 E value
                    131
 Match length
                    11
  % identity
                    Zea mays 22-kDa alpha zein gene cluster, complete sequence
 NCBI Description
                    313848
  Seq. No.
                    ypc700805988.h1
  Seq. ID
                    BLASTX
 Method
  NCBI GI
                    q121472
  BLAST score
                    244
  E value
                    2.0e-22
 Match length
                    85
                    66
  % identity
                    GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)
  NCBI Description
```

(ALCOHOL-SOLUBLE REDUCED GLUTELIN) (ASG) (ZEIN ZC2)

Seq. No.

313854



>gi_72326_pir__ZMZM19 glutelin 2 precursor (clone pME119) maize >gi_22289 emb_CAA26149_ (X02230) glutelin-2 precursor
[Zea mays] >gi_22517_emb_CAA37594_ (X53514) zein Zc2 [Zea
mays] >gi_168485 (M16066) glutelin-2 [Zea mays]

```
Seq. No.
                  313849
                  ypc700806037.hl
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2791834
BLAST score
                  174
                  4.0e-13
E value
                  35
Match length
                  97
% identity
NCBI Description
                  (AF041463) elongation factor 1-alpha [Manihot esculenta]
                  313850
Seq. No.
                  ypc700806050.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g22514
BLAST score
                  48
                  2.0e-18
E value
Match length
                  71
% identity
                  94
NCBI Description
                 Maize Zc1 gene for Zein Zc1 (14 kD zein-2)
Seq. No.
                  313851
Seq. ID
                  ypc700806092.h1
Method
                  BLASTX
NCBI GI
                  q100938
BLAST score
                  234
                  8.0e-20
E value
Match length
                  55
% identity
                  89
                  zein precursor - maize >gi_22442_emb CAA32513_ (X14335)
NCBI Description
                  zein precursor (AA -21 to 90) [Zea mays]
Seq. No.
                  313852
Seq. ID
                  ypc700806149.h1
                  BLASTX
Method
NCBI GI
                  g224509
BLAST score
                  150
E value
                  3.0e-10
Match length
                  43
% identity
                  74
NCBI Description zein E19 [Zea mays]
                  313853
Seq. No.
                  ypc700806157.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g168690
BLAST score
                  105
E value
                  4.0e-52
Match length
                  233
% identity
                  97
NCBI Description Maize zein mRNA, complete cds, clone ZG124
```



```
ypc700806190.h1
Seq. ID
                  BLASTX
Method
                  g141599
NCBI GI
                  324
BLAST score
                  2.0e-30
E value
                  71
Match length
                  92
% identity
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19A2)
NCBI Description
                  >gi_72316_pir__ZIZMA2 19K zein precursor (clone cZ19A2) -
                  maize (fragment) >gi_168670 (M12142) 19 kDa zein protein
                   [Zea mays]
                   313855
Seq. No.
                   ypc700806231.h1
Seq. ID
Method
                   BLASTX
                   g3075392
NCBI GI
                   172
BLAST score
                   1.0e-12
E value
                   78
Match length
                   44
% identity
                   (AC004484) putative steroid dehydrogenase [Arabidopsis
NCBI Description
                   thaliana]
                   313856
Seq. No.
                   ypc700806240.h1
Seq. ID
                   BLASTX
Method
                   g168691
NCBI GI
BLAST score
                   192
                   7.0e-15
E value
                   57
Match length
                   67
% identity
                   (M29628) zein [Zea mays]
NCBI Description
                   313857
Seq. No.
                   ypc700806267.hl
Seq. ID
                   BLASTN
Method
                   g1037129
NCBI GI
BLAST score
                   115
                   4.0e-58
E value
                   167
Match length
% identity
                   92
                   (gamma-zeinA) = opaque2 modifier {5' region} [Zea mays=maize,
NCBI Description
                   Tuxpeno CMS 450, mRNA Partial, 1889 nt]
                   313858
Seq. No.
                   ypc700806274.h1
Seq. ID
Method
                   BLASTX
                   g4063770
NCBI GI
BLAST score
                   269
                   6.0e-24
E value
Match length
                   90
                   58
% identity
```

(AB004906) transposase [Ipomoea purpurea] NCBI Description

Seq. No.

313859

ypc700806282.h1 Seq. ID

Method

BLASTX

E value

Match length

1.0e-61

244

```
g3935148
NCBI GI
BLAST score
                  327
E value
                  9.0e-31
Match length
                  88
% identity
                  69
                  (AC005106) T25N20.12 [Arabidopsis thaliana]
NCBI Description
                  313860
Seq. No.
                  ypc700806365.h1
Seq. ID
Method
                  BLASTN
                  g168679
NCBI GI
BLAST score
                  74
                  7.0e-34
E value
Match length
                  160
                  98
% identity
                  Maize 19 kDa zein mRNA, clone cZ19C2, complete cds.
NCBI Description
                  >gi 270687_gb_I03334_ Sequence 9 from Patent US
                  313861
Seq. No.
                  ypc700806368.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3510253
BLAST score
                  176
E value
                  4.0e-13
Match length
                  42
% identity
                  69
                  (AC005310) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  313862
Seq. No.
Seq. ID
                  ypc700806449.h1
Method
                  BLASTX
NCBI GI
                  g141605
BLAST score
                  144
                  2.0e-09
E value
Match length
                  45
                  67
% identity
                  ZEIN-ALPHA PRECURSOR (19 KD) (CLONE 19C2)
NCBI Description
                  >gi 72312 pir ZIZM92 19K zein precursor (clone cZ19C2) -
                  maize >gi 168680 (M12145) 19 kDa zein protein [Zea mays]
Seq. No.
                  313863
Seq. ID
                  ypc700806520.h1
Method
                  BLASTN
                  g602605
NCBI GI
BLAST score
                  34
                  9.0e-10
E value
Match length
                  58
                  90
% identity
NCBI Description Zea mays tandem genes for alpha1-tubulin and alpha2-tubulin
Seq. No.
                  313864
                  ypc700806554.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g535019
BLAST score
                  121
```

```
% identity
NCBI Description Z.mays Zd1 tandem genes for zein Zd1 (19 kDa Zein)
                   313865
Seq. No.
                   ypc700806564.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g141609
BLAST score
                   294
                   6.0e-27
E value
Match length
                   61
% identity
                   ZEIN-ALPHA PRECURSOR (19 KD) (PMS2) >gi 100944 pir
NCBI Description
                   zein, 19K - maize >gi_22448_emb_CAA4154\overline{3}_ (X58\overline{7}00) \overline{1}9 kDa
                   zein [Zea mays]
                   313866
Seq. No.
Seq. ID
                   ypc700806594.h1
Method
                   BLASTN
                   g168679
NCBI GI
BLAST score
                   150
E value
                   5.0e-79
Match length
                   238
                   91
% identity
NCBI Description
                   Maize 19 kDa zein mRNA, clone cZ19C2, complete cds.
                   >gi_270687_gb_I03334_ Sequence 9 from Patent US
                   313867
Seq. No.
                   ypc700806664.h1
Seq. ID
Method
                   BLASTX
                   q3777600
NCBI GI
                   375
BLAST score
                   2.0e-36
E value
                   84
Match length
% identity
                   87
                   (AF095708) 50S ribosomal protein L5 [Oryza sativa]
NCBI Description
Seq. No.
                   313868
                   ypc700806755.h1
Seq. ID
Method
                   BLASTN
NCBI GI
                   q22514
BLAST score
                   200
                   1.0e-109
E value
Match length
                   214
                   99
% identity
NCBI Description Maize Zc1 gene for Zein Zc1 (14 kD zein-2)
Seq. No.
                   313869
Seq. ID
                   ypc700806801.h1
Method
                   BLASTX
NCBI GI
                   g4539665
BLAST score
                   202
E value
                   5.0e-16
Match length
                   91
% identity
                   46
NCBI Description (AF061282) polyprotein [Sorghum bicolor]
```

313870

Seq. No.

BLAST score

Match length

E value

226

5.0e-19 54

```
vpc700806875.hl
Seq. ID
Method
                  BLASTN
NCBI GI
                  a168673
BLAST score
                   46
                  2.0e-17
E value
                  46
Match length
% identity
                  100
                  Maize 19 kDa zein mRNA, clone cZ19B1, complete cds
NCBI Description
                  313871
Seq. No.
                  ypc700806949.hl
Seq. ID
Method
                   BLASTX
                  g4581164
NCBI GI
                   253
BLAST score
                   4.0e-22
E value
Match length
                   87
% identity
                   55
NCBI Description
                  (AC006220) putative polyprotein [Arabidopsis thaliana]
                   313872
Seq. No.
                   ypc700806955.h1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g168700
BLAST score
                   63
                   2.0e-27
E value
Match length
                   67
                   99
% identity
NCBI Description Z.mays zein mRNA, complete cds
                   313873
Seq. No.
                   ypc700806968.h1
Seq. ID
Method
                   BLASTX
                   g2660670
NCBI GI
BLAST score
                   203
                   3.0e-16
E value
Match length
                   72
% identity
                   (AC002342) putative Cu2+-transporting ATPase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   313874
                   ypc700807142.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4539660
BLAST score
                   277
                   6.0e-25
E value
Match length
                   88
% identity
                   61
                   (AF061282) polyprotein [Sorghum bicolor]
NCBI Description
                   313875
Seq. No.
                   ypc700807249.h1
Seq. ID
Method
                   BLASTX
                   g2832246
NCBI GI
```

```
4
 % identity
 NCBI Description (AF031569) 22-kDa alpha zein 8 [Zea mays]
                    313876
 Seq. No.
                    ypc700807251.hl
 Seq. ID
 Method
                    BLASTN
 NCBI GI
                    q535019
 BLAST score
                    109
                    1.0e-54
E value
                    185
 Match length
 % identity
 NCBI Description Z.mays Zd1 tandem genes for zein Zd1 (19 kDa Zein)
                    313877
 Seq. No.
                    ypc700807271.hl
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g468516
 BLAST score
                    178
                    2.0e-13
 E value
 Match length
                    43
 % identity
                    86
 NCBI Description
                   (X55724) zein [Zea mays]
 Seq. No.
                    313878
                    ypc700807288.h1
 Seq. ID
 Method
                    BLASTX
                    q1346033
 NCBI GI
 BLAST score
                    161
 E value
                    8.0e-16
 Match length
                    61
                    80
 % identity
                    FARNESYL PYROPHOSPHATE SYNTHETASE (FPP SYNTHETASE) (FPS)
 NCBI Description
                    (FARNESYL DIPHOSPHATE SYNTHETASE) (DIMETHYLALLYLTRANSFERASE
                    / GERANYLTRANSTRANSFERASE >gi_662368 (L397/89) farnesyl
                    pyrophosphate synthetase [Zea mays]
 Seq. No.
                    313879
                    ypc700807290.h1
 Seq. ID
 Method
                    BLASTX
                    g224513
 NCBI GI
 BLAST score
                    235
                    3.0e-20
 E value
 Match length
                    47
 % identity
                    91
 NCBI Description zein M6 [Zea mays]
 Seq. No.
                    313880
 Seq. ID
                    ypc700807310.h1
 Method
                    BLASTX
                    q4079800
 NCBI GI
                    231
 BLAST score
                    1.0e-19
 E value
 Match length
                    46
                    96
 % identity
                    (AF052503) S-phase-specific ribosomal protein [Oryza
 NCBI Description
                    sativa]
```

NCBI GI

```
Seq. No.
                  313881
                  ypc700807344.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g82659
BLAST score
                  283
                   1.0e-25
E value
Match length
                  73
                  78
% identity
                  19K zein precursor (clone Z4) - maize
NCBI Description
                  >gi 4388702_emb_CAA24719_ (V01472) zein [Zea mays]
Seq. No.
                   313882
                  ypc700807354.h1
Seq. ID
Method
                   BLASTN
                   q2764801
NCBI GI
                   70
BLAST score
                   1.0e-31
E value
Match length
                   98
% identity
NCBI Description Z.mays yptm3 mRNA
Seq. No.
                   313883
                   yyf700347416.h1
Seq. ID
Method
                   BLASTX
                   g122022
NCBI GI
BLAST score
                   317
                   2.0e-29
E value
                   94
Match length
% identity
                   71
                   HISTONE H2B >gi_283025_pir__S22323 histone H2B - wheat
NCBI Description
                   >gi 21801 emb CAA42530 (X59873) histone H2B [Triticum
                   aestivum]
                   313884
Seq. No.
Seq. ID
                   yyf700347482.h1
Method
                   BLASTN
NCBI GI
                   g22322
BLAST score
                   79
                   1.0e-36
E value
Match length
                   130
% identity
                   91
                  Z.mays mRNA for H2B histone (clone cH2B214)
NCBI Description
Seq. No.
                   313885
                   yyf700347491.h1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g473604
BLAST score
                   167
                   3.0e-89
E value
Match length
                   175
                   99
% identity
                   Zea mays W-22 histone H2B mRNA, complete cds
NCBI Description
Seq. No.
                   313886
                   yyf700347553.h1
Seq. ID
                   BLASTN
Method
```

44892

g3043629



```
BLAST score
                  9.0e-35
E value
                  228
Match length
                  84
% identity
NCBI Description Homo sapiens mRNA for KIAA0553 protein, partial cds
                  313887
Seq. No.
                  yyf700347611.h1
Seq. ID
Method
                  BLASTN
                  g4581063
NCBI GI
BLAST score
                  56
                  3.0e-23
E value
                  106
Match length
                  96
% identity
                  Homo sapiens activation of Sentrin/SUMO protein AOS1 (AOS1)
NCBI Description
                  mRNA, complete cds
                  313888
Seq. No.
                  yyf700347658.h1
Seq. ID
Method
                  BLASTX
                  g4033424
NCBI GI
BLAST score
                  219
                  5.0e-18
E value
Match length
                   41
                   98
% identity
                  SOLUBLE INORGANIC PYROPHOSPHATASE (PYROPHOSPHATE
NCBI Description
                   PHOSPHO-HYDROLASE) (PPASE) >gi_2668746 (AF034947) inorganic
                  pyrophosphatase [Zea mays]
                   313889
Seq. No.
                   yyf700347662.h1
Seq. ID
Method
                   BLASTX
                   g1839188
NCBI GI
                   223
BLAST score
                   2.0e-18
E value
                   69
Match length
                   57
% identity
                  (U86081) root hair defective 3 [Arabidopsis thaliana]
NCBI Description
                   313890
Seq. No.
                   yyf700347801.h1
Seq. ID
Method
                   BLASTX
                   g2982434
NCBI GI
                   229
BLAST score
E value
                   4.0e-19
Match length
                   83
                   53
% identity
                   (AL022224) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   313891
Seq. ID
                   yyf700347848.hl
                   BLASTX
Method
```

Method BLASTX
NCBI GI g418777
BLAST score 207
E value 1.0e-16
Match length 38
% identity 100



```
phosphoprotein phosphatase (EC 3.1.3.16) 2A-alpha catalytic
NCBI Description
                  chain (clone EP7) - Arabidopsis thaliana (fragment)
                  313892
Seq. No.
                  yyf700347858.hl
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2623962
                  389
BLAST score
                  5.0e-38
E value
Match length
                  91
                  81
% identity
                  (Y12540) isocitrate dehydrogenase (NADP+) [Apium
NCBI Description
                  graveolens]
                  313893
Seq. No.
                  yyf700347892.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3169172
                   206
BLAST score
                  2.0e-16
E value
Match length
                  73
                  55
% identity
                  (AC004401) putative serine carboxypeptidase I [Arabidopsis
NCBI Description
                   thaliana] >gi_3445214 (AC004786) putative serine
                   carboxypeptidase I [Arabidopsis thaliana]
                   313894
Seq. No.
                   yyf700347934.h1
Seq. ID
Method
                   BLASTX
                   q232031
NCBI GI
                   211
BLAST score
                   2.0e-17
E value
                   46
Match length
% identity
                  ELONGATION FACTOR 1 BETA' >gi 322851 pir_S29224
NCBI Description
                   translation elongation factor eEF-1 beta chain - rice
                   >qi 218161 dbj BAA02253 (D12821) elongation factor 1 beta'
                   [Oryza sativa]
Seq. No.
                   313895
                   yyf700347948.h1
Seq. ID
Method
                   BLASTX
```

g4559327 NCBI GI

BLAST score 201 5.0e-16 E value Match length 82 % identity

(AC007087) hypothetical protein [Arabidopsis thaliana] NCBI Description

Seq. No. 313896

yyf700347961.h1 Seq. ID Method BLASTX

g4502293 NCBI GI BLAST score 260 7.0e-23 E value 67 Match length 79 % identity



NCBI Description ATP synthase, H+ transporting, mitochondrial >gi_183786 (M73031) coupling factor 6 [Homo sapiens]

Seq. No. 313897

Seq. ID yyf700348005.h1

Method BLASTX
NCBI GI g166384
BLAST score 242
E value 6.0e-21
Match length 55

% identity 98

NCBI Description (M35867) histone H3 (H3-1.1) [Medicago sativa]

Seq. No. 313898

Seq. ID yyf700348006.h1

Method BLASTX
NCBI GI g133820
BLAST score 138
E value 8.0e-09
Match length 29
% identity 93

NCBI Description 40S RIBOSOMAL PROTEIN S17 >gi_304526 (M13933) ribosomal

protein S17 [Cricetulus griseus] >gi_1526555_dbj_BAA04943_

(D25213) ribosomal protein S17 [Mus musculus]

Seq. No. 313899

Seq. ID yyf700348044.h1

Method BLASTN
NCBI GI g22484
BLAST score 56
E value 6.0e-23
Match length 136
% identity 86

NCBI Description Z.mays RNA for superoxide dismutase Sod4A

Seq. No. 313900

Seq. ID yyf700348065.h1

Method BLASTN
NCBI GI g3080381
BLAST score 59
E value 6.0e-25
Match length 132
% identity 87

NCBI Description Homo sapiens DNA sequence from PAC 393P12 on chromosome

Xp11.21. Contains a hypothetical protein KIAA0413

(KIAA0412, KIAA0065, KIAA0569) LIKE Zinc Finger protein pseudogene, a hypothetical Proline-rich protein KIAA0269

Seq. No. 313901

Seq. ID yyf700348076.h1

Method BLASTX
NCBI GI g135398
BLAST score 402
E value 3.0e-39
Match length 94
% identity 85

NCBI Description TUBULIN ALPHA-1 CHAIN >gi_82731_pir__S15773 tubulin alpha-1



chain - maize >gi_22147_emb CAA33734 (X15704) alpha1-tubulin [Zea mays]

313902 Seq. No. Seq. ID yyf700348078.hl Method BLASTX NCBI GI g122106 BLAST score 305 4.0e-28 E value

Match length 89 % identity

HISTONE H4 >gi_70771_pir__HSZM4 histone H4 - maize >gi_81642_pir__S06904 histone H4 - Arabidopsis thaliana NCBI Description

>gi_2119028_pir__S60475 histone H4 - garden pea

>gi_21795_emb_CAA24924 (X00043) histone H4 [Triticum aestivum] >gi_166740 (M17132) histone H4 [Arabidopsis thaliana] >gi_166742 (M17133) histone H4 [Arabidopsis thaliana] >gi_168499 (M36659) histone H4 (H4C13) [Zea mays]

>gi_168501 (M $\overline{1}$ 3370) histone H4 [Zea mays] >gi_168503 $(M1\overline{3}377)$ histone H4 [Zea mays] >gi_498898 (U1 $\overline{0}042$) histone

H4 homolog [Pisum sativum] >gi_1806285_emb_CAB01914_

(Z79638) histone H4 homologue [Sesbania rostrata]

>gi_3927823 (AC005727) histone H4 [Arabidopsis thaliana] >gi_4580385_gb_AAD24364.1_AC007184_4 (AC007184) histone H4 [Arabidopsis thaliana] >gi 225838 prf 1314298A histone H4

[Arabidopsis thaliana]

313903 Seq. No.

yyf700348095.h1 Seq. ID

Method BLASTX g4455356 NCBI GI 225 BLAST score 6.0e-19 E value Match length 72 % identity

NCBI Description (AL035524) putative protein [Arabidopsis thaliana]

Seq. No. 313904

Seq. ID yyf700348110.hl

Method BLASTX NCBI GI g2511531 BLAST score 321 E value 7.0e-30 Match length 63 % identity 94

(AF008120) alpha tubulin 1 [Eleusine indica] NCBI Description

>gi 3163944 emb CAA06618 (AJ005598) alpha-tubulin 1

[Eleusine indica]

313905 Seq. No.

yyf700348134.h1 Seq. ID

Method BLASTN NCBI GI g473602 BLAST score 39 4.0e-13 E value Match length 107 % identity 84



NCBI Description Zea mays W-22 histone H2A mRNA, complete cds

NCBI GI g1087073 BLAST score 196 E value 3.0e-15 Match length 43 % identity 77

NCBI Description (S79243) calmodulin-binding heat-shock protein, CaMBP [Nicotiana tabacum=tobacco, Wisconsin-38, Peptide, 449 aa]

[Nicotiana tabacum]

Seq. No. 313907

Seq. ID yyf700348157.h1

Method BLASTN
NCBI GI g602605
BLAST score 48
E value 5.0e-18
Match length 100
% identity 87

NCBI Description Zea mays tandem genes for alphal-tubulin and alpha2-tubulin

Seq. No. 313908

Seq. ID yyf700348175.h1

Method BLASTX
NCBI GI g2815502
BLAST score 396
E value 9.0e-39
Match length 91
% identity 85

NCBI Description 60S RIBOSOMAL PROTEIN L44 (L36A) >gi_71187_pir__R6RT36 ribosomal protein L36a - rat >gi_206732 (M19635) ribosomal

protein L36a [Rattus norvegicus] >gi_1666702 (U58105) ribosomal protein [Mus musculus] >gi_1684917 (U78027)

L44-like ribosomal protein [Homo sapiens]

>gi_1841302_dbj_BAA19210_ (AB000910) ribosomal protein [Sus

scrofa]

Seq. No. 313909

Seq. ID yyf700348264.h1

Method BLASTX
NCBI GI g3080393
BLAST score 148
E value 5.0e-10
Match length 32
% identity 84

NCBI Description (AL022603) NADH dehydrogenase like protein [Arabidopsis

thaliana]

Seq. No. 313910

Seq. ID yyf700348268.h1

Method BLASTX
NCBI GI g2290528
BLAST score 331
E value 4.0e-31

```
Match length
% identity
                   72
                   (U94746) ATAN11 [Arabidopsis thaliana]
NCBI Description
                   313911
Seq. No.
                  yyf700348292.h1
Seq. ID
Method
                   BLASTX
                   g629641
NCBI GI
                   223
BLAST score
                   1.0e-18
E value
Match length
                   45
                   93
% identity
                   PsHSC71.0 protein - garden pea >gi_1076530_pir__S53500
NCBI Description
                   HSC71.0 protein - garden pea >gi_473217 emb_CAA83548_
                   (Z32537) PsHSC71.0 [Pisum sativum]
                   313912
Seq. No.
                   yyf700348295.h1
Seq. ID
Method
                   BLASTX
                   g4006893
NCBI GI
                   230
BLAST score
                   2.0e-19
E value
                   49
Match length
                   82
% identity
                  (Z99708) aminopeptidase-like protein [Arabidopsis thaliana]
NCBI Description
                   313913
Seq. No.
                   yyf700348301.h1
Seq. ID
                   BLASTN
Method
                   q1778146
NCBI GI
                   36
BLAST score
                   6.0e-11
E value
Match length
                   44
                   95
% identity
                   Zea mays plastid phosphate/phosphoenolpyruvate translocator
NCBI Description
                   precursor (MZPPT1) mRNA, complete cds
                   313914
Seq. No.
                   yyf700348304.h1
Seq. ID
Method
                   BLASTX
                   q3882081
NCBI GI
                   377
BLAST score
                   1.0e-36
E value
                   77
Match length
% identity
                   33
                   (AJ012552) polyubiquitin [Vicia faba]
NCBI Description
                   313915
Seq. No.
Seq. ID
                   yyf700348317.h1
Method
                   BLASTX
                   g231671
NCBI GI
BLAST score
                   242
                   5.0e-21
E value
Match length
                   50
                   88
% identity
                   PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR
NCBI Description
                   >gi_284994_pir__A43291 collagen alpha 2(I) chain precursor
```

Seq. ID

Method

```
collagen [Mus musculus]
                         313916
Seq. No.
                         yyf700348331.h1
Seq. ID
Method
                         BLASTX
NCBI GI
                         g1296955
                         269
BLAST score
                         3.0e-24
E value
Match length
                         55
% identity
                         44
NCBI Description
                         (X95402) duplicated domain structure protein [Oryza sativa]
Seq. No.
                         313917
                         yyf700348341.h1
Seq. ID
Method
                         BLASTX
NCBI GI
                         g231496
BLAST score
                         170
E value
                         1.0e-12
Match length
                         39
% identity
                         85
                         ACTIN 58 >gi_100421_pir__S20094 actin - potato
NCBI Description
                         >gi_21536_emb_CAA39278_ (X55749) actin [Solanum tuberosum]
Seq. No.
                         313918
                         yyf700348395.h1
Seq. ID
Method
                         BLASTX
                         g4506635
NCBI GI
BLAST score
                         394
                         1.0e-38
E value
Match length
                         88
                         88
% identity
                         ribosomal protein L32 >gi_132886_sp_P02433_RL32_HUMAN 60S
RIBOSOMAL PROTEIN L32 >gi_71335_pir__R5HU32_ribosomal
protein L32 - human >gi_71336_pir__R5MS32_ribosomal protein
L32 - mouse >gi_71337_pir__R5RT32_ribosomal protein L32 -
rat >gi_36132_emb_CAA27048_(X03342)_rpL32_(aa 1-135)_[Homo
sapiens] >gi_57117_emb_CAA29777_(X06483)_ribosomal_protein
L32_[Rattus_norvegicus] >gi_200781_(K02060)_ribosomal_protein_L32_37_[Mus_musqulus] >gi_226004_prf__14053337_
NCBI Description
                         protein L32-3A [Mus musculus] >gi_226004_prf__1405339A
                         ribosomal protein L32 [Rattus norvegicus]
Seq. No.
                         313919
Seq. ID
                         yyf700348428.h1
Method
                         BLASTX
NCBI GI
                         g3036796
BLAST score
                         201
E value
                          6.0e-16
                         56
Match length
% identity
                          68
                          (AL022373) putative protein [Arabidopsis thaliana]
NCBI Description
                         >gi 3805858 emb CAA21478 (AL031986) putative protein
                          [Arabidopsis thaliana]
Seq. No.
                         313920
```

- mouse >gi_50489_emb_CAA41205_ (X58251) pro-alpha-2(I)

44899

yyf700348447.h1

BLASTX

```
NCBI GI
                  q3786324
BLAST score
                  202
E value
                  5.0e-16
Match length
                   62
                  55
% identity
                   (AB015139) chlorophyll a oxygenase [Chlamydomonas
NCBI Description
                  reinhardtii]
                  313921
Seq. No.
                  yyf700348452.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1527219
BLAST score
                  411
                  1.0e-40
E value
                  93
Match length
% identity
                  83
                  (U68218) ATP sulphurylase [Brassica napus]
NCBI Description
Seq. No.
                  313922
                  yyf700348489.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2623247
BLAST score
                   60
E value
                   3.0e-25
Match length
                  88
% identity
                  92
                  Zea mays SU1 isoamylase (sugary1) gene, complete cds
NCBI Description
                   313923
Seq. No.
                  yyf700348520.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q168474
BLAST score
                   55
E value
                   9.0e-23
Match length
                   59
% identity
                   98
NCBI Description Maize ferredoxin (Fd) isoprotein mRNA, pFD5
Seq. No.
                   313924
                   yyf700348534.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3600035
BLAST score
                   200
E value
                   8.0e-16
Match length
                   95
                   44
% identity
NCBI Description
                   (AF080119) contains similarity to GTP-binding proteins
                   [Arabidopsis thaliana]
```

Seq. No. 313925

Seq. ID yyf700348617.h1

Method BLASTX
NCBI GI g119355
BLAST score 193
E value 2.0e-15
Match length 38
% identity 100

```
NCBI Description ENOLASE 1 (2-PHOSPHOGLYCERATE DEHYDRATASE 1)
(2-PHOSPHO-D-GLYCERATE HYDRO-LYASE 1)
>gi_100869_pir__S16257 phosphopyruvate hydratase (EC
4.2.1.11) - maize >gi_22273_emb_CAA39454_ (X55981) enolase
[Zea mays]

Seq. No. 313926
Seq. ID yyf700348691.h1
Method BLASTX
NCBI GI g2104908
```

NCBI GI g210490: BLAST score 297 E value 2.0e-27 Match length 81 % identity 79

NCBI Description (Y07632) potassium channel [Zea mays]

Seq. No. 313927

Seq. ID yyf700348745.h1

Method BLASTX
NCBI GI g2687358
BLAST score 419
E value 2.0e-41
Match length 81
% identity 99

NCBI Description (AF033263) nonphototropic hypocotyl 1 [Zea mays]

Seq. No. 313928

Seq. ID yyf700348756.h1

Method BLASTX
NCBI GI g3024018
BLAST score 368
E value 1.0e-35
Match length 69
% identity 100

NCBI Description INITIATION FACTOR 5A (EIF-5A) (EIF-4D)

>gi_1546919_emb_CAA69225_ (Y07920) translation initiation factor 5A [Zea mays] >gi_2668738 (AF034943) translation

initiation factor 5A [Zea mays]

Seq. No. 313929

Seq. ID yyf700348809.h1

Method BLASTX
NCBI GI g3643598
BLAST score 419
E value 2.0e-41
Match length 102
% identity 81

NCBI Description (AC005395) putative poly(A) polymerase [Arabidopsis

thaliana]

Seq. No. 313930

Seq. ID yyf700348812.h1

Method BLASTX
NCBI GI g2959781
BLAST score 365
E value 4.0e-35
Match length 103



% identity (AJ223508) Zwille protein [Arabidopsis thaliana] NCBI Description Seq. No. 313931 yyf700348989.h1 Seq. ID Method BLASTX NCBI GI q123378 BLAST score 281 2.0e-25 E value Match length 81 % identity

NCBI Description DNA-BINDING PROTEIN MNB1B (HMG1-LIKE PROTEIN)

>gi_100886_pir__S16670 high mobility group protein - maize
>gi_539062_pir__B47150 DNA-binding protein MNB1b - maize >gi 22329 emb CAA41220 (X58282) high mobility group

protein [Zea mays]

Seq. No. 313932

yyf700349003.h1 Seq. ID

Method BLASTN NCBI GI q4499947 BLAST score 43 E value 2.0e-15 Match length 104 90 % identity

NCBI Description Homo sapiens mRNA; cDNA DKFZp564I1916 (from clone

DKFZp564I1916)

Seq. No. 313933

yyf700349017.h1 Seq. ID

Method BLASTX NCBI GI q3121828 BLAST score 300 E value 1.0e-27 Match length 87 % identity 63

BENE PROTEIN >gi_2135423 pir I38891 hypothetical protein -NCBI Description

human (fragment) >gi 1000712 (U17077) unknown [Homo

sapiens]

Seq. No. 313934

Seq. ID yyf700349049.h1

Method BLASTX NCBI GI g1707928 BLAST score 350 3.0e-36 E value Match length 87 % identity 88

GLUCOSE-1-PHOSPHATE ADENYLYLTRANSFERASE LARGE SUBUNIT 2 NCBI Description

PRECURSOR (ADP-GLUCOSE SYNTHASE) (ADP-GLUCOSE

PYROPHOSPHORYLASE) (AGPASE S) (ALPHA-D-GLUCOSE-1-PHOSPHATE

ADENYL TRANSFERASE) >gi_1076806_pir__S49439

glucose-1-phosphate adenylyltransferase (EC 2.7.7.27) maize >gi_558365_emb_CAA86227_ (Z38111) ADP-glucose

pyrophosphorylase [Zea mays]

Seq. No. 313935

```
yyf700349088.h1
Seq. ID
Method
                  BLASTX
                  q1498053
NCBI GI
                  200
BLAST score
                  4.0e-16
E value
Match length
                  55
                  73
% identity
                  (U64436) ribosomal protein S8 [Zea mays]
NCBI Description
                  313936
Seq. No.
                  yyf700349095.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4505750
BLAST score
                  117
                  3.0e-59
E value
                  167
Match length
                  93
% identity
                  Homo sapiens profilin 2 (PFN2) mRNA
NCBI Description
                  >gi_190387_gb_L10678_HUMPROFII Human profilin II mRNA,
                  complete cds
                                                               4
                  313937
Seq. No.
                  yyf700349140.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1076678
BLAST score
                  173
                  5.0e-13
E value
Match length
                  56
                  73
% identity
NCBI Description ubiquitin / ribosomal protein S27a - potato (fragment)
                  313938
Seq. No.
                  yyf700349166.h1
Seq. ID
Method
                  BLASTX
                  g3335355
NCBI GI
BLAST score
                  182
E value
                   4.0e-19
Match length
                   69
% identity
                   20
                   (AC004512) Match to polyubiquitin DNA gb_L05401 from A.
NCBI Description
                   thaliana. Contains insertion of mitochondrial NADH
                   dehydrogenase gb_X82618 and gb_X98301. May be a pseudogene
                   with an expressed insert. EST gb_AA586248 comes from this
                   region. [Arabi
                   313939
Seq. No.
                   yyf700349173.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3334138
BLAST score
                   158
E value
                   8.0e-12
```

Match length 58 57

% identity

CALNEXIN HOMOLOG PRECURSOR >gi_669003 (U20502) calnexin NCBI Description

[Glycine max]

Seq. No.

```
yyf700349182.hl
Seq. ID
Method
                  BLASTX
NCBI GI
                  q122022
BLAST score
                  184
                  9.0e-14
E value
Match length
                  65
% identity
                  62
                  HISTONE H2B >gi_283025_pir__S22323 histone H2B - wheat
NCBI Description
                  >gi 21801 emb CAA42530 (X59873) histone H2B [Triticum
                  aestivum]
Seq. No.
                  313941
Seq. ID
                  yyf700349190.h1
Method
                  BLASTX
                  q802111
NCBI GI
                  193
BLAST score
                  2.0e-27
E value
Match length
                  100
% identity
                   74
                   (S74802) zero beta-globin [Rattus norvegicus=rats, Peptide,
NCBI Description
                  146 aa] [Rattus norvegicus]
Seq. No.
                  313942
                  yyf700349192.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                   g4558459
BLAST score
                   70
                   4.0e-31
E value
Match length
                   93
                   94
% identity
                  Zea mays replication origin activator ROA2 (roa2) gene,
NCBI Description
                  partial cds
Seq. No.
                   313943
                   yyf700349202.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q35053
BLAST score
                   294
E value
                   4.0e-27
Match length
                   63
% identity
                   89
                  (X53778) uracil DNA glycosylase [Homo sapiens]
NCBI Description
Seq. No.
                   313944
Seq. ID
                   yyf700349226.h1
Method
                   BLASTN
NCBI GI
                   g4507754
BLAST score
                   196
                   1.0e-106
E value
Match length
                   256
% identity
                   94
                  Homo sapiens TYRO protein tyrosine kinase binding protein
NCBI Description
                   (TYROBP) mRNA, and translated products
                   >gi_2905993_gb_AF019562_AF019562 Homo sapiens DAP12 mRNA,
```

Seq. No. 313945

complete cds



```
Seq. ID
                  yyf700349232.hl
Method
                  BLASTX
                  g114778
NCBI GI
                  238
BLAST score
                  2.0e-20
E value
Match length
                  86
% identity
                  71
                  BETA-2-MICROGLOBULIN PRECURSOR >gi 92006 pir A26842
NCBI Description
                  beta-2-microglobulin precursor - rat
                  >gi_55808_emb_CAA68498_ (Y00441) beta-2-microglobulin
                  precursor [Rattus norvegicus] >gi 1619327_emb_CAA69847_
                  (Y08531) beta 2 microglobulin [Rattus norvegicus]
Seq. No.
                  313946
                  yyf700349233.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4406810
BLAST score
                  249
                  1.0e-21
E value
Match length
                  82
% identity
                  61
                  (AC006201) unknown protein [Arabidopsis thaliana]
NCBI Description
                  313947
Seq. No.
Seq. ID
                  yyf700349271.h1
Method
                  BLASTX
NCBI GI
                  g4557787
BLAST score
                  193
                  3.0e-15
E value
Match length
                  38
                  95
% identity
                  neutrophil cytosolic factor 2; p67phox
NCBI Description
                  >qi 105160 pir A34855 67K neutrophil oxidase factor -
                  human >gi 189268 (M32011) neutrophil oxidase factor [Homo
                  sapiens]
Seq. No.
                  313948
Seq. ID
                  yyf700349294.h1
Method
                  BLASTX
NCBI GI
                  q1326372
BLAST score
                  149
E value
                  4.0e-10
Match length
                  56
% identity
                  62
NCBI Description
                  (U58750) Similar to Histone. [Caenorhabditis elegans]
Seq. No.
                  313949
Seq. ID
                  yyf700349319.h1
Method
                  BLASTN
NCBI GI
                  g4588027
BLAST score
                  73
```

E value 5.0e-33 Match length 197 % identity 86

NCBI Description Mus musculus steroid receptor RNA activator mRNA, complete



```
313950
Seq. No.
Seq. ID
                  yyf700349326.hl
Method
                  BLASTX
NCBI GI
                  q3421123
                  146
BLAST score
                  5.0e-12
E value
Match length
                  62
% identity
                  65
                  (AF043538) 20S proteasome beta subunit PBG1 [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  313951
Seq. ID
                  yyf700349349.h1
Method
                  BLASTX
NCBI GI
                  g3021272
BLAST score
                  190
                  1.0e-14
E value
Match length
                  72
% identity
                  46
                   (AL022347) serine /threonine kinase - like protein
NCBI Description
                   [Arabidopsis thaliana]
                  313952
Seq. No.
Seq. ID
                  yyf700349355.h1
Method
                  BLASTX
                                                                               -
                  g226471
NCBI GI
BLAST score
                  336
E value
                  1.0e-31
Match length
                  90
% identity
                  74
NCBI Description
                  Cu/Zn superoxide dismutase [Mus musculus]
                  313953
Seq. No.
Seq. ID
                  yyf700349365.hl
Method
                  BLASTX
NCBI GI
                  g2501011
BLAST score
                   195
E value
                   4.0e-15
Match length
                   44
% identity
                   80
                  ISOLEUCYL-TRNA SYNTHETASE (ISOLEUCINE--TRNA LIGASE) (ILERS)
NCBI Description
                  >gi_1652625_dbj_BAA17545_ (D90907) isoleucyl-tRNA
                   synthetase [Synechocystis sp.]
Seq. No.
                   313954
                  yyf700349374.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4504960
BLAST score
                   51
E value
                   5.0e-20
Match length
                   125
% identity
                   94
                  Homo sapiens lamin B receptor (LBR) mRNA
NCBI Description
                  >gi 438638 gb L25931 HUMLBR Human lamin B receptor (LBR)
```

Seq. No. 313955

mRNA, complete cds

NCBI GI

E value

BLAST score

g2511531

2.0e-38

394

بن -

```
yyf700349383.h1
Seq. ID
                  BLASTX
Method
                  q1332579
NCBI GI
BLAST score
                  317
                  2.0e-40
E value
                  98
Match length
% identity
NCBI Description (X98063) polyubiquitin [Pinus sylvestris]
                  313956
Seq. No.
                  yyf700349387.h1
Seq. ID
                  BLASTX
Method
                   g214113
NCBI GI
BLAST score
                   220
                   2.0e-18
E value
                   48
Match length
                   92
% identity
                   (M25504) elongation factor-1 alpha-chain protein
NCBI Description
                   (EF-1-alpha) [Xenopus laevis]
                   313957
Seq. No.
                   yyf700349393.hl
Seq. ID
                   BLASTX
Method
                   g2342724
NCBI GI
BLAST score
                   260
                   6.0e-23
E value
                   88
Match length
                   58
% identity
NCBI Description (AC002341) unknown protein [Arabidopsis thaliana]
                   313958
Seq. No.
                   yyf700349396.h1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4587550
BLAST score
                   149
E value
                   8.0e-10
                   42
Match length
% identity
                   67
                   (AC006577) EST gb R64848 comes from this gene. [Arabidopsis
NCBI Description
                   thaliana]
                   313959
Seq. No.
                   yyf700349462.h1
Seq. ID
                   BLASTN
Method
NCBI GI
                   q516551
                   81
BLAST score
                   3.0e-38
E value
                   107
Match length
% identity
                   94
NCBI Description Zea mays B73 cyclin IbZm mRNA, complete cds
                   313960
Seq. No.
Seq. ID
                   yyf700349493.h1
Method
                   BLASTX
```

```
Match length 78
% identity 94
NCBI Description (AF008120) alpha tubulin 1 [Eleusine indica]
>gi_3163944_emb_CAA06618_ (AJ005598) alpha-tubulin 1
[Eleusine indica]

Seq. No. 313961
Seq. ID yyf700349506.h1
Method BLASTX
NCBI GI g3093294
```

NCBI GI g3093294
BLAST score 412
E value 1.0e-40
Match length 106
% identity 78

NCBI Description (Y12782) putative villin [Arabidopsis thaliana]

Seq. ID yyf700349530.h1
Method BLASTX
NCBI GI g4220529
BLAST score 326
E value 2.0e-30

Match length 105 % identity 63

Seq. No.

NCBI Description (AL035356) putative protein [Arabidopsis thaliana]

Seq. No. 313963

Seq. ID yyf700349556.h1

313962

Method BLASTX
NCBI GI g2828296
BLAST score 215
E value 1.0e-32
Match length 76
% identity 91

NCBI Description (AL021687) RNase L inhibitor [Arabidopsis thaliana]

Seq. No. 313964

Seq. ID yyf700349568.h1

Method BLASTX
NCBI GI g3962377
BLAST score 324
E value 2.0e-30
Match length 62
% identity 98

NCBI Description (AJ002551) heat shock protein 70 [Arabidopsis thaliana]

Seq. No. 313965

Seq. ID yyf700349615.h1

Method BLASTX
NCBI GI g3063700
BLAST score 183
E value 7.0e-14
Match length 59
% identity 61

NCBI Description (AL022537) putative protein [Arabidopsis thaliana]

Seq. No. 313966

```
yyf700349631.h1
Seq. ID
                   BLASTX
Method
                   g4193320
NCBI GI
                   502
BLAST score
                   3.0e-51
E value
                   93
Match length
                   100
% identity
                  (AF045473) histone deacetylase [Zea mays]
NCBI Description
                   313967
Seq. No.
                   yyf700349642.h1
Seq. ID
                   BLASTX
Method
                   g70774
NCBI GI
BLAST score
                   233
                   8.0e-20
E value
                   47
Match length
                   100
% identity
                   histone H4 (TH091) - wheat >gi_170747 (M12277) histone H4
NCBI Description
                   [Triticum aestivum]
                   313968
Seq. No.
                   yyf700349736.h1
Seq. ID
                   BLASTX
Method
                   g3402749
NCBI GI
BLAST score
                   258
                   1.0e-22
E value
                   94
Match length
                   46
% identity
                  (AL031187) putative protein [Arabidopsis thaliana]
NCBI Description
                   313969
Seq. No.
                   yyf700349765.h1
Seq. ID
                   BLASTX
Method
                   g3861068
NCBI GI
                   151
BLAST score
E value
                   4.0e-10
Match length
                   50
                   50
% identity
                  (AJ235272) unknown [Rickettsia prowazekii]
NCBI Description
Seq. No.
                   313970
Seq. ID
                   yyf700349777.h1
                   BLASTX
Method
                   q3746071
NCBI GI
BLAST score
                   157
                   9.0e-11
E value
                   33
Match length
                   85
% identity
                   (AC005311) putative GTP-binding protein [Arabidopsis
NCBI Description
                   thaliana]
```

thal

Method BLASTX
NCBI GI g4508068
BLAST score 164
E value 6.0e-12

```
Match length
% identity
                   69
                  (AC005882) 3063 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  313972
                  yyf700349869.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g21800
BLAST score
                  111
                  1.0e-55
E value
Match length
                  223
                  88
% identity
NCBI Description T.aestivum L mRNA for histone H2B
                  313973
Seq. No.
                  yyf700349879.hl
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2649435
BLAST score
                  155
E value
                  1.0e-10
Match length
                  96
                  39
% identity
NCBI Description
                   (AE001024) conserved hypothetical protein [Archaeoglobus
                  fulgidus]
Seq. No.
                   313974
                  yyf700349890.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2511531
BLAST score
                   238
                  1.0e-22
E value
Match length
                   51
                   94
% identity
NCBI Description
                   (AF008120) alpha tubulin 1 [Eleusine indica]
                  >gi_3163944_emb_CAA06618_ (AJ005598) alpha-tubulin 1
                   [Eleusine indica]
Seq. No.
                   313975
                  yyf700349960.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q902524
BLAST score
                   147
E value
                   3.0e-77
Match length
                   214
% identity
                   93
                  Zea mays clone MubG10 ubiquitin fusion protein gene,
NCBI Description
                  complete cds
                  313976
Seq. No.
Seq. ID
                  yyf700349963.hl
Method
                  BLASTX
NCBI GI
                  g2739044
BLAST score
                  172
E value
                  1.0e-12
Match length
                   45
                   67
% identity
                  (AF024651) polyphosphoinositide binding protein Ssh1p
NCBI Description
```



[Glycine max]

```
Seq. No.
                   313977
                   yyf700349991.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2191152
BLAST score
                   170
                   6.0e-13
E value
Match length
                   59
                   58
% identity
                   (AF007269) A IG002N01.31 gene product [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   313978
                   yyf700350025.hl
Seq. ID
Method
                   BLASTN
NCBI GI
                   g169818
BLAST score
                   51
E value
                   7.0e-20
Match length
                   67
                   94
% identity
NCBI Description Rice 25S ribosomal RNA gene
                   313979
Seq. No.
Seq. ID
                   yyf700350092.h1
Method
                   BLASTX
                   g2673906
NCBI GI
                   201
BLAST score
                   6.0e-16
E value
Match length
                   64
                   66
% identity
                   (AC002561) putative DNA polymerase delta small subunit
NCBI Description
                   [Arabidopsis thaliana]
                   313980
Seq. No.
                   yyf700350102.h1
Seq. ID
Method
                   BLASTX
                   q3176714
NCBI GI
                   230
BLAST score
E value
                   1.0e-19
                   59
Match length
                   73
% identity
                   (AC002392) putative tRNA-splicing endonuclease positive
NCBI Description
                   effector [Arabidopsis thaliana]
                   313981
Seq. No.
                   yyf700350122.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4432841
BLAST score
                   320
                   7.0e-30
E value
Match length
                   96
% identity
                   62
                   (AC006283) hypothetical protein [Arabidopsis thaliana]
NCBI Description
```

313982

yyf700350156.h1

Seq. No.

Seq. ID



Method BLASTX
NCBI GI g312179
BLAST score 229
E value 6.0e-27
Match length 67
% identity 97

NCBI Description (X73151) glyceraldehyde 3-phosphate dehydrogenase

(phosphorylating) [Zea mays] >gi_1184772 (U45855) cytosolic glyceroldehyde-3-phosphate dehydrogenase GAPC2 [Zea mays]

>gi_1185554 (U45858) glyceraldehyde-3-phosphate

dehydrogenase [Zea mays]

Seq. No. 313983

Seq. ID yyf700350160.h1

Method BLASTX
NCBI GI g2984709
BLAST score 192
E value 3.0e-15
Match length 68
% identity 60

NCBI Description (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]

Seq. No. 313984

Seq. ID yyf700350193.h1

Method BLASTX
NCBI GI g4585966
BLAST score 154
E value 1.0e-10
Match length 37
% identity 81

NCBI Description (AC005287) Putative dihyrdolipoamide acetyltransferase

[Arabidopsis thaliana]

Seq. No. 313985

Seq. ID yyf700350210.h1

Method BLASTX
NCBI GI g642134
BLAST score 152
E value 2.0e-10
Match length 41
% identity 73

NCBI Description (D45355) protein kinase [Arabidopsis thaliana]

>gi 3063704 emb CAA18595.1 (AL022537) protein kinase AME3

[Arabidopsis thaliana]

Seq. No. 313986

Seq. ID yyf700350234.h1

Method BLASTX
NCBI GI g3600039
BLAST score 407
E value 5.0e-40
Match length 100
% identity 70

NCBI Description (AF080119) similar to Schizosaccharomyces pombe isp4

protein (GB:D14061) [Arabidopsis thaliana]

Seq. No. 313987

```
yyf
```

```
yyf700350249.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2181184
                   181
BLAST score
E value
                   2.0e-13
Match length
                  103
                   41
% identity
                  (Y13577) JR3 protein [Arabidopsis thaliana]
NCBI Description
                   313988
Seq. No.
                   yyf700350266.h1
Seq. ID
Method
                   BLASTX
                   g2668744
NCBI GI
BLAST score
                   216
                   1.0e-17
E value
                   37
Match length
                   100
% identity
                  (AF034946) ubiquitin conjugating enzyme [Zea mays]
NCBI Description
                   313989
Seq. No.
                   yyf700350286.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3676246
BLAST score
                   507
E value
                   8.0e-52
Match length
                   93
                   100
% identity
                   (AJ011607) DNA polymerase alpha subunit III (primase)
NCBI Description
                   [Rattus norvegicus]
                   313990
Seq. No.
                   yyf700350326.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2914703
                   169
BLAST score
                   2.0e-12
E value
Match length
                   48
% identity
                   58
                   (AC003974) unknown protein [Arabidopsis thaliana]
NCBI Description
                   313991
Seq. No.
                   yyf700350355.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2598227
BLAST score
                   234
E value
                   4.0e-20
Match length
                   65
                   71
% identity
                  (AJ222585) AT-hook protein 1 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   313992
                   yyf700350371.h1
Seq. ID
Method
                   BLASTN
                   g644491
NCBI GI
BLAST score
                   41
```

44913

3.0e-14

84

E value Match length

```
% identity
NCBI Description Corn mRNA for elongation factor 1A
                  313993
Seq. No.
                  yyf700350378.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3309575
                  293
BLAST score
E value
                  5.0e-27
Match length
                  71
% identity
                  79
NCBI Description
                  (AF060553) calcium sensor homolog [Arabidopsis thaliana]
                  >gi 4538989 emb CAB39731.1 (Y18870) CBL4 protein
                  [Arabidopsis thaliana]
Seq. No.
                  313994
Seq. ID
                  yyf700350422.h1
Method
                  BLASTX
                  g2853084
NCBI GI
BLAST score
                  150
                                                                                 6.0e-10
E value
Match length
                  52
% identity
                  56
NCBI Description
                  (AL021768) putative protein [Arabidopsis thaliana]
Seq. No.
                  313995
Seq. ID
                  yyf700350431.h1
Method
                  BLASTX
NCBI GI
                  g2245030
BLAST score
                  200
                  4.0e-16
E value
Match length
                  59
% identity
                  66
NCBI Description
                  (Z97341) apetala2 domain TINY homolog [Arabidopsis
                  thaliana]
Seq. No.
                  313996
Seq. ID
                  yyf700350440.h1
Method
                  BLASTX
NCBI GI
                  q3152613
BLAST score
                  211
E value
                  4.0e-17
Match length
                  94
% identity
                  49
                  (AC004482) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  313997
Seq. ID
                  yyf700350507.hl
Method
                  BLASTN
NCBI GI
                  g4503504
BLAST score
                  38
E value
                  2.0e-12
Match length
                  62
                  90
% identity
NCBI Description
                  Homo sapiens eukaryotic translation initiation factor 2,
                  subunit 2 (beta, 38kD ) (EIF2S2) mRNA
                  >gi_182066 gb M29536 HUMELF2 Human translational initiation
```

NCBI GI

g600855



factor 2 beta subunit (elF-2-beta) mRNA, complete cds

```
313998
Seq. No.
                  yyf700350517.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4263721
BLAST score
                   247
                  1.0e-21
E value
Match length
                   61
                  77
% identity
NCBI Description
                   (ACO06223) putative DNA repair protein RAD50 [Arabidopsis
                   thaliana]
                   313999
Seq. No.
                   yyf700350572.h1
Seq. ID
Method
                  BLASTN
                  g397395
NCBI GI
BLAST score
                   161
E value
                   2.0e-85
Match length
                  165
% identity
                   99
NCBI Description Z.mays MNB1b mRNA for DNA-binding protein
Seq. No.
                   314000
                   yyf700350610.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3461820
BLAST score
                   188
                   2.0e-14
E value
Match length
                   45
% identity
                   71
NCBI Description
                  (AC004138) unknown protein [Arabidopsis thaliana]
Seq. No.
                   314001
Seq. ID
                   yyf700350663.h1
Method
                   BLASTX
NCBI GI
                   q66615
BLAST score
                   385
E value
                   2.0e-37
Match length
                   74
% identity
                   99
NCBI Description
                  glutathione transferase (EC 2.5.1.18) I - maize
Seq. No.
                   314002
                   yyf700350737.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4097575
BLAST score
                   193
                   2.0e-24
E value
Match length
                   62
% identity
                  (U64913) NTFP1 [Nicotiana tabacum]
NCBI Description
Seq. No.
                   314003
Seq. ID
                   yyf700350763.h1
Method
                   BLASTX
```

NCBI Description

```
BLAST score
                   2.0e-11
E value
Match length
                   59
% identity
                   53
NCBI Description
                  (U17887) bZIP protein [Arabidopsis thaliana]
Seq. No.
                   314004
                   yyf700350765.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2342724
BLAST score
                   302
E value
                   8.0e-28
Match length
                   90
% identity
                   62
NCBI Description
                   (AC002341) unknown protein [Arabidopsis thaliana]
Seq. No.
                   314005
Seq. ID
                   yyf700350788.h1
Method
                   BLASTN
NCBI GI
                   g22511
BLAST score
                   139
E value
                   2.0e-72
Match length
                   155
% identity
                   97
NCBI Description
                   Z.mays whp (white pollen) gene for chalcone synthase
Seq. No.
                   314006
Seq. ID
                   yyf700350844.h1
Method
                   BLASTX
NCBI GI
                   g1944330
BLAST score
                   174
E value
                   9.0e-13
Match length
                   43
% identity
                   84
NCBI Description
                  (D49545) KIFC2 [Mus musculus]
                   314007
Seq. No.
Seq. ID
                   yyf700350884.h1
Method
                   BLASTX
NCBI GI
                   g1172836
BLAST score
                   379
                   8.0e-37
E value
                   72
Match length
% identity
                   96
                   GTP-BINDING NUCLEAR PROTEIN RAN-B1 >gi 496272 (L16787)
NCBI Description
                   small ras-related protein [Nicotiana tabacum]
                   314008
Seq. No.
Seq. ID
                   yyf700350907.h1
Method
                   BLASTX
NCBI GI
                   g2827710
BLAST score
                   332
E value
                   2.0e-31
Match length
                   87
                   78
% identity
```

[Arabidopsis thaliana]

(AL021684) lysosomal Pro-X carboxypeptidase - like protein



```
Seq. No.
                  314009
                  yyf700350912.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q399213
                   253
BLAST score
E value
                   5.0e-22
                   53
Match length
                   94
% identity
                  ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPA HOMOLOG
NCBI Description
                   CD4B PRECURSOR >gi_100190_pir__B35905 CD4B protein - tomato
                   >gi_170435 (M32604) ATP-dependent protease (CD4B)
                   [Lycopersicon esculentum]
                   314010
Seq. No.
                   yyf700350950.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3252868
BLAST score
                   289
                   3.0e-26
E value
                   90
Match length
                   58
% identity
NCBI Description
                  (AF033536) putative zinc transporter [Arabidopsis thaliana]
Seq. No.
                   314011
                   yyf700350977.h1
Seq. ID
Method
                   BLASTN
                   q312180
NCBI GI
BLAST score
                   34
                   1.0e-09
E value
Match length
                   42
                   95
% identity
NCBI Description Z.mays GapC4 gene
Seq. No.
                   314012
                   yyf700351006.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4455255
BLAST score
                   148
E value
                   1.0e-09
Match length
                   78
                   44
% identity
NCBI Description
                  (AL035523) putative protein [Arabidopsis thaliana]
Seq. No.
                   314013
Seq. ID
                   yyf700351050.h1
Method
                   BLASTN
NCBI GI
                   g168500
BLAST score
                   67
E value
                   2.0e-29
Match length
                   178
% identity
                   87
NCBI Description Maize (Zea mays) histone H4 gene (H4C14), complete cds
```

Seq. No. 314014

Seq. ID yyf700351110.h1

Method BLASTX

```
NCBI GI
                  q4585991
BLAST score
                  164
                  7.0e-12
E value
                  41
Match length
% identity
                  (AC005287) very similar to mouse Dhm1 and Dhm2 [Arabidopsis
NCBI Description
                  thaliana]
                  314015
Seq. No.
                  yyf700351114.h1
Seq. ID
Method
                  BLASTX
                  g3242709
NCBI GI
BLAST score
                  222
                  2.0e-18
E value
                  78
Match length
% identity
                  63
                  (AC003040) putative quanine nucleotide-binding protein
NCBI Description
                  [Arabidopsis thaliana]
                  314016
Seq. No.
                  yyf700351209.h1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3256066
BLAST score
                  197
                  1.0e-15
E value
Match length
                  73
                  52
% identity
NCBI Description (Y13987) chloroplast NAD-MDH [Arabidopsis thaliana]
                  314017
Seq. No.
                  yyf700351224.h1
Seq. ID
Method
                  BLASTX
                  g1076820
NCBI GI
BLAST score
                  321
                  5.0e-30
E value
Match length
                  57
% identity
                  100
                  phosphoglycerate mutase (EC 5.4.2.1) - maize
NCBI Description
Seq. No.
                  314018
Seq. ID
                  yyf700351302.h1
Method
                  BLASTX
NCBI GI
                  q2196672
BLAST score
                  333
E value
                  2.0e-31
Match length
                  84
                  76
% identity
NCBI Description
                  (Y08807) HMGd1 [Zea mays]
Seq. No.
                  314019
Seq. ID
                  yyf700351307.h1
Method
                  BLASTX
                  q134598
NCBI GI
BLAST score
                  206
E value
                  3.0e-28
Match length
                  86
                  80
% identity
```

Method

BLASTX



```
NCBI Description SUPEROXIDE DISMUTASE-4AP (CU-ZN)
                     314020
  Seq. No.
  Seq. ID
                     yyf700351383.h1
  Method
                     BLASTN
  NCBI GI
                     g4589503
                     209
  BLAST score
  E value
                     1.0e-114
                     233
  Match length
🗽 % identity
                     97
  NCBI Description Homo sapiens mRNA for KIAA0930 protein, partial cds
                     314021
  Seq. No.
  Seq. ID
                     yyf700351410.hl
  Method
                     BLASTX
  NCBI GI
                     g1172977
  BLAST score
                     247
                     2.0e-34
  E value
                     98
  Match length
                     77
  % identity
                     60S RIBOSOMAL PROTEIN L18 >gi 606970 (U15741) cytoplasmic
  NCBI Description
                     ribosomal protein L18 [Arabidopsis thaliana]
  Seq. No.
                     314022
  Seq. ID
                     yyf700351492.h1
  Method
                     BLASTX
                     g1899060
  NCBI GI
  BLAST score
                     313
  E value
                     3.0e-29
  Match length
                     80
                     72
  % identity
  NCBI Description
                     (U79669) endosperm C-24 sterol methyltransferase [Zea mays]
                     314023
  Seq. No.
                     yyf700351536.h1
  Seq. ID
  Method
                     BLASTX
                     g3413888
  NCBI GI
  BLAST score
                     154
  E value
                     2.0e-10
  Match length
                     31
                     97
  % identity
                     (AB007932) KIAA0463 protein [Homo sapiens]
  NCBI Description
  Seq. No.
                     314024
                     yyf700351548.h1
  Seq. ID
  Method
                     BLASTX
  NCBI GI
                     g4432867
  BLAST score
                     149
                     8.0e-10
  E value
  Match length
                     87
  % identity
                     4 Õ
  NCBI Description
                     (AC006300) putative dnaJ-like protein [Arabidopsis
                     thaliana]
  Seq. No.
                     314025
                     yyf700351549.h1
  Seq. ID
```

q4502095 NCBI GI 180 BLAST score 9.0e-14 E value

Match length 35 % identity

NCBI Description alanyl (membrane) aminopeptidase (aminopeptidase N, aminopeptidase M, microsomal aminopeptidase, CD13, p150)

>gi_105598_pir__A30325 membrane alanyl aminopeptidase (EC

3.4.11.2) precursor - human >gi_178536 (M22324) aminopeptidase N precursor (EC 3.4.11.2) [Homo sapiens]

Seq. No. 314026

Seq. ID yyf700351567.h1

Method BLASTX NCBI GI q4584545 BLAST score 228 E value 4.0e-19 Match length 63 % identity 65

NCBI Description (AL049608) putative protein [Arabidopsis thaliana]

Seq. No. 314027

Seq. ID yyf700351629.hl

Method BLASTN NCBI GI q4160401 BLAST score 112 3.0e-56 E value 172 Match length % identity

NCBI Description Zea mays eIF-5 gene, exons 1-2

Seq. No. 314028

Seq. ID yyf700351633.hl

Method BLASTX NCBI GI g417103 BLAST score 361 1.0e-34 E value 72 Match length % identity 100

HISTONE H3.2, MINOR >gi 282871 pir S24346 histone NCBI Description

H3.3-like protein - Arabidopsis thaliana

>gi_16324_emb_CAA42957 (X60429) histone H3.3 like protein
[Arabidopsis thaliana] >gi_404825_emb_CAA42958 (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_488563 (U09458) histone H3.2 [Medicago sativa] >gi 488567 (U09460) histone H3.2 [Medicago sativa] >gi 488569 ($\overline{\text{U}}$ 09461) histone H3.2 [Medicago sativa] >gi_488575 (U09464) histone H3.2

[Medicago sativa] $>gi_488577$ (U09465) histone H3.2

[Medicago sativa] >gi_510911_emb_CAA56153_ (X79714) histone H3 [Lolium temulentum] >gi 1435157 emb CAA58445 (X83422)

histone H3 variant H3.3 [Lycopersicon esculentum]

>gi 2558944 (AF024716) histone 3 [Gossypium hirsutum] >gi_3273350_dbj_BAA31218 (AB015760) histone H3 [Nicotiana tabacum] >gi 3885890 (AFO93633) histone H3 [Oryza sativa] >gi_4038469 gb AAC97380 (AF109910) histone H3 [Porteresia coarctata] >gi 4490754_emb_CAB38916.1_ (AL035708) histone H3.3 [Arabidopsis thaliana] >gi_4490755_emb_CAB38917.1_

E value

Match length

% identity

2.0e-18

46

89



(AL035708) Histon H3 [Arabidopsis thaliana]

314029 Seq. No. Seq. ID yyf700351694.h1 Method BLASTN NCBI GI g4585826 BLAST score 227 E value 1.0e-125 265 Match length 96 % identity Rattus norvegicus mRNA for ribosome associated membrane NCBI Description protein RAMP4 314030 Seq. No. Seq. ID yyf700351717.h1 Method BLASTX NCBI GI g3335354 BLAST score 156 E value 1.0e-10 Match length 71 % identity 45 NCBI Description (AC004512) This gene is continued from gene F5I14.1 from BAC sequence gb AC001229 from A. thaliana. EST gb AA585814 comes from this gene. [Arabidopsis thaliana] Seq. No. 314031 Seq. ID yyf700351805.h1 Method BLASTX NCBI GI g130708 BLAST score 440 E value 6.0e-44Match length 99 78 % identity SERINE/THREONINE PROTEIN PHOSPHATASE PP1 NCBI Description >gi 81693_pir__S12985 phosphoprotein phosphatase (EC 3.1.3.16) 1 catalytic chain - rape (fragment) >gi 17846 emb CAA40686 (X57438) phosphatase 1 catalytic subunit [Brassica napus] 314032 Seq. No. Seq. ID yyf700351851.h1 Method BLASTN NCBI GI g685177 BLAST score 271 E value 1.0e-151 Match length 275 % identity 100 NCBI Description Homo sapiens troponin T cardiac isoform mRNA, 3' end of cds Seq. No. 314033 yyf700351859.h1 Seq. ID 24. Method BLASTX NCBI GI g3122800 BLAST score 222



```
40S RIBOSOMAL PROTEIN S16 >gi 2641209 (AF031546) ribosomal
NCBI Description
                  protein S16 [Fritillaria agrestis]
                  314034
Seq. No.
                  yyf700351873.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3582311
BLAST score
                  234
E value
                  1.0e-129
Match length
                  254
% identity
NCBI Description
                  Human Chromosome 16 BAC clone CIT987SK-A-972D3, complete
                  sequence [Homo sapiens]
                  314035
Seq. No.
Seq. ID
                  yyf700351888.h1
Method
                  BLASTX
                  g1172977
NCBI GI
                  190
BLAST score
                  6.0e-15
E value
Match length
                  57
% identity
                  70
                  60S RIBOSOMAL PROTEIN L18 >gi 606970 (U15741) cytoplasmic
NCBI Description
                  ribosomal protein L18 [Arabidopsis thaliana]
                  314036
Seq. No.
                  yyf700351890.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2808656
BLAST score
                  110
E value
                  4.0e-55
Match length
                  145
                   92
% identity
NCBI Description
                  Homo sapiens complete genomic sequence between D16S3070 and
                  D16S3275, containing Familial Mediterranean Fever gene
                  314037
Seq. No.
                  yyf700351905.h1
Seq. ID
Method
                  BLASTX
                  q4510395
NCBI GI
BLAST score
                  178
                   4.0e-13
E value
Match length
                  74
% identity
                   53
                   (AC006587) putative beta-galactosidase precursor
NCBI Description
                   [Arabidopsis thaliana]
                  314038
Seq. No.
Seq. ID
                  yyf700351912.h1
Method
                  BLASTX
NCBI GI
                  q3912921
                   433
```

NCBI GI g3912921 BLAST score 433 E value 5.0e-43 Match length 88

% identity 86

NCBI Description (AF001308) G/T DNA mismatch repair enzyme [Arabidopsis



thaliana]

```
Seq. No.
                   314039
Seq. ID
                   yyf700351933.h1
Method
                   BLASTN
NCBI GI
                   g3790132
BLAST score
                   150
E value
                   5.0e-79
Match length
                   242
% identity
                   91
```

Human DNA sequence from clone 191N21 on chromosome 6q27 NCBI Description

Contains genes for PDCD2 (PROGRAMMED CELL DEATH-2/RP8

HOMOLOG), TATA factor (TFIID), proteasome subunit HC5, EST,

STS, GSS, complete sequence [Homo sapiens]

```
Seq. No.
                   314040
                   yyf700352005.h1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g4519193
```

36 BLAST score E value 7.0e-11 Match length 52 % identity 92

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MDC11, complete sequence

```
Seq. No.
                   314041
                   yyf700352014.h1
Seq. ID
Method
                   BLASTX
```

NCBI GI q722379 BLAST score 142 E value 5.0e-09 Match length 95 39 % identity

NCBI Description (U23139) similar to NIFS protein (nitrogen fixation)

[Caenorhabditis elegans]

```
Seq. No.
                   314042
Seq. ID
                   yyf700352049.h1
```

Method BLASTX NCBI GI q2832617 BLAST score 206 E value 8.0e-17 Match length 54 % identity

NCBI Description (AL021711) putative protein [Arabidopsis thaliana]

Seq. No. 314043

Seq. ID yyf700352054.h1

Method BLASTX NCBI GI g1171865 BLAST score 316 E value 2.0e-29 Match length 80 79 % identity

The second of th

NADH-UBIQUINONE OXIDOREDUCTASE 20 KD SUBUNIT PRECURSOR NCBI Description

ASSESSED TO A COLOR

(COMPLEX I-20KD) (CI-20KD) (PSST SUBUNIT)

44923

and the second second

>gi_108826_pir__S22371 NADH dehydrogenase (EC 1.6.99.3)
chain PSST - bovine >gi_599691_emb_CAA46154_ (X65020) PSST
subunit of the NADH: ubiquinone oxidoreductase complex [Bos taurus]

 Seq. No.
 314044

 Seq. ID
 yyf700352112.h1

 Method
 BLASTX

NCBI GI g4415937
BLAST score 200
E value 2.0e-19
Match length 63
% identity 74

NCBI Description (AC006418) hypothetical protein [Arabidopsis thaliana]

Seq. No. 314045

Seq. ID yyf700352126.h1

Method BLASTX
NCBI GI g2996140
BLAST score 244
E value 6.0e-21
Match length 67
% identity 70

NCBI Description (AF051743) fibrillarin [Picea mariana] >gi_2996142 (AF051744) fibrillarin [Picea mariana] >gi_2996144

(AF051745) fibrillarin [Picea mariana]

Seq. No. 314046

Seq. ID yyf700352133.h1

Method BLASTN
NCBI GI g3413877
BLAST score 245
E value 1.0e-135
Match length 261
% identity 98

NCBI Description Homo sapiens mRNA for KIAA0458 protein, complete cds

Seq. No. 314047

Seq. ID yyf700352160.h1

Method BLASTX
NCBI GI g2809247
BLAST score 191
E value 9.0e-15
Match length 95
% identity 22

NCBI Description (AC002560) F21B7.16 [Arabidopsis thaliana]

Seq. No. 314048

Seq. ID yyf700352188.h1

Method BLASTX
NCBI GI g547909
BLAST score 366
E value 2.0e-35
Match length 88

% identity 6
NCBI Description ZINC FINGER PROTEIN MLZ-4 (ZINC FINGER PROTEIN 46)
>gi 423617 pir JN0533 finger protein pMLZ-4 - mouse

Method

BLASTX





>gi_200407 (M98502) pMLZ-4 [Mus musculus]

```
Seq. No.
                   314049
Seq. ID
                   yyf700352206.h1
Method
                   BLASTN
                   g4503078
NCBI GI
                   194
BLAST score
                   1.0e-105
E value
Match length
                   286
                   93
% identity
                  Homo sapiens colony stimulating factor 3 (granulocyte)
NCBI Description
                   (CSF3) mRNA
                   314050
Seq. No.
Seq. ID
                   yyf700352211.h1
                   BLASTX
Method
                   g2959781
NCBI GI
BLAST score
                   432
                   5.0e-43
E value
Match length
                  .99
                             - A.
% inentity 4
                   08
                  (AJ223508) Zwille protein [Arabidopsis thaliana]
NCBI Description
                   314051
Seq. No.
Seq. ID
                   yyf700352238.h1
Method
                   BLASTX
                   g4191789
NCBI GI
BLAST score
                   276
                   8.0e-25
E value
Match length
                   87
% identity
                   67
                   (AC005917) putative transmembrane transport protein
NCBI Description
                   [Arabidopsis thaliana]
                   314052
Seq. No.
Seq. ID
                   yyf700352305.h1
                   BLASTX
Method
                   g4006866
NCBI GI
BLAST score
                   372
                   5.0e-36
E value
Match length
                   95
                   76
% identity
NCBI Description
                   (Z99707) putative protein [Arabidopsis thaliana]
                   314053
Seq. No.
                   yyf700352334.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g557472
BLAST score
                   169
E value
                   3.0e-12
Match length
                   65
% identity
                   49
NCBI Description
                   (U15178) arabinosidase [Bacteroides ovatus]
Seq. No.
                   314054
                   yyf700352343.h1
Seq. ID
```

E value

Match length

2.0e-36

96

```
NCBI GI
                   q729671
                   207
BLAST score
                   1.0e-16
E value
                   43
Match length
                   100
% identity
                  HISTONE H2A >gi 473603 (U08225) histone H2A [Zea mays]
NCBI Description
                   314055
Seq. No.
Seq. ID
                   yyf700352384.h1
Method
                   BLASTX
                   g629641
NCBI GI
BLAST score
                   328
                   5.0e-31
E value
Match length
                   63
% identity
                   98
                   PsHSC71.0 protein - garden pea >gi 1076530 pir S53500
NCBI Description
                   HSC71.0 protein - garden pea >gi 473217 emb CAA83548
                   (Z32537) PsHSC71.0 [Pisum sativum]
Seq. No.
                   314056
Seq. ID
                   yyf700352436.h1
Method
                   BLASTX
NCBI GI
                   g3688174
                   205
BLAST score
                   2.0e-16
E value
Match length
                   74
% identity
NCBI Description
                   (AL031804) putative protein [Arabidopsis thaliana]
                   314057
Seq. No.
                   yyf700352452.h1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3953470
BLAST score
                   288
                   2.0e-26
E value
Match length
                   64
                   78
% identity
                   (AC002328) F20N2.15 [Arabidopsis thaliana]
NCBI Description
                   314058
Seq. No.
Seq. ID
                   yyf700352459.h1
Method
                   BLASTN
NCBI GI
                   g6478880
BLAST score
                   77
E value
                   2.0e-35
Match length
                   161
% identity
                   Coix lacryma-jobi dihydrodipicolinate synthase (dapA) gene,
NCBI Description
                   complete cds
                   314059
Seq. No.
Seq. ID
                   yyf700352577.h1
                   BLASTX
Method
NCBI GI
                   q4587516
BLAST score
                   376
```

```
% identity
                   (AC007060) Strong similarity to gb U80583 proteinase TMP
NCBI Description
                   from Lycopersicon esculentum and is a member of the
                  PF 00082 subtilase family. [Arabidopsis thaliana]
Seq. No.
                  314060
Seq. ID
                  yyf700352578.h1
Method
                  BLASTX
NCBI GI
                  g1345587
BLAST score
                  296
E value
                  2.0e-30
Match length
                  77
% identity
                   99
                  14-3-3-LIKE PROTEIN GF14-6 >gi 998430 bbs 164522 (S77133)
NCBI Description
                  GF14-6=14-3-3 protein homolog [Zea mays, XL80, Peptide, 261
                  aa] [Zea mays]
Seq. No.
                   314061
                   zla700379659.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q4206306
BLAST score
                   471
E value
                   1.0e-47
Match length
                   95
                   97
% identity
NCBI Description
                  (AF049110) prpol [Zea mays]
                   314062
Seq. No.
                   zla700379678.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g729671
BLAST score
                   198
E value
                   1.0e-15
Match length
                   89
% identity
                   58
NCBI Description HISTONE H2A >gi 473603 (U08225) histone H2A [Zea mays]
                   314063
Seq. No.
                   zla700379687.h1
Seq. ID
                   BLASTX
Method
                   g3928098
NCBI GI
                   177
BLAST score
                   4.0e-13
E value
                   37
Match length
                   95
% identity
                   (AC005770) similar to guanylate binding protein, 5' partial
NCBI Description
                   [Arabidopsis thaliana]
                   314064
Seq. No.
                   zla700379705.h1
Seq. ID
                   BLASTN
Method
                   g2626751
NCBI GI
BLAST score
                   43
                   5.0e-15
E value
                   182
Match length
                   82
% identity
```

NCBI Description Triticum aestivum retrotransposon Tarl, partial sequence

```
314065
Seq. No.
                  zla700379750.h1
Seq. ID
                  BLASTN
Method
                  g1129083
NCBI GI
BLAST score
                  37
                  1.0e-11
E value
Match length
                  57
                  91
% identity
NCBI Description Wheat mRNA for protein H2A, complete cds, clone wcH2A-2
Seq. No.
                  314066
                  zla700379778.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3415134
                  225
BLAST score
                  5.0e-19
E value
Match length
                  50
% identity
                  80
                  (AF082024) Phyb1 [Pimpinella brachycarpa]
NCBI Description
                  314067
Seq. No.
                  zla700379791.h1
Seq. ID
Method
                  BLASTX
                  q70654
NCBI GI
                  337
BLAST score
                  8.0e-32
E value
Match length
                  74
                   92
% identity
                  ubiquitin / ribosomal protein CEP52 - Chlamydomonas
NCBI Description
                  reinhardtii >gi_18244_emb_CAA43216_ (X60826) ubiquitin
                   extension protein (UbCEP52) [Chlamydomonas reinhardtii]
                   >gi_18246_emb_CAA33466_ (X15427) ubiquitin/ribosomal
                  protein [Chlamydomonas reinhardtii]
Seq. No.
                   314068
Seq. ID
                   zla700379837.h1
Method
                   BLASTX
NCBI GI
                   q806299
BLAST score
                   237
E value
                   4.0e-20
Match length
                   95
                   46
% identity
NCBI Description
                  (M25427) unknown protein [Zea mays]
Seq. No.
                   314069
Seq. ID
                   zla700379881.h1
Method
                   BLASTX
                   g4056495
NCBI GI
BLAST score
                   150
                   3.0e-10
E value
Match length
                   33
% identity
                   91
                  (AC005896) putative TKRP125 [Arabidopsis thaliana]
NCBI Description
                   314070
Seq. No.
                   zla700379913.h1
Seq. ID
```

```
BLASTX
Method
                  q4204265
NCBI GI
                  225
BLAST score
                  5.0e-19
E value
Match length
                  59
% identity
                  66
                  (AC005223) 45643 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  314071
Seq. ID
                  zla700379969.h1
Method
                  BLASTX
NCBI GI
                  q3953467
BLAST score
                  154
                  2.0e-10
E value
Match length
                  39
% identity
                  39
NCBI Description (AC002328) F20N2.12 [Arabidopsis thaliana]
Seq. No.
                  314072
Seq. ID
                  zla700380007.h1
Method
                  BLASTN
NCBI GI
                  g1945608
BLAST score
                  94
E value
                  6.0e-46
Match length
                  118
% identity
                  95
NCBI Description
                  Homo sapiens mRNA for 26S proteasome subunit p44.5,
                  complete cds
Seq. No.
                  314073
                   zla700380080.h1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1350977
BLAST score
                  138
                  7.0e-09
E value
Match length
                  29
                  90
% identity
NCBI Description PROBABLE 40S RIBOSOMAL PROTEIN S30
Seq. No.
                  314074
Seq. ID
                  zla700380094.h1
Method
                  BLASTX
NCBI GI
                  g4514631
BLAST score
                  146
E value
                  8.0e-10
Match length
                  66
% identity
                  48
NCBI Description
                  (AB017020) JKTBP [Mus musculus]
Seq. No.
                  314075
Seq. ID
                  zla700380127.h1
Method
                  BLASTN
NCBI GI
                  g3327087
BLAST score
                  218
E value
                  1.0e-119
```

44929

- 4

Match length

% identity

266

3 B. .



```
314076
Seq. No.
Seq. ID
                  zla700380141.h1
Method
                  BLASTX
NCBI GI
                  g549051
BLAST score
                  150
E value
                  3.0e-10
Match length
                  34
% identity
                  82
                  TUBULIN ALPHA CHAIN >gi 630810 pir S43425 tubulin alpha
NCBI Description
                  chain - giant octopus >gi 159725 (L10110) alpha tubulin
                   [Octopus dofleini]
                  314077
Seq. No.
Seq. ID
                  zla700380152.h1
Method
                  BLASTN
                  g3808091
NCBI GI
BLAST score
                  106
                √ 9.0e-53
E value
Match length
                  198
% identity
                  94
NCBI Description
                  Homo sapiens chromosome 17, clone hCIT.211 P 7, complete
                  sequence [Homo sapiens]
Seq. No.
                  314078
                  zla700380155.h1
Seq. ID
Method
                  BLASTN
                  g4508154
NCBI GI
                  75
BLAST score
                  2.0e-34
E value
Match length
                  129
% identity
                  89
NCBI Description Homo sapiens clone DJ0555N02, complete sequence
                  314079
Seq. No.
Seq. ID
                  zla700380231.h1
Method
                  BLASTX
NCBI GI
                  q728837
BLAST score
                  161
E value
                  3.0e-11
                  63
Match length
                  26
% identity
NCBI Description ALU SUBFAMILY SQ WARNING ENTRY !!!!
Seq. No.
                  314080
Seq. ID
                  zla700380255.h1
Method
                  BLASTX
NCBI GI
                  g2282584
BLAST score
                  379
E value
                  9.0e-37
                  77
Match length
                  96
% identity
```

NCBI Description Homo sapiens mRNA for KIAA0637 protein, complete cds

Seq. No. 314081

NCBI Description

Seq. ID zla700380261.h1

(U76259) elongation factor 1-alpha [Zea mays]

```
BLASTX
Method
                  q4322327
NCBI GI
                  302
BLAST score
                  1.0e-27
E value
                  91
Match length
                  59
% identity
NCBI Description (AF080545) peptide transporter [Nepenthes alata]
                  314082
Seq. No.
                  zla700380272.h1
Seq. ID
                  BLASTN
Method
NCBI GI
                  q4589928
BLAST score
                  107
E value
                  1.0e-53
Match length
                  131
% identity
                  95
NCBI Description Homo sapiens mRNA for fls353, complete cds
Seq. No.
                  314083
                  zla700380274.hl
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1065506
BLAST score
                  244
E value
                  6.0e-21
Match length
                  95
                  48
% identity
                  (U40419) nearly identical to C. elegans predicted protein
NCBI Description
                  F17C8.5 (GB:Z35719) [Caenorhabditis elegans]
                  314084
Seq. No.
Seq. ID
                  zla700380282.h1
Method
                  BLASTN
NCBI GI
                  g37423
                  209
BLAST score
E value
                  1.0e-114
                  241
Match length
                  97
% identity
NCBI Description Human 2.5 kb mRNA for cytoskeletal tropomyosin TM30(nm)
                  314085
Seq. No.
                   zla700380462.h1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q121982
BLAST score
                  188
                  2.0e-14
E value
Match length
                  58
% identity
                   67
NCBI Description
                  HISTONE H2A.2.2
                   314086
Seq. No.
Şeq. ID
                  zla700380481.h1
                  BLASTX
Method
NCBI GI
                   g2623160
BLAST score
                  159
```

4.0e-11

66 47

E value Match length

% identity



NCBI Description (AF030178) N-acetylglucosaminyl transferase component Gpi1 [Mus musculus]

Seq. No. 314087

Seq. ID zla700380490.h1

Method BLASTN
NCBI GI g902524
BLAST score 85
E value 3.0e-40

Match length 181 % identity 92

NCBI Description Zea mays clone MubG10 ubiquitin fusion protein gene,

complete cds

Seq. No. 314088

Seq. ID zla700380515.hl

Method BLASTX
NCBI GI g3935148
BLAST score 442
E value 4.0e-44
Match length 107
% identity 77

NCBI Description (AC005106) T25N20.12 [Arabidopsis thaliana]

Seq. No. 314089

Seq. ID zla700380547.h1

Method BLASTX
NCBI GI g3024018
BLAST score 366
E value 2.0e-35
Match length 71
% identity 99

NCBI Description INITIATION FACTOR 5A (EIF-5A) (EIF-4D)

>gi_1546919_emb_CAA69225_ (Y07920) translation initiation factor 5A [Zea mays] >gi_2668738 (AF034943) translation

initiation factor 5A [Zea mays]

Seq. No. 314090

Seq. ID zla700380613.h1

Method BLASTX
NCBI GI g399854
BLAST score 172
E value 2.0e-12
Match length 54
% identity 70

NCBI Description HISTONE H2B.2 >gi 283042 pir S28049 histone H2B - maize

>gi_22325_emb_CAA40565_ (X57313) H2B histone [Zea mays]

Seq. No. 314091

Seq. ID zla700380725.h1

Method BLASTX
NCBI GI g3341697
BLAST score 220
E value 4.0e-18
Match length 71
% identity 58

NCBI Description (AC003672) hypothetical protein [Arabidopsis thaliana]

Match length

```
Seq. No.
                     314092
                     zla700380747.h1
Seq. ID
Method
                     BLASTX
NCBI GI
                     q1703380
                     188
BLAST score
E value
                     1.0e-14
                     44
Match length
% identity
                     ADP-RIBOSYLATION FACTOR >gi 1132483 dbj BAA04607 (D17760)
NCBI Description
                     ADP-ribosylation factor [Oryza sativa]
Seq. No.
                     314093
Seq. ID
                     zla700380756.h1
                     BLASTN
Method
NCBI GI
                     g22149
                     45
BLAST score
E value
                     3.0e-16
                     105
Match length
                     86
% identity
NCBI Description Z.mays mRNA for alpha-tubulin
                     314094
Seq. No.
Seq. ID
                     zuv700352614.h1
Method
                     BLASTX
                     g4502693
NCBI GI
                     282
BLAST score
                     1.0e-25
E value
Match length
                     73
                     74
% identity
                     CD9 antigen (p24) >gi 231724 sp P21926 CD9 HUMAN CD9
NCBI Description
                     ANTIGEN (P24) (LEUKOCYTE ANTIGEN MIC3) (MOTILITY-RELATED
                     PROTEIN) (MRP-1) >gi 105588 pir A40402 CD9 antigen - human >gi 34769 emb CAA42708 (X60111) MRP-1 (motility related protein) [Homo sapiens] >gi 300115 bbs 131345 (S60702) CD9 antigen [human, leukocytes, Peptide, 228 aa] [Homo sapiens]
                     >gi_508496 (L34068) membrane protein [Homo sapiens]
                     >gi 1048989 (M38690) CD9 antigen [Homo sapiens]
                     314095
Seq. No.
                     zuv700352619.h1
Seq. ID
Method
                     BLASTN
NCBI GI
                     g1518693
BLAST score
                     164
                      2.0e-87
E value
Match length
                      215
% identity
                     Human ubiquitin-homology domain protein PIC1 mRNA, complete
NCBI Description
                      cds
                      314096
Seq. No.
Seq. ID
                      zuv700352637.h1
                     BLASTX
Method
NCBI GI
                     g123650
BLAST score
                      381
                      2.0e-40
E value
```

```
% identity
                   HEAT SHOCK COGNATE 70 KD PROTEIN >gi_82245 pir__S03250 heat
NCBI Description
                   shock protein 70 (clone pMON9743) - garden petunia
                   >gi_20557_emb_CAA30018_ (X06932) heat shock protein 70
                   [Petunia x hybrida]
Seq. No.
                   314097
Seq. ID
                   zuv700352727.h1
Method
                   BLASTX
NCBI GI
                   q3928084
BLAST score
                   250
E value
                   1.0e-21
Match length
                   67
% identity
                   66
                   (AC005770) retrotransposon-like protein [Arabidopsis
NCBI Description
Seq. No.
                   314098
                   zuv700352772.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g66009
                   380
BLAST score
E value
                   6.0e-37
Match length
                   75
% identity
                   glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) C,
NCBI Description
                   cytosolic - maize >gi_22238_emb_CAA30151_ (X07156) GADPH
                    (AA 1-337) [Zea mays]
                   314099
Seq. No.
                   zuv700352775.h1
Seq. ID
                   BLASTX
Method
                   q548492
NCBI GI
BLAST score
                   400
                   2.0e-39
E value
Match length
                   89
% identity
                   EXOPOLYGALACTURONASE PRECURSOR (EXOPG) (PECTINASE)
NCBI Description
                    (GALACTURAN 1,4-ALPHA-GALACTURONIDASE)
                   >gi_629853_pir__S30066 polygalacturonase - maize
>gi_288379_emb_CAA45751_ (X64408) polygalacturonase [Zea
                   mays]
                   314100
Seq. No.
Seq. ID
                    zuv700352776.h1
Method
                   BLASTX
NCBI GI
                   q1362008
BLAST score
                   320
E value
                    6.0e-30
Match length
                   79
% identity
                   17
                   ubiquitin-like protein 12 - Arabidopsis thaliana
NCBI Description
```

Seq. No. 314101

Seq. ID zuv700352824.h1

Method BLASTX NCBI GI g3249065

```
BLAST score
E value
                  9.0e-22
                                               - 5
Match length
                  56
% identity
                  84
                  (AC004473) Similar to HAK1 gb U22945 high affinity
NCBI Description
                  potassium transporter from Schwanniomyces occidentalis.
                  [Arabidopsis thaliana]
Seq. No.
                  . 314102
Seq. ID
                  zuv700352836.h1
Method
                  BLASTN
NCBI GI
                  q4140643
BLAST score
                  53
E value
                  5.0e-21
Match length
                  77
% identity
                  92
NCBI Description
                  Zea mays cosmid II.2E10 22-kDa alpha zein gene cluster,
                  complete sequence
Seq. No.
                  314103
Seq. ID
                  zuv700352848.h1
Method
                  BLASTX
NCBI GI
                  q548493
BLAST score
                  224
E value
                  6.0e-19
Match length
                  59
                  76
% identity
NCBI Description
                  EXOPOLYGALACTURONASE PRECURSOR (EXOPG) (PECTINASE)
                   (GALACTURAN 1, 4-ALPHA-GALACTURONIDASE)
                  >gi_629854_pir__S30067 polygalacturonase - maize
                  >gi_288612_emb_CAA47052_ (X66422) polygalacturonase [Zea
                  mays]
Seq. No.
                  314104
Seq. ID
                  zuv700352873.h1
Method
                  BLASTN
NCBI GI
                  g3492893
BLAST score
                  143
E value
                  5.0e-75
Match length
                  163
                  97
% identity
                  Homo sapiens chromosome 17, clone hCIT.131 K 11, complete
NCBI Description
                  sequence [Homo sapiens]
                  314105
Seq. No.
Seq. ID
                  zuv700352875.h1
Method
                  BLASTX
NCBI GI
                  g2245136
BLAST score
                  226
E value
                  1.0e-28
                  94
Match length
                  59
% identity
NCBI Description
                  (Z97344) trehalose-6-phosphate synthase homolog
                   [Arabidopsis thaliana]
```

Seq. ID zuv700352882.h1

314106

Seq. No.

Match length

% identity

110

```
BLASTX
Method
                  q4150963
NCBI GI
BLAST score
                  145
                  2.0e-09
E value
Match length
                  56
% identity
                  54
NCBI Description (Y18620) DsPTP1 protein [Arabidopsis thaliana]
                  314107
Seq. No.
                  zuv700353081.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3135271
BLAST score
                  174
                  4.0e-13
E value
                  50
Match length
% identity
                  64
NCBI Description
                   (AC003058) putative receptor-like protein kinase
                   [Arabidopsis thaliana]
Seq. No.
                  314108
                  zuv700353105.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2827551
BLAST score
                  161
                  3.0e-11
E value
Match length
                  56
% identity
                  48
NCBI Description (AL021635) predicted protein [Arabidopsis thaliana]
                  314109
Seq. No.
                  zuv700353135.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4432825
                  221
BLAST score
                  2.0e-23
E value
Match length
                  66
                  80%
% identity
NCBI Description
                  (AC006593) putative SOP2p protein [Arabidopsis thaliana]
Seq. No.
                  314110
Seq. ID
                  zuv700353136.h1
Method
                  BLASTX
NCBI GI
                  g1518259
BLAST score
                  245
                  3.0e-21
E value
Match length
                  68
% identity
                  69
NCBI Description (Y07596) gpi8 [Homo sapiens]
Seq. No.
                  314111
                  zuv700353146.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4206125
BLAST score
                  58
E value
                  4.0e-24
```

Seq. No.

```
Homo sapiens map 3p22; 9.65 cR from CHLC.GATA87B02 repeat
NCBI Description
                  region, complete sequence
                  314112
Seq. No.
                  zuv700353147.h1
Seq. ID
Method
                  BLASTN
                  g2832242
NCBI GI
                  34
BLAST score
                  9.0e-10
E value
Match length
                  54
% identity
                  91
                  Zea mays 22-kDa alpha zein gene cluster, complete sequence
NCBI Description
Seq. No.
                  314113
                  zuv700353151.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g425194
BLAST score
                  201
E value
                  4.0e-16
Match length
                  42
% identity
                  88
                   (L26243) heat shock protein [Spinacia oleracea] >gi 2660772
NCBI Description
                   (AF034618) cytosolic heat shock 70 protein [Spinacia
                  oleracea]
Seq. No.
                  314114
Seq. ID
                  zuv700353168.h1
Method
                  BLASTX
NCBI GI
                  g1184774
BLAST score
                   311
                  7.0e-29
E value
Match length
                   64
                   92
% identity
                   (U45856) cytosolic glyceroldehyde-3-phosphate dehydrogenase
NCBI Description
                  GAPC3 [Zea mays]
Seq. No.
                   314115
                   zuv700353178.h1
Seq. ID
Method
                  BLASTN
                   g22458
NCBI GI
BLAST score
                   223
                   1.0e-122
E value
                   247
Match length
% identity
                   98
                  Z.mays pollen specific mRNA C-terminal (clone 4H7)
NCBI Description
                   314116
Seq. No.
Seq. ID
                   zuv700353239.h1
                   BLASTX
Method
NCBI GI
                   g2739370
BLAST score
                   251
                   8.0e-22
E value
                   97
Match length
% identity
                   54
                  (AC002505) putative pectinesterase [Arabidopsis thaliana]
NCBI Description
```

```
Seq. ID
                   zuv700353257.h1
Method
                   BLASTN
NCBI GI
                   q4191249
BLAST score
                   104
                   2.0e-51
E value
                   279
Match length
% identity
NCBI Description
                   Cloning vector pSLJ8313, T-DNA region
                   314118
Seq. No.
Seq. ID
                   zuv700353258.h1
Method
                   BLASTX
NCBI GI
                   q1911582
                   244
BLAST score
                   6.0e-21
E value
                   69
Match length
% identity
                   62
NCBI Description
                   (S83343) Cyn d 1=major allergen [Cynodon dactylon=Bermuda
                   grass, pollen, Peptide Partial, 246 aa] [Cynodon dactylon]
Seq. No.
                   314119
Seq. ID
                   zuv700353267.h1
Method
                   BLASTX
                   g3879192
NCBI GI
BLAST score
                   200
                   9.0e-16
E value
                   87
Match length
% identity
                   45
NCBI Description
                   (Z50795) weak similarity with yeast cat8 regulatory protein
                   (Swiss Prot accession number P39113); cDNA EST EMBL: Z14554
                   comes from this gene; cDNA EST EMBL: T02057 comes from this
                   gene; cDNA EST EMBL:D75504 comes from this gene;
Seq. No.
                   314120
Seq. ID
                   zuv700353524.h1
Method
                   BLASTX
NCBI GI
                   g399940
BLAST score
                   157
E value
                   5.0e-11
Match length
                   32
% identity
                   97
                   MITOCHONDRIAL HEAT SHOCK 70 KD PROTEIN PRECURSOR
NCBI Description
                   >gi_100004_pir__S25005 heat shock protein, 70K - kidney bean >gi_22636_emb_CAA47345_ (X66874) 70 kDa heat shock
                   protein [Phaseolus vulgaris]
Seq. No.
                   314121
Seq. ID
                   zuv700353575.h1
Method
                   BLASTX
NCBI GI
                   q4567251
BLAST score
                   150
E value
                   3.0e-10
                   34
Match length
```

NCBI Description (AC007070) unknown protein [Arabidopsis thaliana]

% identity

Seq. No.

76

```
zuv700353586.h1
Seq. ID
Method
                    BLASTX
                    g2827544
NCBI GI
                    161
BLAST score
                    1.0e-11
E value
Match length
                    50
% identity
                    68
                    (AL021635) HSP associated protein like [Arabidopsis
NCBI Description
                    thaliana]
Seq. No.
                    314123
Seq. ID
                    zuv700353657.h1
Method
                    BLASTX
NCBI GI
                    g283049
BLAST score
                    366
                    2.0e-35
E value
                    76
Match length
% identity
                    93
                    polygalacturonase (EC 3.2.1.15) precursor (clone W2247) -
NCBI Description
                    maize (fragment) >gi 481079 pir S37718 polygalacturonase -
                    maize >gi_22426_emb_CAA44248_ (X62384) polygalacturonase
                    [Zea mays] >gi_287830_emb_CAA47234_ (X66692)
                    polygalacturonase [Zea mays]
Seq. No.
                    314124
Seq. ID
                    zuv700353696.h1
Method
                    BLASTX
NCBI GI
                    a1710032
BLAST score
                    178
E value
                    1.0e-13
Match length
                    58
                    57
% identity
NCBI Description
                    RETINOBLASTOMA BINDING PROTEIN 2 (RBBP-2)
                    >gi_2136106_pir__I78879 retinoblastoma binding protein 2 -
human >gi_435778_bbs_138858 (S66431) retinoblastoma binding
protein 2, RBP2 [human, Nalm-6 pre-B cell leukemia,
                    Peptide, 1722 aa] [Homo sapiens]
Seq. No.
                    314125
Seq. ID
                    zuv700353715.h1
Method
                    BLASTX
NCBI GI
                    g3808101
BLAST score
                    197
E value
                    2.0e-22
Match length
                    73
% identity
                    84
NCBI Description
                    (AJ012165) chloroplast protease [Capsicum annuum]
                    314126
Seq. No.
Seq. ID
                    zuv700353723.h1
Method
                    BLASTX
NCBI GI
                    q169705
BLAST score
                    146
E value
                    9.0e-10
                    37
Match length
% identity
                    81
NCBI Description (M64737) ATP:pyruvate phosphotransferase [Ricinus communis]
```

Seq. No.

Seq. ID

314132

zuv700354129.h1

```
Seq. No.
                   314127
Seq. ID
                   zuv700353726.h1
Method
                   BLASTX
NCBI GI
                   q548774
BLAST score
                   193
E value
                   2.0e-15
Match length
                   51
                   76
% identity
                   60S RIBOSOMAL PROTEIN L7A >gi_542158_pir__S38360 ribosomal protein L7a - rice >gi_303855_dbj_BAA02156_ (D12631)
NCBI Description
                   ribosomal protein L7A [Oryza sativa]
Seq. No.
                   314128
Seq. ID
                   zuv700353742.h1
Method
                   BLASTX
NCBI GI
                   g3885880
BLAST score
                   354
E value
                   6.0e - 34
Match length
                   93
                   75
% identity
NCBI Description
                   (AF093628) protochlorophyllide reductase homolog [Oryza
                   sativa]
Seq. No.
                   314129
Seq. ID
                   zuv700353855.h1
Method
                   BLASTX
NCBI GI
                   q3377517
BLAST score
                   318
                   9.0e-30
E value
Match length
                   85
% identity
                   66
NCBI Description (AF073361) nitrate transporter NTL1 [Arabidopsis thaliana]
Seq. No.
                   314130
                   zuv700353857.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g576509
BLAST score
                   243
                   6.0e-21
E value
                   88
Match length
                   56
% identity
NCBI Description (L36857) GTP-binding protein [Pisum sativum]
Seq. No.
                   314131
                   zuv700353950.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g629852
BLAST score
                   266
E value
                   2.0e-29
                   79
Match length
                   89
% identity
NCBI Description polygalacturonase - maize >gi 288367 emb CAA46680 (X65845)
                   polygalacturonase [Zea mays]
```

E value

9.0e-46

```
Method
                  BLASTX
                  g4006978
NCBI GI
BLAST score
                  147
                  1.0e-09
E value
Match length
                  82
                   41
% identity
NCBI Description
                  (AJ131335) pollen allergen (group II) [Cynodon dactylon]
Seq. No.
Seq. ID
                  zuv700354261.h1
Method
                  BLASTX
NCBI GI
                  q1934972
BLAST score
                  155
E value
                  8.0e-11
Match length
                  41
                   68
% identity
NCBI Description
                  (Y08611) dihydropterin pyrophosphokinase /dihydropteroate
                  synthase [Pisum sativum]
Seq. No.
                  314134
Seq. ID
                  zuv700354274.h1
Method
                  BLASTN
NCBI GI
                  q2285789
BLAST score
                  141
E value
                  1.0e-73
Match length
                  291
% identity
                  88
NCBI Description Rattus norvegicus mRNA for p47, complete cds
Seq. No.
                  314135
Seq. ID
                  zuv700354285.h1
Method
                  BLASTN
NCBI GI
                  g4505578
BLAST score
                  253
E value
                  1.0e-140
                  289
Match length
% identity
                   97
                  Homo sapiens paired basic amino acid cleaving enzyme
NCBI Description
                   (furin, membrane associated receptor protein) (PACE) mRNA
                  >gi 31477 emb X17094 HSFUR Human fur mRNA for furin
Seq. No.
                  314136
Seq. ID
                  zuv700354308.h1
Method
                  BLASTN
NCBI GI
                  g22458
BLAST score
                  298
E value
                  1.0e-167
Match length
                  306
                  99
% identity
NCBI Description
                  Z.mays pollen specific mRNA C-terminal (clone 4H7)
Seq. No.
                  314137
Seq. ID
                  zuv700354316.h1
Method
                  BLASTX
NCBI GI
                  g4406528
BLAST score
                  456
```



```
Match length
                  89
% identity
                  (AF126799) delta-6 fatty acid desaturase [Homo sapiens]
NCBI Description
Seq. No.
                  314138
Seq. ID
                  zuv700354357.h1
Method
                  BLASTN
NCBI GI
                  q461187
BLAST score
                  133
E value
                  4.0e-69
Match length
                  157
% identity
                  96
                  Human mRNA for fructose-bisphosphate aldolase A, 5'UTR
NCBI Description
                  (sequence from the 5'cap to the start codon)
Seq. No.
                  314139
Seq. ID
                  zuv700354365.hl
Method
                  BLASTN
NCBI GI
                  g1877217
BLAST score
                  70
E value
                  3.0e - 31
Match length
                  155
% identity
                  97
NCBI Description
                  Human DNA sequence from cosmid U105G4, between markers
                  DXS366 and DXS87 on chromosome X contains ESTs
Seq. No.
                  314140
Seq. ID
                  zuv700354391.h1
Method
                  BLASTX
NCBI GI
                  q4204312
BLAST score
                  215
                  7.0e-18
E value
Match length
                  53
% identity
                  74
NCBI Description
                   (AC003027) lcl prt seq No definition line found
                   [Arabidopsis thaliana]
Seq. No.
                  314141
Seq. ID
                  zuv700354395.h1
Method
                  BLASTN
NCBI GI
                  q2781403
BLAST score
                  104
                  8.0e-52
E value
Match length
                  120
                  97
% identity
NCBI Description Homo sapiens clone DT1P1A7 mRNA, CAG repeat region
Seq. No.
                  314142
Seq. ID
                  zuv700354407.h1
Method
                  BLASTX
```

q4539404 NCBI GI BLAST score 329 E value 6.0e-31 94 Match length

% identity

(AL049524) putative protein [Arabidopsis thaliana] NCBI Description



```
Seq. No.
                   314143
Seq. ID
                  zuv700354414.hl
Method
                  BLASTN
NCBI GI
                  g4416300
BLAST score
                  158
E value
                   1.0e-83
Match length
                  281
                   45
% identity
NCBI Description Zea mays chromosome 4 22 kDa zein-associated intercluster
                  region, complete sequence
Seq. No.
                   314144
Seq. ID
                   zuv700354418.h1
Method
                  BLASTN
NCBI GI
                  q190892
BLAST score
                   58
                   2.0e-24
E value
Match length
                  104
                  100
% identity
NCBI Description Human ras inhibitor mRNA, partial cds
Seq. No.
                   314145
Seq. ID
                   zuv700354451.h1
Method
                   BLASTX
NCBI GI
                   q3688181
                   148
BLAST score
E value
                   2.0e-12
Match length
                   62
% identity
                   71
NCBI Description
                   (AL031804) putative protein (fragment) [Arabidopsis
                   thaliana]
Seq. No.
                   314146
Seq. ID
                   zuv700354594.h1
Method
                   BLASTX
NCBI GI
                   q4530126
BLAST score
                   153
                   1.0e-10
E value
Match length
                   47
% identity
                   62
                   (AF078082) receptor-like protein kinase homolog RK20-1
NCBI Description
                   [Phaseolus vulgaris]
Seq. No.
                   314147
                   zuv700354682.h1
Seq. ID
                   BLASTN
Method
NCBI GI
                   g22458
BLAST score
                   153
                   9.0e-81
E value
                   273
Match length
                   89
% identity
NCBI Description Z.mays pollen specific mRNA C-terminal (clone 4H7)
```

Seq. No. 314148

Seq. ID zuv700354686.h1

Method BLASTN NCBI GI g4240040

% identity

NCBI Description

96

```
BLAST score
E value
                   7.0e-38
Match length
                  85
                   99
% identity
NCBI Description Zea mays ZmGR2c mRNA, complete cds
Seq. No.
                   314149
                   zuv700354705.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g4586036
BLAST score
                   205
E value
                   2.0e-16
Match length
                   95
                   40
% identity
                  (AC007109) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   314150
Seq. ID
                   zuv700354748.h1
Method
                   BLASTX
NCBI GI
                   g3928519
BLAST score
                   249
                   1.0e-21
E value
Match length
                   67
% identity
                   76
                  (AB011670) wpk4 protein kinase [Triticum aestivum]
NCBI Description
Seq. No.
                   314151
Seq. ID
                   zuv700354757.h1
Method
                  BLASTX
NCBI GI
                   q2149640
BLAST score
                   219
E value
                   2.0e-18
Match length
                   49
% identity
                   86
NCBI Description
                  (U91995) Argonaute protein [Arabidopsis thaliana]
Seq. No.
                   314152
                   zuv700354816.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3337361
BLAST score
                   213
E value
                   3.0e-20
Match length
                  86
% identity
                   55
                  (AC004481) ankyrin-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   314153
                   zuv700354820.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                   g1914844
BLAST score
                  235
E value
                   1.0e-129
Match length
                  278
```

44944

Zea mays liguleless1 protein (liguleless1) mRNA, complete

E value

Match length

NCBI Description

% identity

1.0e-12

[Arabidopsis thaliana]

50

62

```
Seq. No.
                   314154
Seq. ID
                   zuv700354831.h1
Method
                   BLASTX
NCBI GI
                   g3953507
BLAST score
                   289
E value
                   2.0e-26
Match length
                   89
                   82
% identity
NCBI Description
                   (AC005035) nik-like; similar to U88984 (PID:g1872546) [Homo
Seq. No.
                   314155
Seq. ID
                   zuv700354866.h1
Method
                   BLASTX
NCBI GI
                   q283049
BLAST score
                   369
E value
                   1.0e-35
Match length
                   83
% identity
                   polygalacturonase (EC 3.2.1.15) precursor (clone W2247) -
NCBI Description
                   maize (fragment) >gi_481079_pir__S37718 polygalacturonase -
                   maize >gi_22426_emb_CAA44248_ (X62384) polygalacturonase
                   [Zea mays] >gi_\(\overline{2}878\)\(\overline{3}0\)\(_\overline{emb}\(_\overline{CAA}47234\)\((X66692)\)
                   polygalacturonase [Zea mays]
Seq. No.
                   314156
Seq. ID
                   zuv700354870.h1
Method
                   BLASTX
NCBI GI
                   g1086860
BLAST score
                   156
E value
                   1.0e-10
Match length
                   86
% identity
                   38
                    (U41272) Similar to man(9)-alpha-mannosidase.
NCBI Description
                    [Caenorhabditis elegans]
                   314157
Seq. No.
                   zuv700354963.h1
Seq. ID
Method
                   BLASTN
NCBI GI
                   q485376
BLAST score
                   121
E value
                   7.0e-62
Match length
                   177
% identity
                   92
                   Zea mays alpha-3-tubulin gene, complete cds
NCBI Description
Seq. No.
                   314158
Seq. ID
                   zuv700354964.h1
Method
                   BLASTX
NCBI GI
                   q3128168
BLAST score
                   170
```

44945

(AC004521) putative carboxyl-terminal peptidase

```
Seq. No.
                   314159
Seq. ID
                   zuv700354972.h1
Method
                   BLASTX
NCBI GI
                   g2258469
BLAST score
                   218
E value
                   3.0e-18
Match length
                   63
% identity
                   63
NCBI Description
                   (AF009179) replication protein Al [Oryza sativa]
Seq. No.
                   314160
Seq. ID
                   zuv700355028.h1
Method
                   BLASTX
NCBI GI
                   q3482913
BLAST score
                   164
E value
                   2.0e-11
Match length
                   91
% identity
                   38
                   (AC003970) Similar to MtN21, gi_2598575, Megicago
NCBI Description
                   truncatula nodulation induced gene [Arabidopsis thaliana]
Seq. No.
                   314161
Seq. ID
                   zuv700355048.h1
Method
                   BLASTX
                   g4185796
NCBI GI
BLAST score
                   170
                   1.0e-12 ~
E value
Match length
                   55
% identity
                   60
NCBI Description
                   (AF103796) placenta-specific ATP-binding cassette
                   transporter [Homo sapiens]
Seq. No.
                   314162
Seq. ID
                   zuv700355237.h1
Method
                   BLASTX
NCBI GI
                   g1203832
BLAST score
                   270
E value
                   5.0e-24
Match length
                   96
                   53
% identity
NCBI Description
                   (U46003) beta-D-glucan exohydrolase, isoenzyme ExoII
                   [Hordeum vulgare] >gi_1588407_prf 2208395A beta-D-glucan
                   exohydrolase [Hordeum vulgare]
Seq. No.
                   314163
Seq. ID
                   zuv700355407.h1
Method
                   BLASTX
NCBI GI
                   g3093294
BLAST score
                   305
E value
                   4.0e-28
Match length
                   88
% identity
                  64
NCBI Description
                  (Y12782) putative villin [Arabidopsis thaliana]
Seq. No.
                   314164
Seq. ID
                   zuv700355460.h1
Method
                  BLASTX
```

```
q3719211
NCBI GI
BLAST score
                  203
                  3.0e-16
E value
Match length
                  63
                  59
% identity
NCBI Description (U97021) UIP2 [Arabidopsis thaliana]
                  314165
Seq. No.
                  zuv700355541.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2832242
BLAST score
                  41
E value
                  7.0e-14
Match length
                  41
                  100
% identity
NCBI Description Zea mays 22-kDa alpha zein gene cluster, complete sequence
                  314166
Seq. No.
Seq. ID
                  zuv700355542.h1
Method
                  BLASTN
NCBI GI
                  g433042
BLAST score
                  54
                  1.0e-21
E value
Match length
                  168
% identity
                  89
NCBI Description
                  Zea mays W-22 clone PREM-1C retroelement PREM-1, partial
                  sequence
Seq. No.
                  314167
                  zuv700355553.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3093294
BLAST score
                  159
E value
                  5.0e-11
                  93
Match length
% identity
                  43
NCBI Description (Y12782) putative villin [Arabidopsis thaliana]
Seq. No.
                  314168
                  zuv700355559.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2827709
BLAST score
                  160
E value
                  2.0e-11
Match length
                  48
% identity
                  69
NCBI Description (AL021684) predicted protein [Arabidopsis thaliana]
Seq. No.
                  314169
Seq. ID
                  zuv700355627.h1
Method
                  BLASTN
NCBI GI
                  g902583
```

Method BLASTN
NCBI GI g902583
BLAST score 64
E value 5.0e-28
Match length 104
% identity 34

NCBI Description Zea mays clone MubG1 ubiquitin gene, complete cds

Match length

```
Seq. No.
                    314170
                    zuv700355634.h1
Seq. ID
Method
                    BLASTX
                    g1703302
NCBI GI
BLAST score
                    311
                    6.0e-29
E value
Match length
                    87
                    75
% identity
                    BETA-AMYLASE (1,4-ALPHA-D-GLUCAN MALTOHYDROLASE)
NCBI Description
                    >gi_480593_pir__S37075 beta-amylase (EC 3.2.1.2) - maize
                    >gi 397959 emb CAA81091 (Z25871) beta-amylase [Zea mays]
Seq. No.
                    314171
                    zuv700355644.h1
Seq. ID
Method
                    BLASTN
NCBI GI
                    q4506666
                    68
BLAST score
                    3.0e-30
E value
Match length
                    154
                    86
% identity
                    Homo sapiens ribosomal protein, large, PO (RPLPO) mRNA
NCBI Description
                    >gi_190231_gb_M17885_HUMPPARPO Human acidic ribosomal
                    phosphoprotein PO mRNA, complete cds
Seq. No.
                    314172
                    zuv700355649.h1
Seq. ID
Method
                    BLASTX
NCBI GI
                    g1172836
BLAST score
                    164
                    1.0e-11
E value
                    50
Match length
% identity
                    70
NCBI Description
                    GTP-BINDING NUCLEAR PROTEIN RAN-B1 >gi 496272 (L16787)
                    small ras-related protein [Nicotiana tabacum]
Seq. No.
                    314173
                    zuv700355659.h1
Seq. ID
Method
                    BLASTX
NCBI GI
                    q283049
BLAST score
                    145
E value
                    2.0e-09
                    68
Match length
                    50
% identity
NCBI Description
                    polygalacturonase (EC 3.2.1.15) precursor (clone W2247) -
                    maize (fragment) >gi_481079_pir__S37718 polygalacturonase -
                    maize >gi 22426 emb \overline{\text{CAA44248}} (\overline{\text{X62384}}) polygalacturonase [Zea mays] >gi 287830 emb \overline{\text{CAA47234}} (\overline{\text{X666692}})
                    polygalacturonase [Zea mays]
Seq. No.
                    314174
                    zuv700355692.h1
Seq. ID
Method
                    BLASTX
                    g1332579
NCBI GI
BLAST score
                    198
                    1.0e-26
E value
```

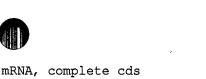
% identity

89



```
% identity
NCBI Description
                  (X98063) polyubiquitin [Pinus sylvestris]
                   314175
Seq. No.
                   zuv700355701.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                  g548492
BLAST score
                   175
                   1.0e-13
E value
Match length **
                   58
% identity
                   84
NCBI Description
                  EXOPOLYGALACTURONASE PRECURSOR (EXOPG) (PECTINASE)
                   (GALACTURAN 1,4-ALPHA-GALACTURONIDASE)
                   >gi_629853_pir__S30066 polygalacturonase - maize
                   >gi 288379 emb CAA45751 (X64408) polygalacturonase [Zea
                  mays]
                   314176
Seq. No.
                   zuv700355742.h1
Seq. ID
Method
                   BLASTX
                   g1176004
NCBI GI
BLAST score
                   169
E value
                   3.0e-12
Match length
                   79
% identity
                   49
NCBI Description
                  HYPOTHETICAL 40.4 KD PROTEIN IN PES4-HIS2 INTERGENIC REGION
                  >gi 836779 dbj BAA09263.1 (D50617) YFR024C [Saccharomyces
                   cerevisiae]
Seq. No.
                   314177
                   zuv700355816.h1
Seq. ID
Method
                   BLASTN
                   g396148
NCBI GI
BLAST score
                   56
                   8.0e-23
E value
Match length
                   80
% identity
                   93
NCBI Description
                  Z.mays CHI gene
Seq. No.
                   314178
                   zuv700355826.h1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4469023
BLAST score
                   311
E value
                   6.0e-29
Match length
                   69
% identity
                   84
NCBI Description
                  (AL035602) putative protein [Arabidopsis thaliana]
Seq. No.
                   314179
Seq. ID
                   zuv700355878.h1
Method -
                   BLASTN
NCBI GI
                   q293901
BLAST score
                   72
E value
                   2.0e-32
Match length
                   128
```

```
NCBI Description Zea mays Zea mI gene, complete cds
Seq. No.
                  314180
Seq. ID
                  zuv700355892.h1
Method
                  BLASTN
NCBI GI
                  q4505288
BLAST score
                  110
E value
                  2.0e-55
Match length
                  130
                  96
% identity
                  Homo sapiens mevalonate (diphospho) decarboxylase (MVD)
NCBI Description
                  mRNA >gi_1235681_gb_U49260_HSU49260 Human mevalonate
                  pyrophosphate decarboxylase (MPD) mRNA, complete cds
Seq. No.
                  314181
Seq. ID
                  zuv700355934.h1
Method
                  BLASTX
NCBI GI
                  g70774
BLAST score
                   419
E value
                  1.0e-41
Match length
                  84
                  100
% identity
NCBI Description
                  histone H4 (TH091) - wheat >gi 170747 (M12277) histone H4
                   [Triticum aestivum]
Seq. No.
                  314182
Seq. ID
                  zuv700355941.h1
Method
                  BLASTX
                  q100665
NCBI GI
BLAST score
                  308
E value
                  2.0e-28
Match length
                   60
% identity
                  100
NCBI Description
                  calmodulin 2 (clone lambda DASH) - rice
                  >gi 20190 emb CAA78288 (Z12828) calmodulin [Oryza sativa]
                  >gi 310313 (L18914) calmodulin [Oryza sativa]
Seq. No.
                  314183
Seq. ID
                  zuv700355972.h1
Method
                  BLASTX
NCBI GI
                  g4139188
BLAST score
                  414
E value
                  6.0e-41
Match length
                  89
% identity
                  94
NCBI Description
                   (AF095257) heterogeneous nuclear ribonucleoprotein C1/C2;
                  hnRNP C1/C2 [Mus musculus]
Seq. No.
                  314184
Seq. ID
                  zuv700355984.h1
Method
                  BLASTN
NCBI GI
                  g178083
BLAST score
                  93
                  3.0e-45
E value
Match length
                  141
                  91
% identity
NCBI Description Homo sapiens adenylyl cyclase-associated protein (CAP)
```



```
314185
Seq. No.
Seq. ID
                   zuv700356002.h1
Method
                   BLASTX
NCBI GI
                   g627468
BLAST score
                   232
E value
                   1.0e-19
Match length
                  88
% identity
                   58
NCBI Description
                  hypothetical protein 1 - human >gi 285983 dbj BAA02799
                   (D13635) KIAA0010 [Homo sapiens]
Seq. No.
                   314186
Seq. ID
                   zuv700356029.h1
Method
                  BLASTX
NCBI GI
                   g4539009
BLAST score
                   262
E value
                   4.0e-23
Match length
                   96
% identity
                   53
NCBI Description
                  (AL049481) putative protein [Arabidopsis thaliana]
Seq. No.
                   314187
Seq. ID
                   zuv700356055.h1
Method
                  BLASTX
NCBI GI
                  q548492
BLAST score
                   487
E value
                   2.0e-49
Match length
                   94
% identity
                   99
NCBI Description
                  EXOPOLYGALACTURONASE PRECURSOR (EXOPG) (PECTINASE)
                   (GALACTURAN 1,4-ALPHA-GALACTURONIDASE)
                   >gi_629853 pir S30066 polygalacturonase - maize
                   >gi_288379_emb_CAA45751_ (X64408) polygalacturonase [Zea
                  mays]
Seq. No.
                  314188
Seq. ID
                  zuv700356069.h1
Method
                  BLASTX
NCBI GI
                  g1172835
BLAST score
                  151
E value
                  2.0e-10
Match length
                  40
                  72
% identity
NCBI Description
                  GTP-BINDING NUCLEAR PROTEIN RAN-A1 >qi 496268 (L16767)
                  GTP-binding protein [Nicotiana tabacum]
Seq. No.
                  314189
Seq. ID
                  zuv700356086.h1
Method
                  BLASTX
NCBI GI
                  g479357
BLAST score
                  183
                  7.0e-14
E value
Match length
                  93
                  42
% identity
```

NCBI Description hypothetical protein 612 - maize transposon MuA2

Method

NCBI GI

BLASTN

g313139



>gi 22375 emb CAA44165 (X62251) ORF [Zea mays]

```
314190
Seq. No.
                  zuv700356133.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2827631
BLAST score
                  275
E value
                  1.0e-29
Match length
                  87
                  66
% identity
NCBI Description
                  (AL021636) putative protein [Arabidopsis thaliana]
Seq. No.
                  314191
                   zuv700356141.h1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q2262105
BLAST score
                  160
E value
                   4.0e-11
                   96
Match length
% identity
                  34
                  (AC002343) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   314192
Seq. ID
                   zuv700356209.h1
Method
                  BLASTN
                   g293886
NCBI GI
BLAST score
                  77
                  1.0e-35
E value
Match length
                  159
                   97
% identity
                  Zea mays glyceraldehyde-3-phosphate dehydrogenase mRNA, 3'
NCBI Description
                  end, (clone GAPC3)
Seq. No.
                   314193
Seq. ID
                   zuv700356288.h1
                  BLASTX
Method
NCBI GI
                   q1076678
BLAST score
                   271
E value
                   4.0e-24
Match length
                   57
% identity
NCBI Description
                  ubiquitin / ribosomal protein S27a - potato (fragment)
Seq. No.
                  314194
                   zuv700356467.h1
Seq. ID
Method
                  BLASTN
NCBI GI
                   q602605
BLAST score
                   104
E value
                  8.0e-52
Match length
                  136
                   94
% identity
                  Zea mays tandem genes for alpha1-tubulin and alpha2-tubulin
NCBI Description
Seq. No.
                  314195
                   zuv700356637.h1
Seq. ID
```

Method

NCBI GI

BLASTN

g288611

```
BLAST score
E value
                    7.0e-68
Match length
                    167
                    95
% identity
NCBI Description Z.mays ZmPRO2 mRNA for profilin
Seq. No.
                    314196
Seq. ID
                    zuv700356739.h1
Method
                    BLASTX
NCBI GI
                    g22422
BLAST score
                    171
E value
                    1.0e-12
Match length
                    53
% identity
                    68
NCBI Description
                    (X57743) polygalacturonase [Zea mays]
Seq. No.
                    314197
Seq. ID
                    zuv700356762.h1
Method
                    BLASTX
NCBI GI
                    q3608128
                    256
BLAST score
                    1.0e-22
E value
Match length
                    58
% identity
                    76
NCBI Description
                    (AC005314) hypothetical protein [Arabidopsis thaliana]
                    >gi_4263794_gb_AAD15454_ (AC006068) hypothetical protein
                    [Arabidopsis thaliana]
Seq. No.
                    314198
                    zuv700356779.h1
Seq. ID
Method
                    BLASTX
NCBI GI
                    g2190543
BLAST score
                    148
E value
                    5.0e-10
Match length
                    60
% identity
                    52
NCBI Description
                    (AC001229) EST gb N37484 comes from this gene. [Arabidopsis
                    thaliana]
                    314199
Seq. No.
Seq. ID
                    zuv700356834.h1
Method
                    BLASTX
NCBI GI
                    g283049
BLAST score
                    495
                    2.0e-50
E value
Match length
                    94
% identity
                    100
NCBI Description
                    polygalacturonase (EC 3.2.1.15) precursor (clone W2247) -
                    maize (fragment) >gi_481079_pir__S37718 polygalacturonase -maize >gi_22426_emb_CAA44248 (X62384) polygalacturonase [Zea mays] >gi_287830_emb_CAA47234 (X66692)
                    polygalacturonase [Zea mays]
                    314200
Seq. No.
Seq. ID
                    zuv700356847.h1
```

```
BLAST score
E value
                   7.0e-18
Match length
                   98
                   96
% identity
NCBI Description
                  Z.mays PG gene for polygalacturonase
Seq. No.
                   314201
Seq. ID
                   zuv700356993.h1
Method
                  BLASTX
NCBI GI
                  q3201554
BLAST score
                  254
E value
                   2.0e-22
Match length
                   58
                  83
% identity
                  (AJ006501) beta-D-glucosidase [Tropaeolum majus]
NCBI Description
Seq. No.
                   314202
Seq. ID
                   zuv700357140.h1
Method
                  BLASTX
NCBI GI
                   g1169186
BLAST score
                   241
E value
                  1.0e-20
Match length
                  101
% identity
                   50
NCBI Description
                  THIOL PROTEASE SEN102 PRECURSOR >gi_1085732_pir__S36421
                   cysteine proteinase - Hemerocallis sp
                   >gi 1364024 pir S57777 cysteine protease precursor -
                   Hemerocallis x hybrida >gi_396568_emb_CAA52425_ (X74406)
                   thiol-protease [Hemerocallis sp.]
                   314203
Seq. No.
Seq. ID
                   zuv700357171.h1
Method
                   BLASTN
NCBI GI
                   q288611
BLAST score
                   77
E value
                   2.0e-35
Match length
                   144
% identity
                   89
NCBI Description Z.mays PG gene for polygalacturonase
Seq. No.
                   314204
Seq. ID
                   zuv700357410.h1
Method
                   BLASTX
NCBI GI
                   g4218011
BLAST score
                   339
E value
                   4.0e-32
Match length
                   98
% identity
                   81
```

NCBI Description (AC006135) putative protein kinase [Arabidopsis thaliana]

>gi_4309721_gb_AAD15491_ (AC006439) putative

serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No. 314205

Seq. ID zuv700357419.h1

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Method BLASTX NCBI GI g553073 BLAST score 315

Match length

% identity

52

81

```
3.0e-29
 E value
                    98
 Match length
 % identity
                    68
 NCBI Description (M94481) reverse transcriptase [Zea mays]
 Seq. No.
                    314206
 Seq. ID
                    zvd700460542.h1
 Method
                    BLASTX
 NCBI GI
                  - q3935181
 BLAST score
                    179
                    1.0e-13
 E value
 Match length
                    37
 % identity
                    89
 NCBI Description (AC004557) F17L21.24 [Arabidopsis thaliana]
 Seq. No.
                    314207
 Seq. ID
                    zvd700460589.h1
 Method
                    BLASTN
 NCBI GI
                    g2198850
 BLAST score
                    44
 E value
                    6.0e-16
 Match length
                    48
 % identity
                    98
 NCBI Description
                   Zea mays cystathionine gamma-synthase (CGS1) mRNA, complete
 Seq. No.
                    314208
 Seq. ID
                    zvd700460657.h1
 Method
                    BLASTX
 NCBI GI
                    g3360289
 BLAST score
                    240
 E value
                    8.0e-21
 Match length
                    48
 % identity
                    96
 NCBI Description
                    (AF023164) leucine-rich repeat transmembrane protein kinase
                    1 [Zea mays]
 Seq. No.
                    314209
 Seq. ID
                    zvd700460669.h1
 Method
                    BLASTX
 NCBI GI
                    q3860277
 BLAST score
                    240
 E value
                    1.0e-20
 Match length
                    89
 % identity
                    60
 NCBI Description
                    (AC005824) putative ribosomal protein L10 [Arabidopsis
                    thaliana] >gi_4314394_gb_AAD15604_ (AC006232) putative
                   ribosomal protein L10A [Arabidopsis thaliana]
 Seq. No.
                   314210
Seq. ID
                   zvd700460692.h1
 Method
                   BLASTX
 NCBI GI
                   g4581109
 BLAST score
                   230
                   1.0e-19
 E value
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44955

, 75,10



NCBI	Description	(AC005825)	unknown protein	[Arabidopsis	thaliana]
Seq. Seq.		314211 LIB143-001-	-Q1-E1-A11		
Seq. Seq.	No. ID	314212 LIB143-001-	-Q1-E1-C10		
Seq. Seq.		314213 LIB143-001-	-Q1-E1-C11		
Seq. Seq.		314214 LIB143-001-	-Q1-E1-C3		
Seq. Seq.	No. ID	314215 LIB143-001-	-Q1-E1-C4		
Seq. Seq.	No. ID	314216 LIB143-001-	-Q1-E1-D5		
_	No. ID	314217 LIB143-001-	-Q1-E1-E11		
Seq. Seq.	No. ID	314218 LIB143-001-	-Q1-E1-E3		
Seq. Seq.	No. ID	314219 LIB143-001-	-Q1-E1-F4		· ·
	No. ID	314220 LIB143-001-	-Q1-E1-F9		
Seq. Seq.		314221 LIB143-001-	-Q1-E1-G3		
Seq. Seq.	No. ID	314222 LIB143-001	-Q1-E1-G6		
-	No. ID	314223 LIB143-001	-Q1-E1-G7		
Seq. Seq.		314224 LIB143-001-	-Q1-E1-G8		
Seq. Seq.		314225 LIB143-001-	-Q1-E1-G9		
Seq. Seq.		314226 LIB143-001-	-Q1-E1-H2		
Seq. Seq.		314227 LIB143-001-	-Q1-E1-H3		
Seq. Seq.		314228 LIB143-002-	-Q1-E1-B3		
Seq.	No.	314229			

Seq.	ID	LIB143-002-Q1-E1-B5
Seq. Seq.	No. ID	314230 LIB143-002-Q1-E1-B6
Seq. Seq.		314231 LIB143-002-Q1-E1-C10
Seq. Seq.		314232 LIB143-002-Q1-E1-C5
Seq. Seq.	No. ID	314233 LIB143-002-Q1-E1-D12
Seq. Seq.		314234 LIB143-002-Q1-E1-D7
Seq. Seq.		314235 LIB143-002-Q1-E1-E11
Seq. Seq.		314236 LIB143-002-Q1-E1-E6
Seq. Seq.		314237 LIB143-002-Q1-E1-F10
Seq. Seq.		314238 LIB143-002-Q1-E1-F6
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Seq. Seq.		314240 LIB143-003-Q1-E1-A1
Seq. Seq.		314241 LIB143-003-Q1-E1-A6
Seq. Seq.	No. ID	314242 LIB143-003-Q1-E1-A8
Seq. Seq.		314243 LIB143-003-Q1-E1-B3
Seq. Seq.		314244 LIB143-003-Q1-E1-B6
Seq. Seq.		314245 LIB143-003-Q1-E1-B9
Seq. Seq.		314246 LIB143-003-Q1-E1-C2
Seq. Seq.		314247 LIB143-003-Q1-E1-C4

Seq. No.

		THE P
Seq.	ID	LIB143-003-Q1-E1-C7
Seq. Seq.		314249 LIB143-003-Q1-E1-D2
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Seq. Seq.		314252 LIB143-003-Q1-E1-E8
Seq. Seq.		314253 LIB143-003-Q1-E1-F11
Seq.		314254 LIB143-003-Q1-E1-F8
Seq. Seq.		314255 LIB143-003-Q1-E1-G12
Seq. Seq.		314256 LIB143-003-Q1-E1-G2
Seq. Seq.		314257 LIB143-003-Q1-E1-G3
Seq. Seq.		314258 LIB143-003-Q1-E1-H10
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Seq. Seq.		314265 LIB143-004-Q1-E1-B1
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Seq.	No.	314267

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Seq. Seq.		314273 LIB143-004-Q1-E1-F4
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Seq. Seq.		314283 LIB143-004-Q1-E1-H8
Seq. Seq.		314284 LIB143-005-Q1-E1-B5
Seq. Seq.		314285 LIB143-005-Q1-E1-C11
Seq.	No.	314286

		am.
Seq.	ID	LIB143-005-Q1-E1-C3
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Seq. Seq.		314289 LIB143-005-Q1-E1-C6
Seq. Seq.		314290 LIB143-005-Q1-E1-C8
Seq. Seq.	No. ID	314291 LIB143-005-Q1-E1-D1
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Seq. Seq.		314293 LIB143-005-Q1-E1-D7
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Seq. Seq.		314296 LIB143-005-Q1-E1-E5
Seq. Seq.		314297 LIB143-005-Q1-E1-E7
Seq.	No. ID	314298 LIB143-005-Q1-E1-F3
Seq. Seq.		314299 LIB143-005-Q1-E1-F9
Seq. Seq.		314300 LIB143-005-Q1-E1-H2
Seq. Seq.		314301 LIB143-005-Q1-E1-H3
Seq. Seq.		314302 LIB143-006-Q1-E1-A2
Seq. Seq.		314303 LIB143-006-Q1-E1-A6
Seq. Seq.		314304 LIB143-006-Q1-E1-C3
Seq.	No.	314305

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	Seq. Seq.		314307 LIB143-006-Q1-E1-D9
	Seq.		314308 LIB143-006-Q1-E1-F12
	Seq. Seq.	No. ID	314309 LIB143-006-Q1-E1-F5
	Seq. Seq.		314310 LIB143-006-Q1-E1-F7
7	Seq. Seq.		314311 LIB143-006-Q1-E1-G10
	Seq. Seq.		314312 LIB143-006-Q1-E1-G7
	Seq. Seq.		314313 LIB143-006-Q1-E1-H10
	Seq. Seq.		314314 LIB143-006-Q1-E1-H2
	Seq. Seq.		314315 LIB143-006-Q1-E1-H3
	Seq. Seq.		314316 LIB143-006-Q1-E1-H8
	Seq. Seq.		314317 LIB143-011-Q1-E1-A12
	Seq. Seq.		314318 LIB143-011-Q1-E1-A9
	Seq. Seq.		314319 LIB143-011-Q1-E1-B10
	Seq. Seq.		314320 LIB143-011-Q1-E1-B4
	Seq. Seq.		314321 LIB143-011-Q1-E1-C1
	Seq. Seq.		314322 LIB143-011-Q1-E1-C10
	Seq. Seq.		314323 LIB143-011-Q1-E1-C3
	Seq.	No.	314324

Seq.	ID	LIB143-011-Q1-E1-C8
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Seq. Seq.		314327 LIB143-011-Q1-E1-E10
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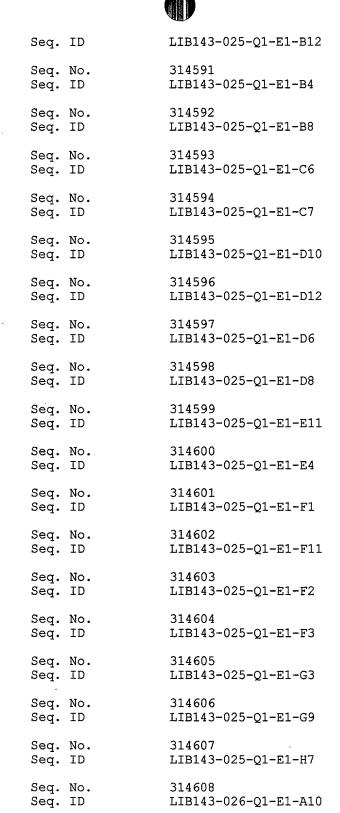
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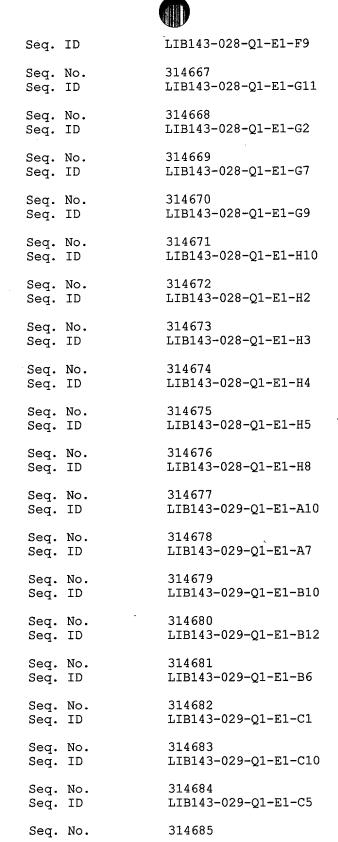
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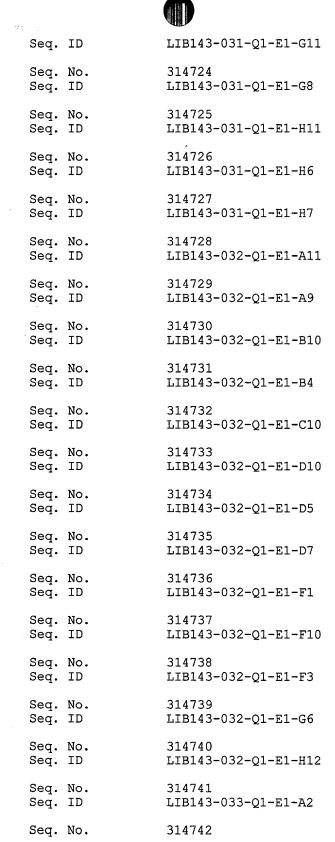
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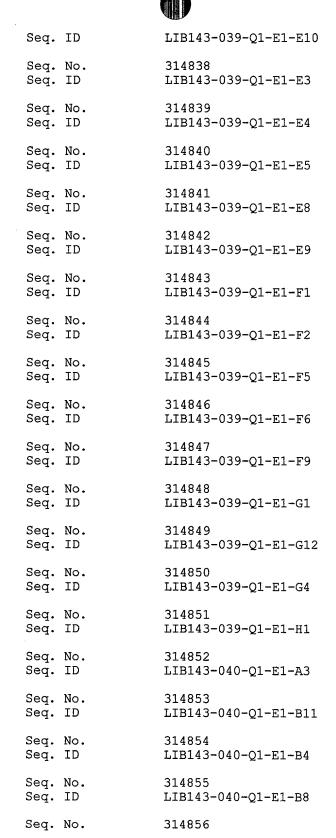
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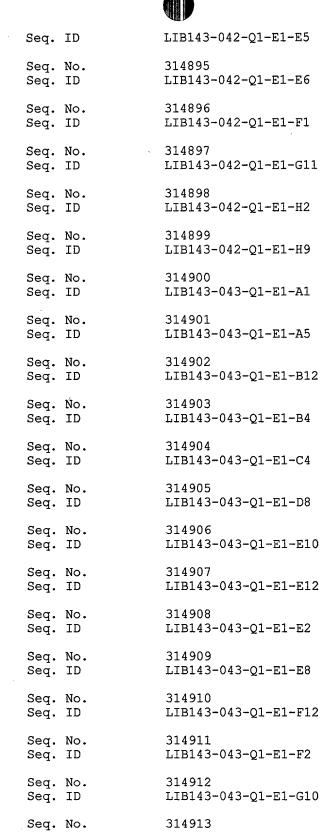
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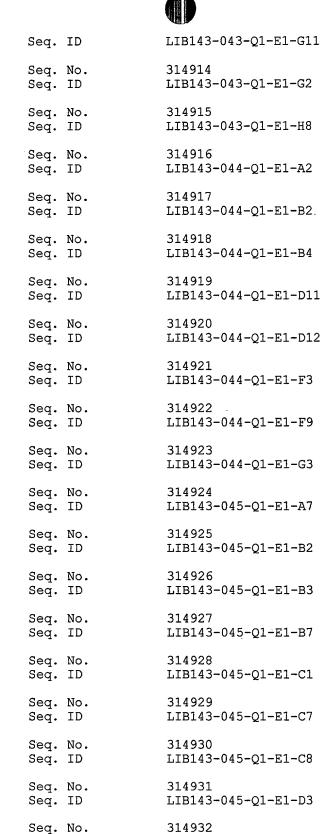


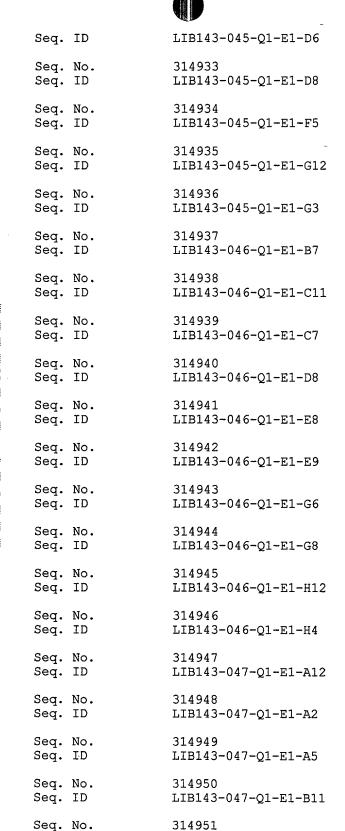
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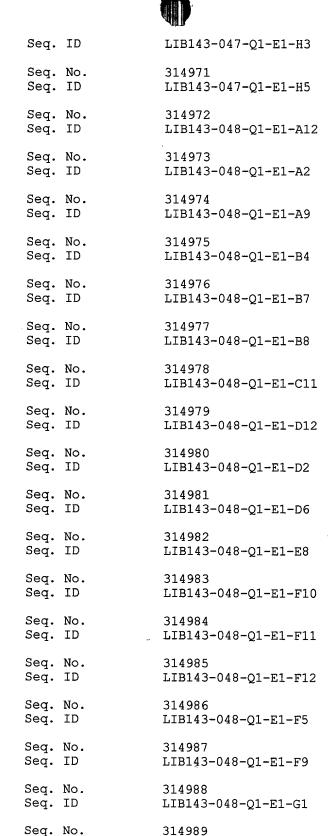


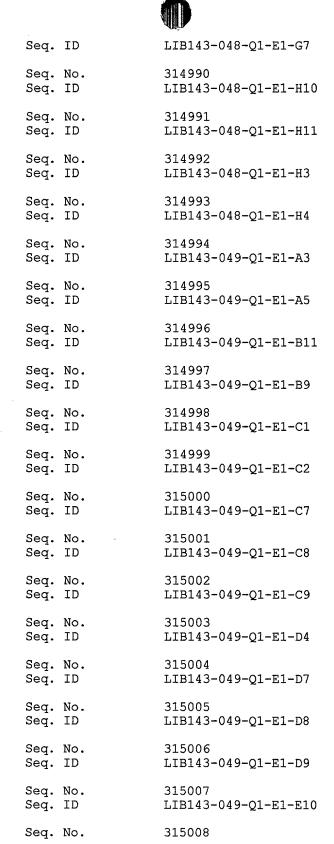


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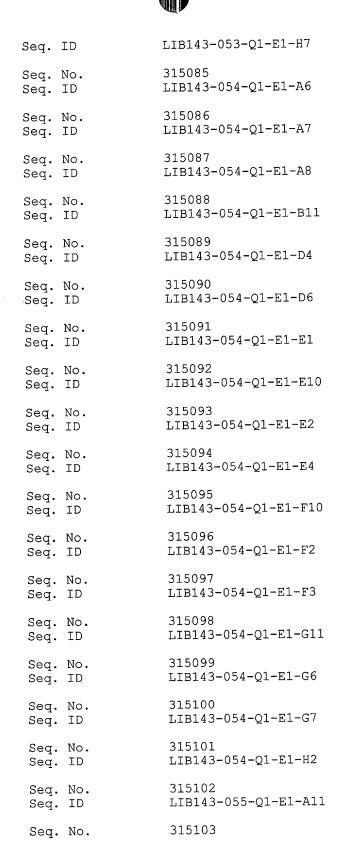
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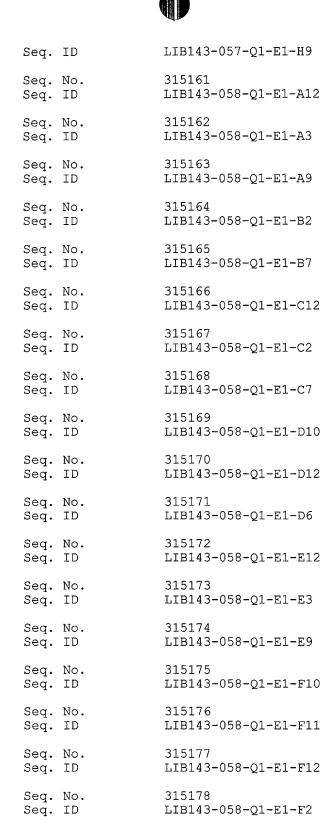


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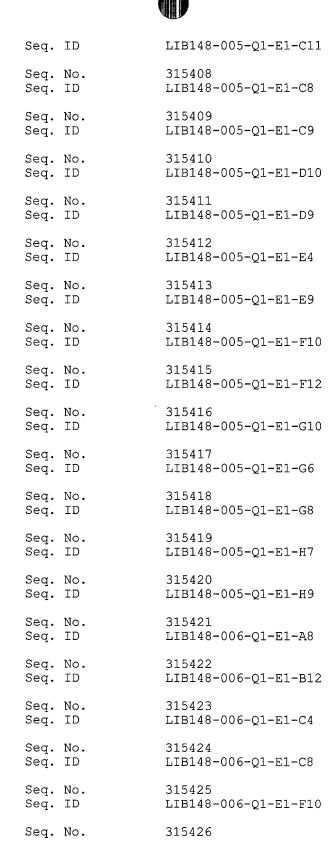
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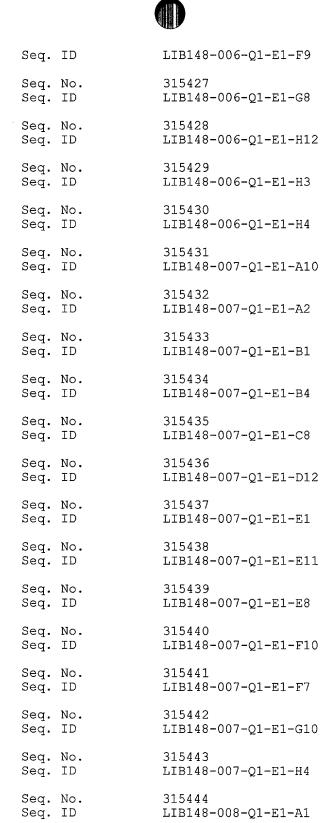
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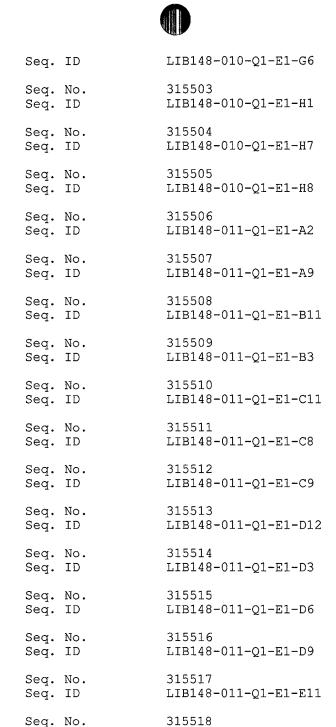
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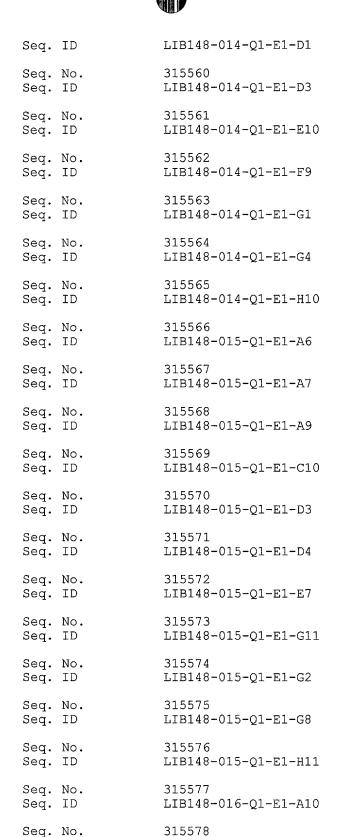
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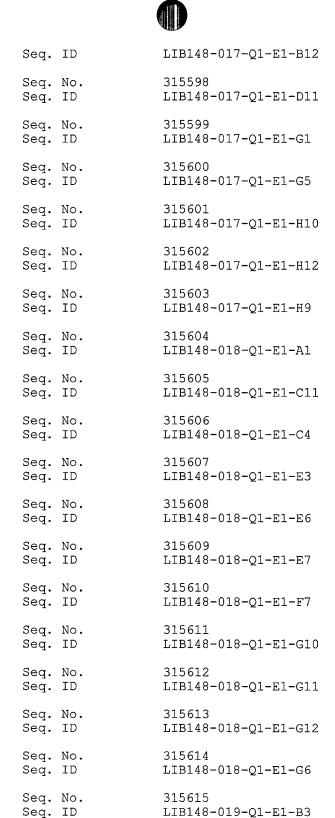


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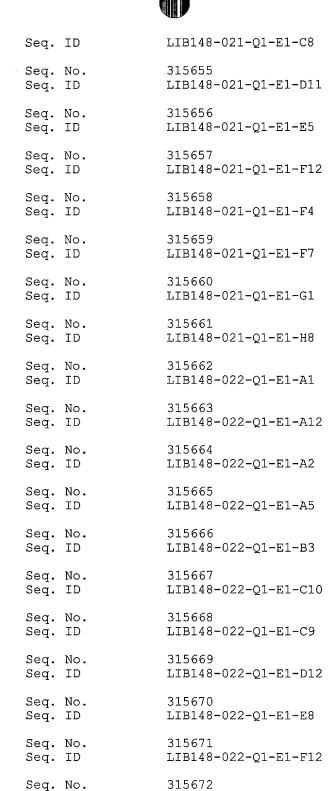


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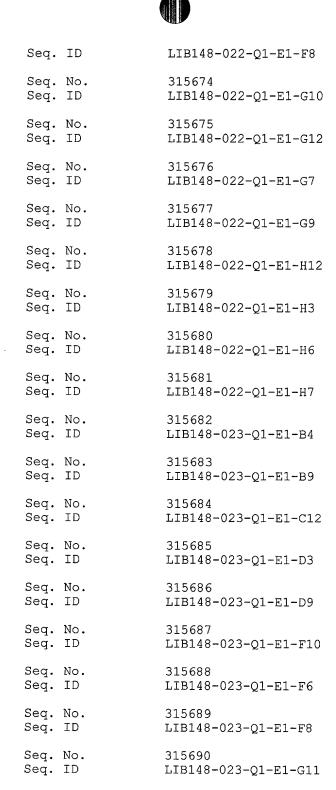
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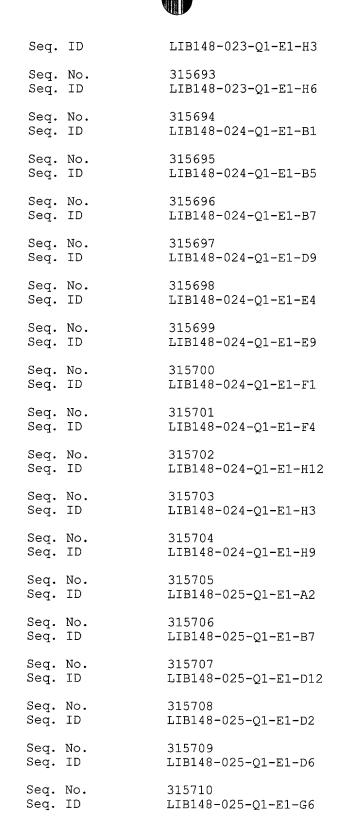


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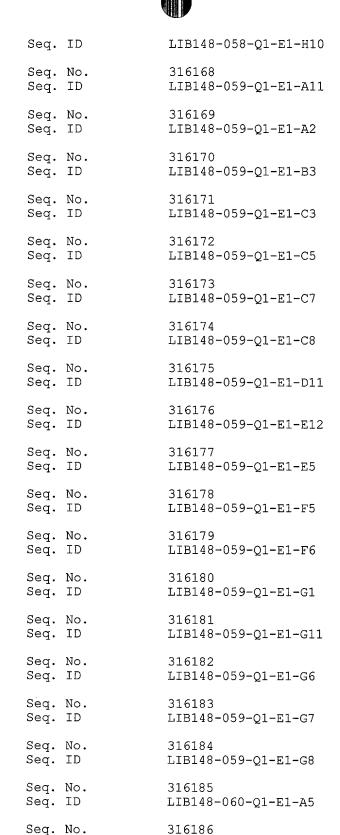
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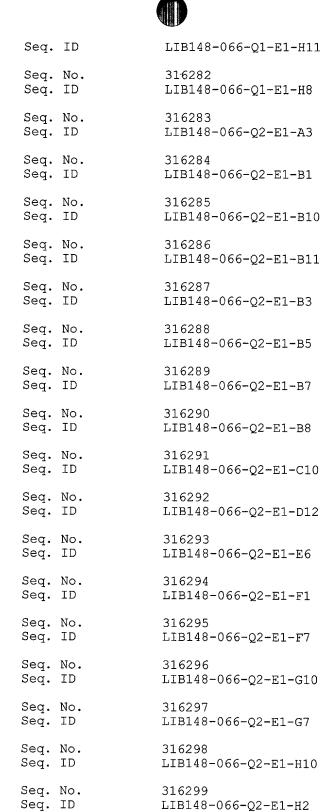
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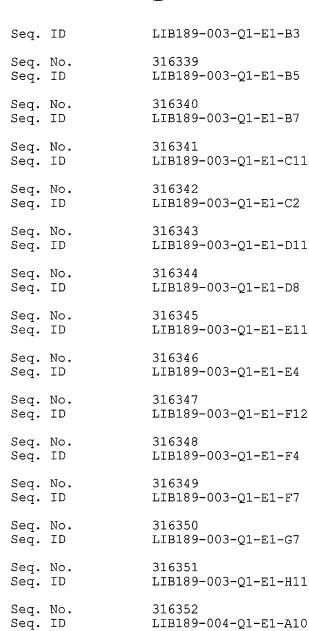
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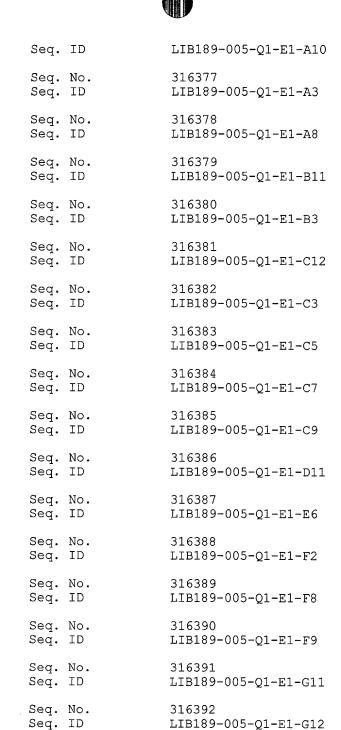
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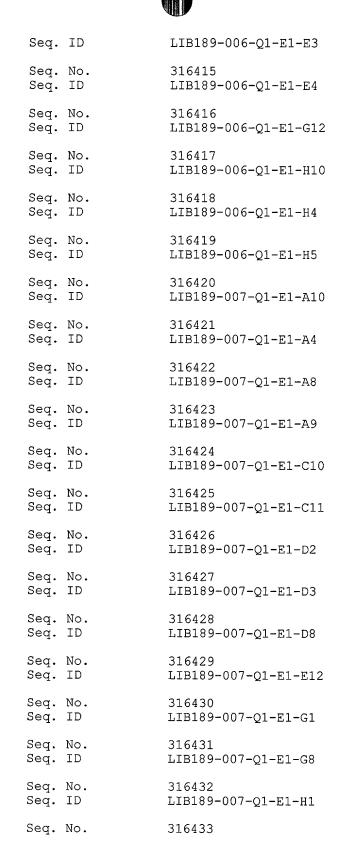
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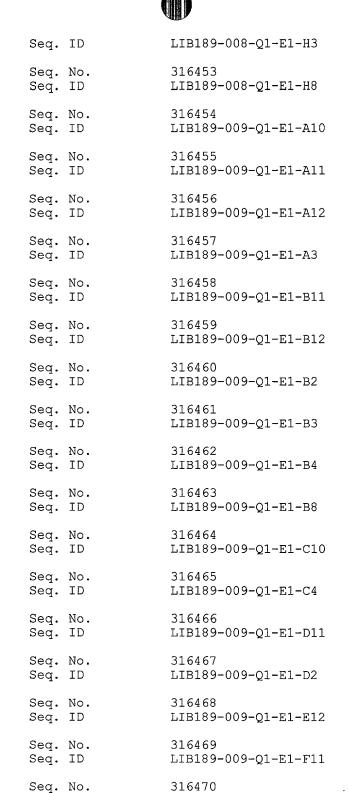
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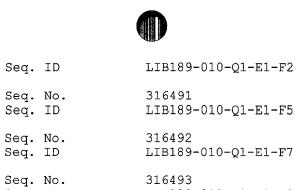
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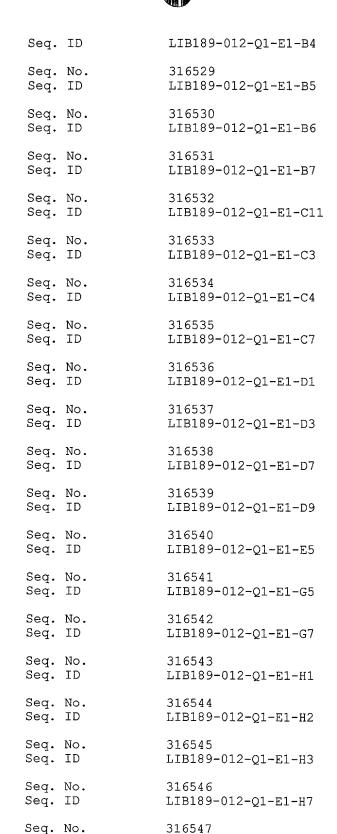
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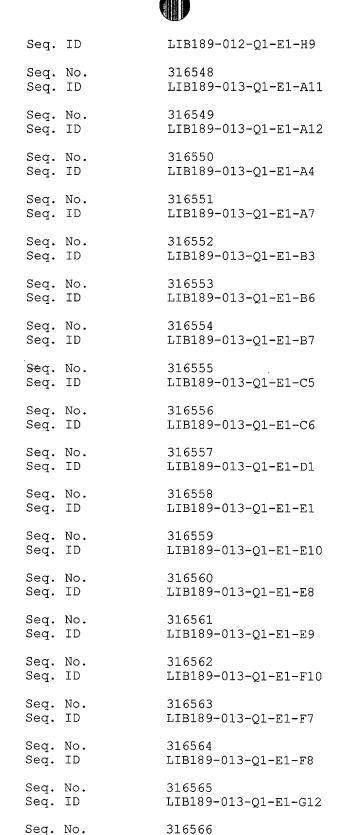
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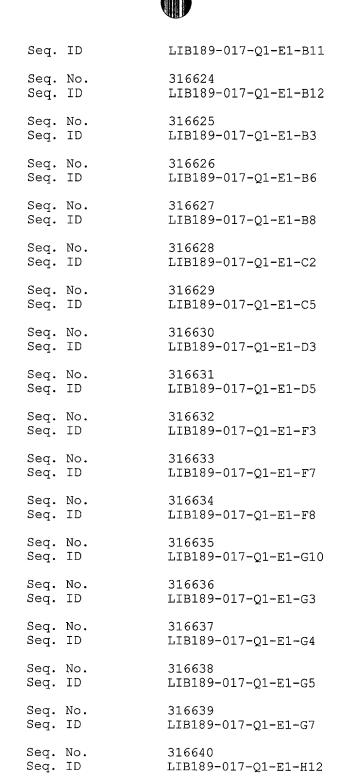
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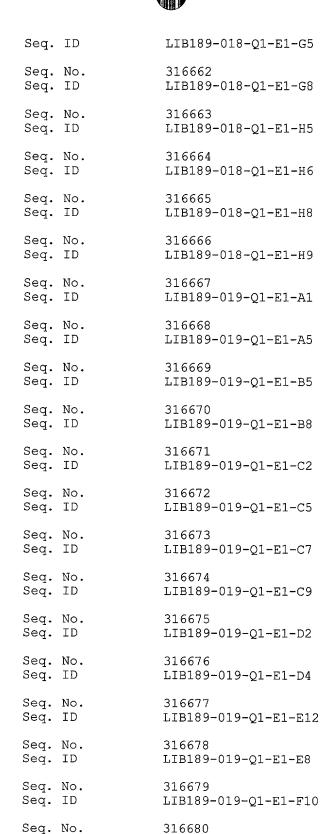


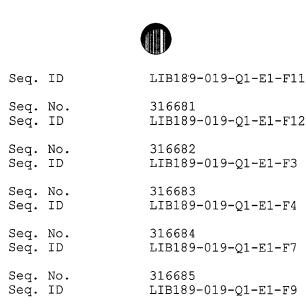
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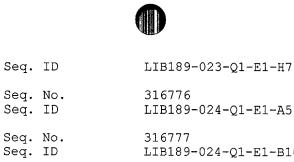
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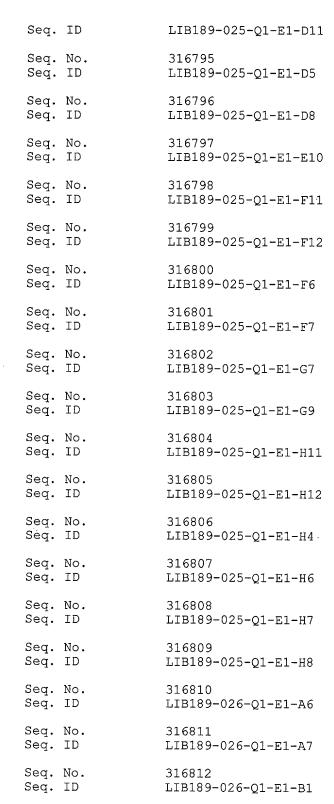


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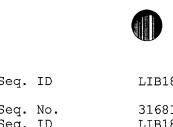
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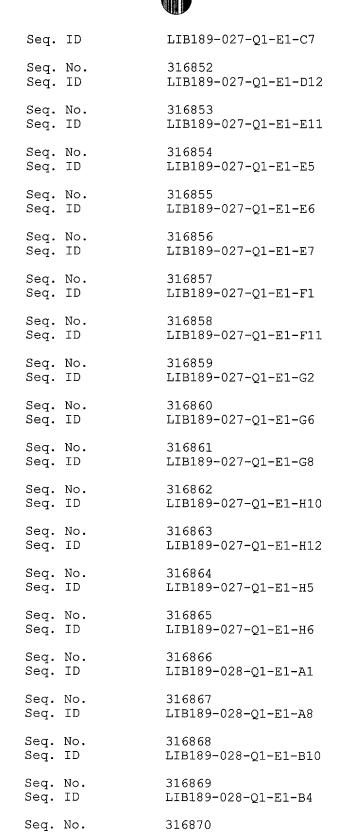


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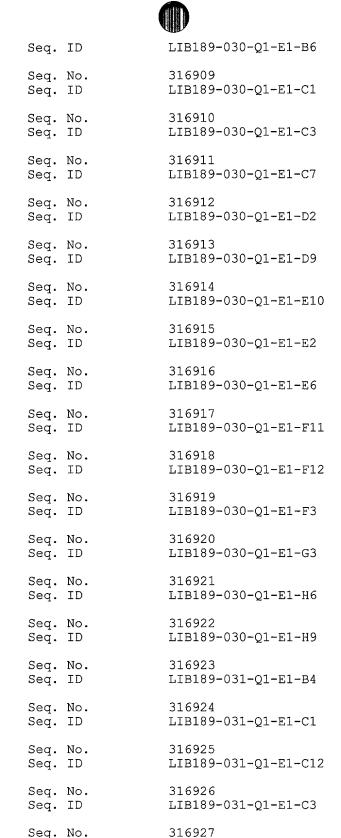
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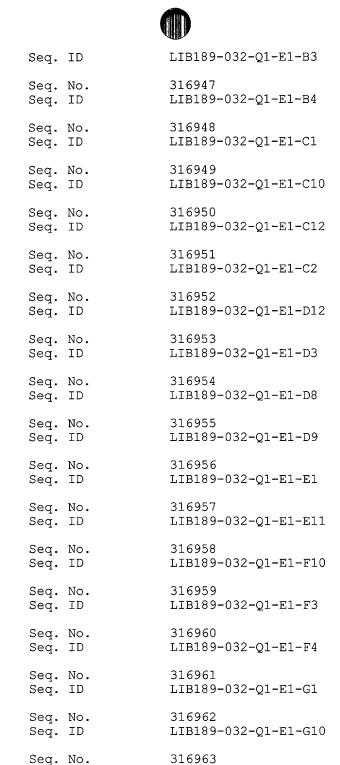


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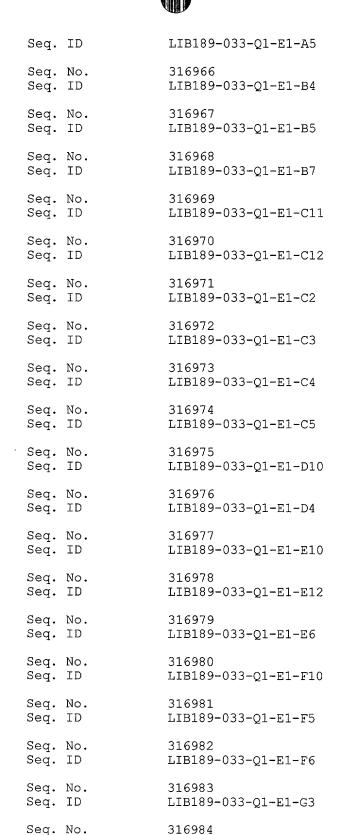


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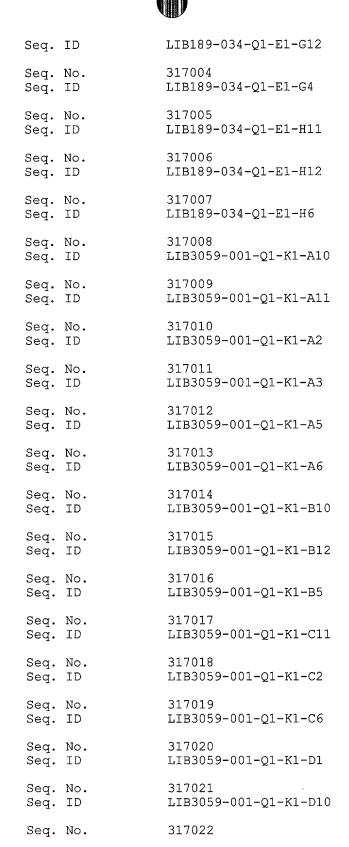
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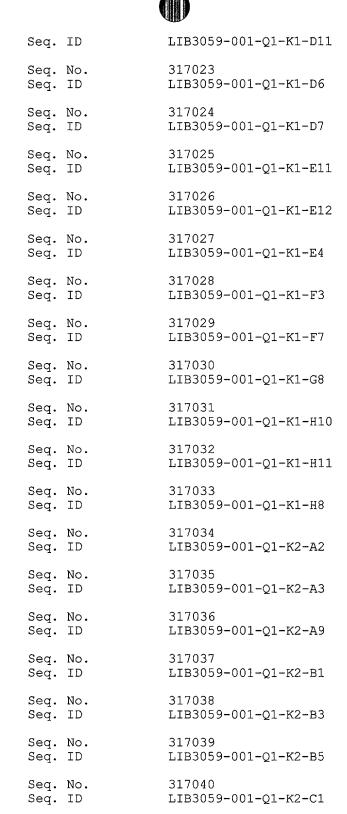




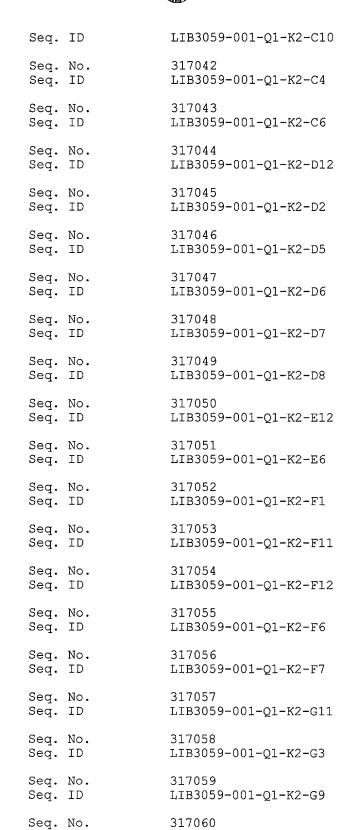
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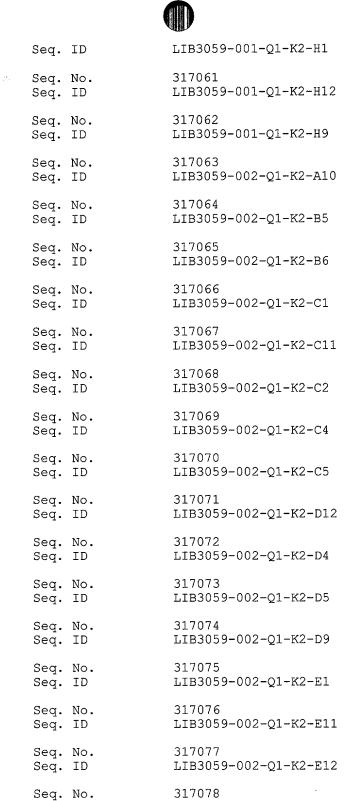


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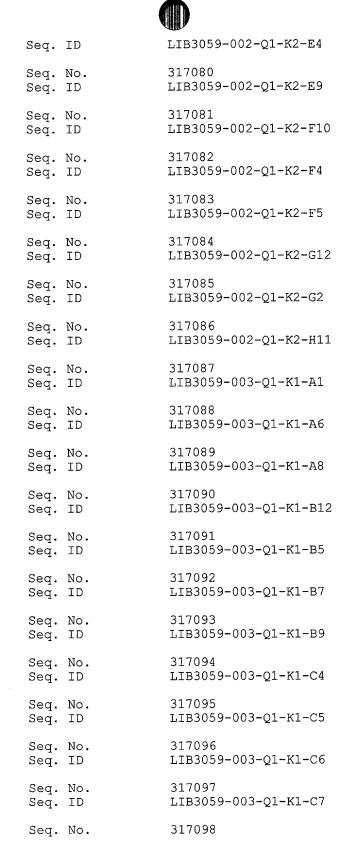
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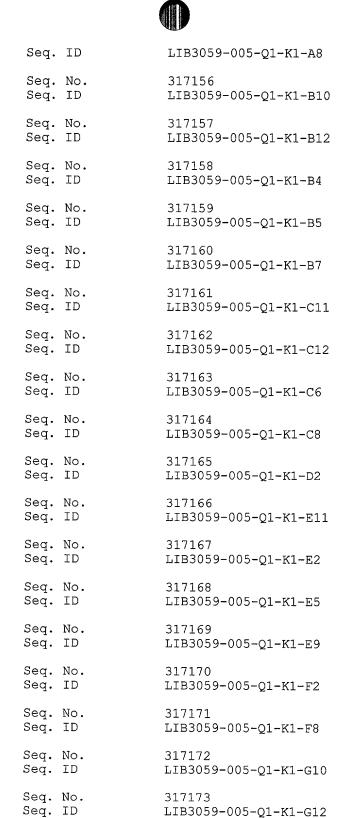
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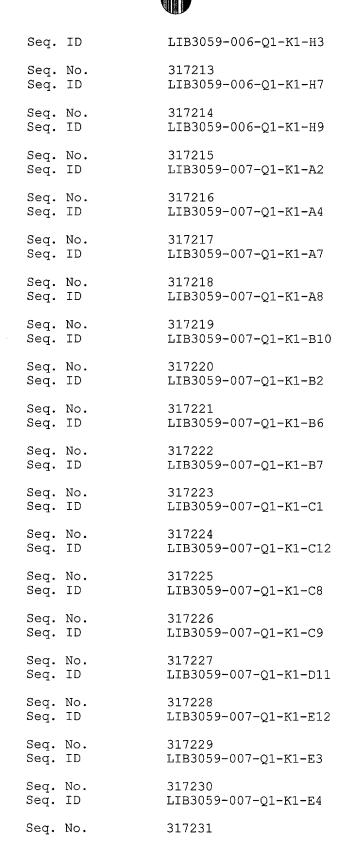




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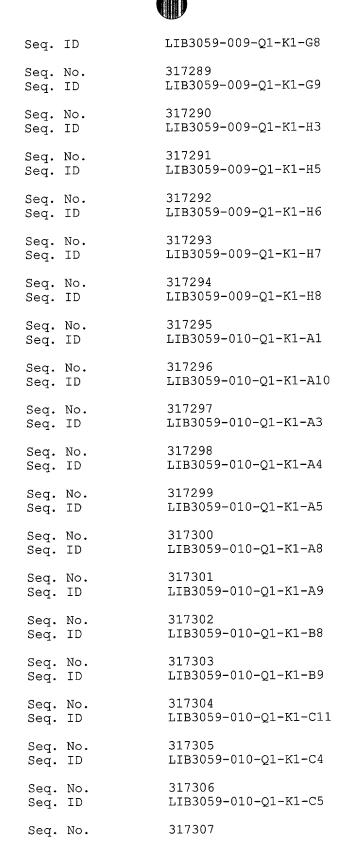


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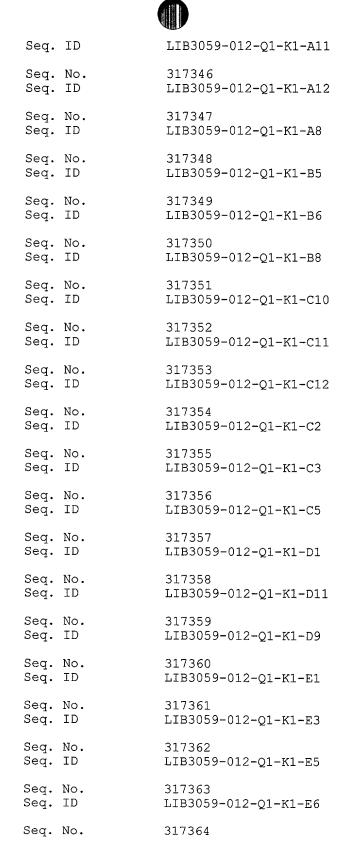




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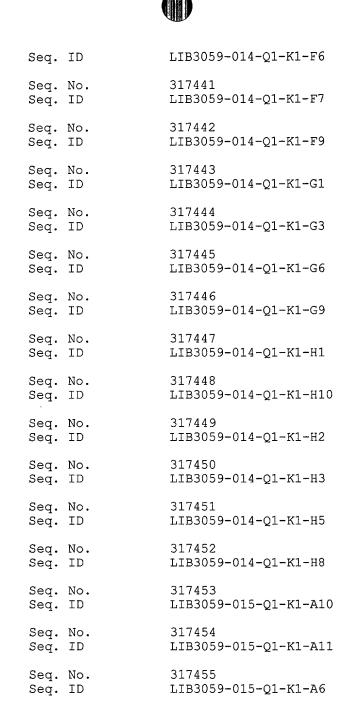
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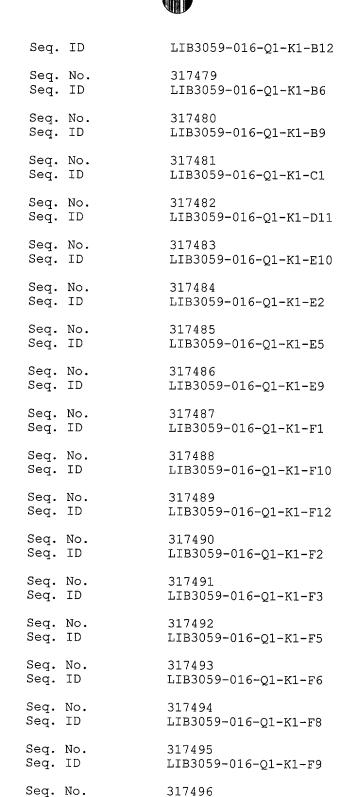
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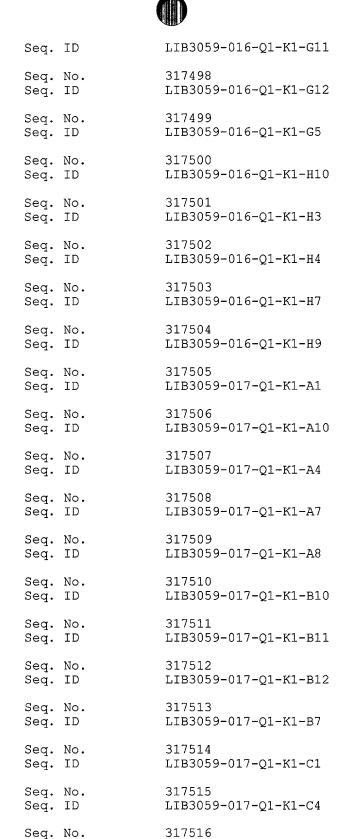
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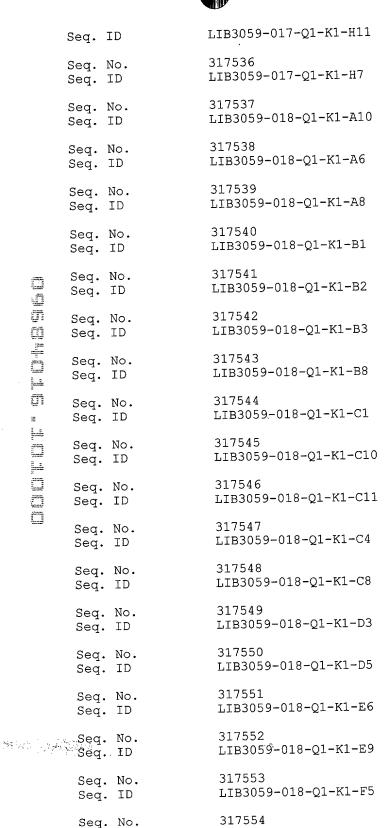
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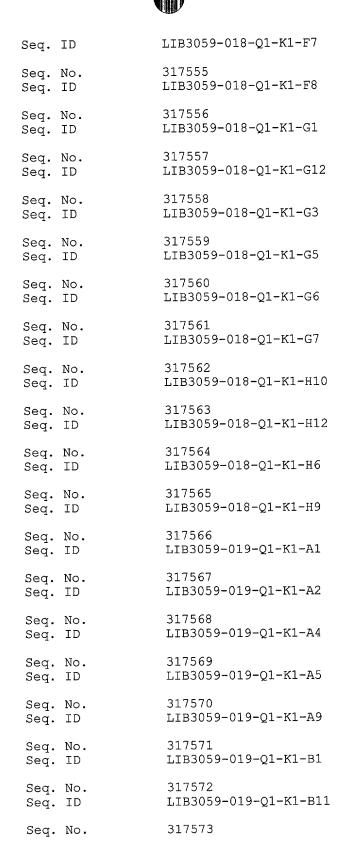
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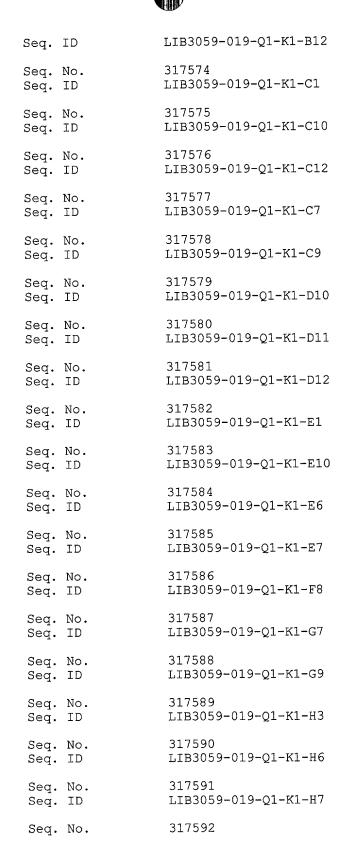




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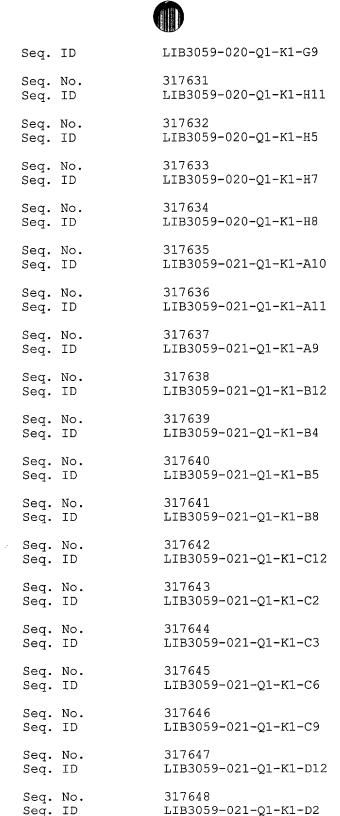




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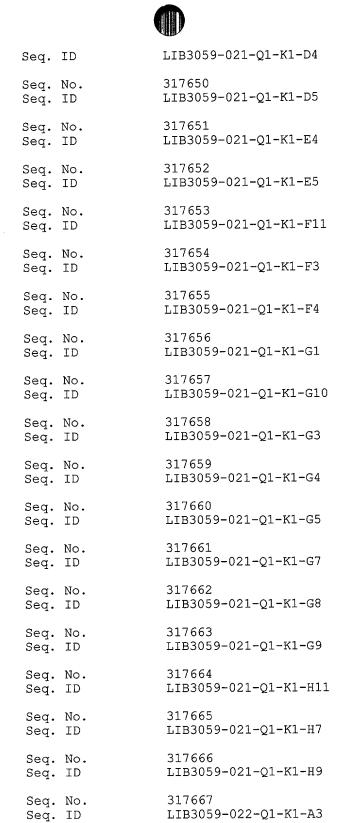
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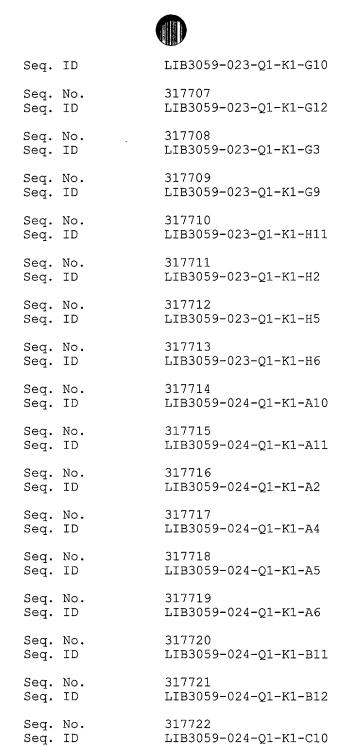




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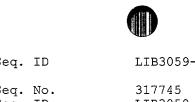
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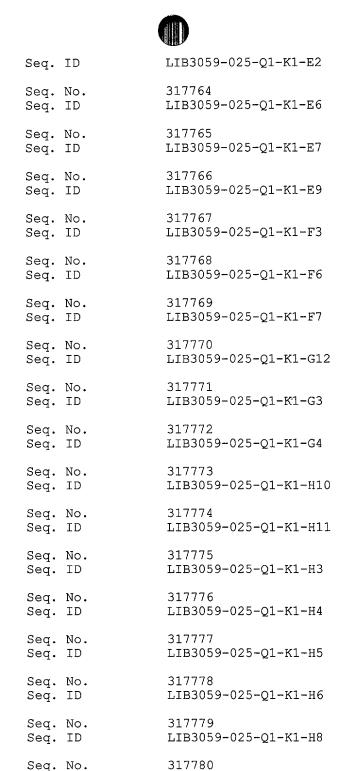
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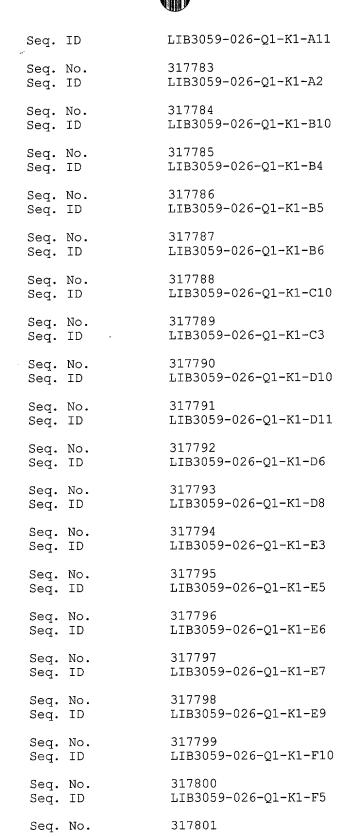


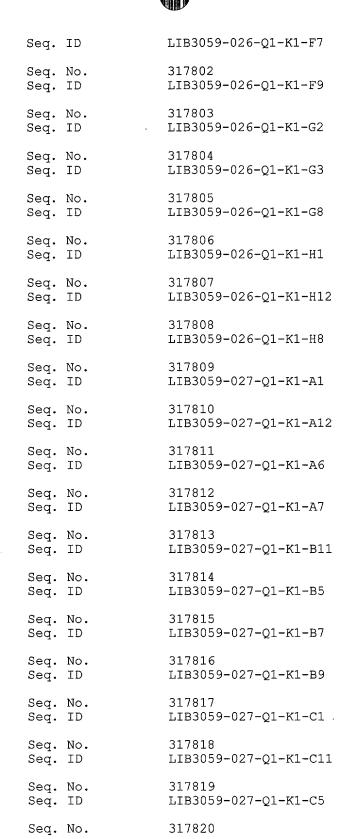
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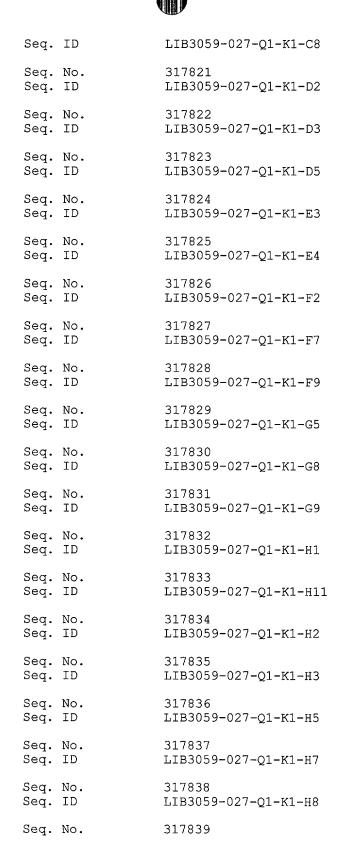
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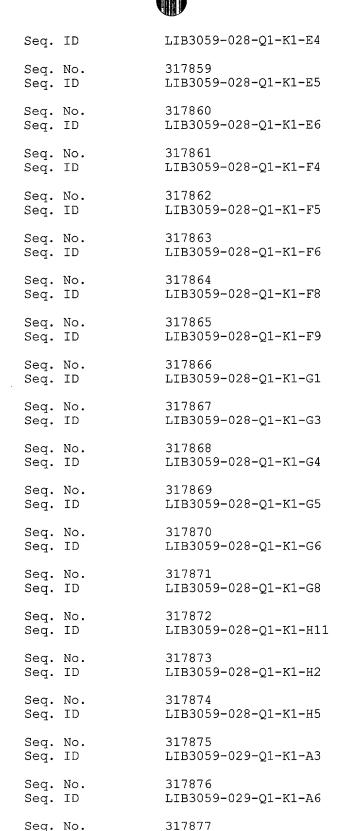






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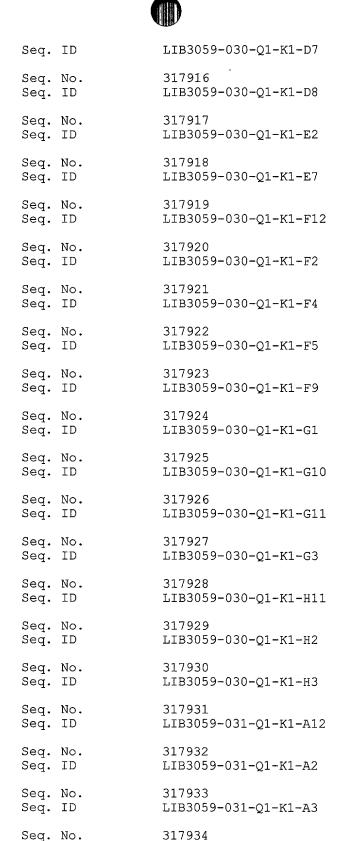




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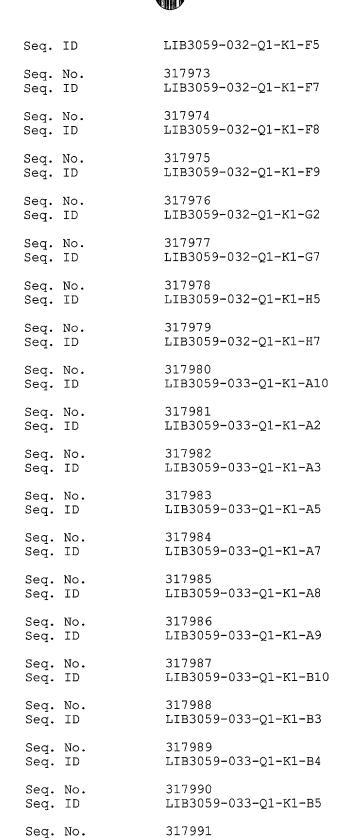


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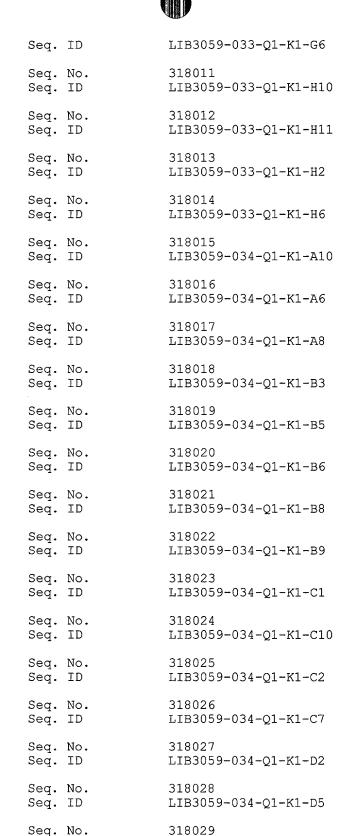
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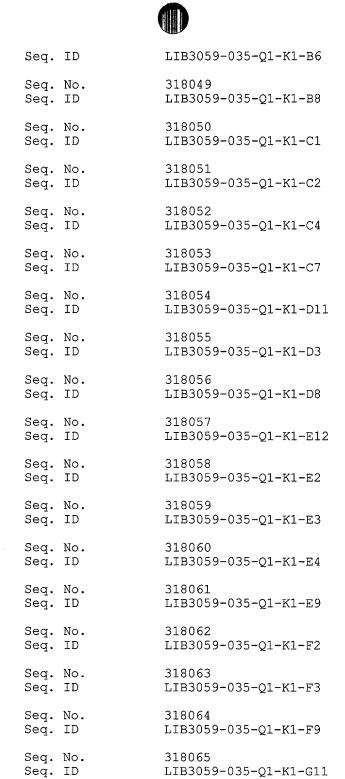
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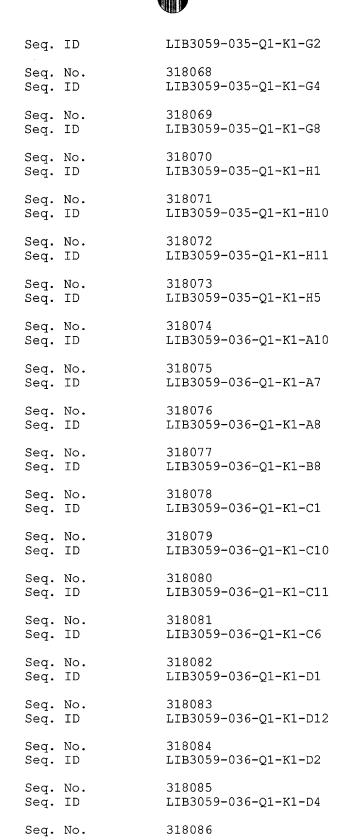
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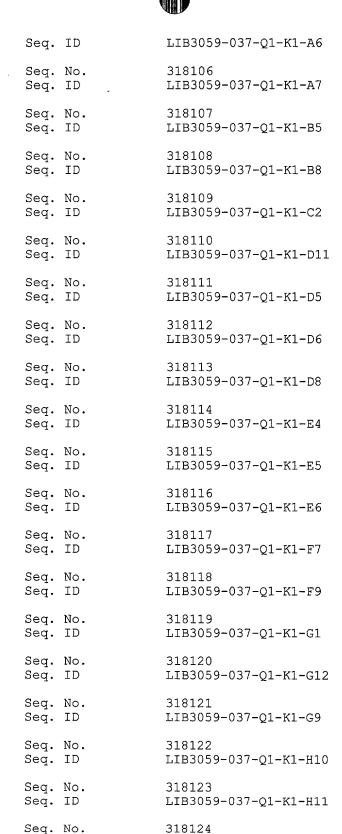
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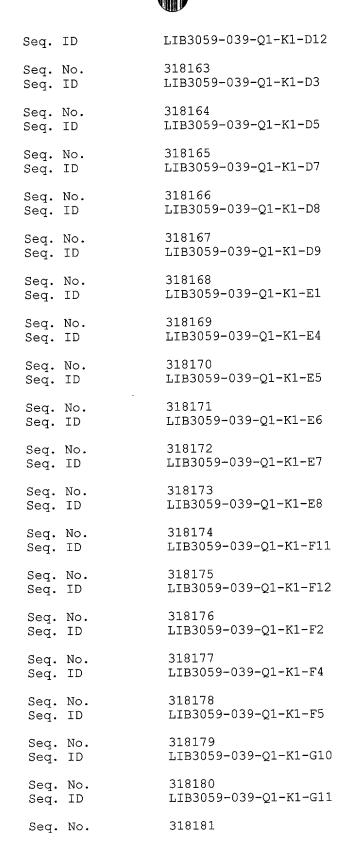
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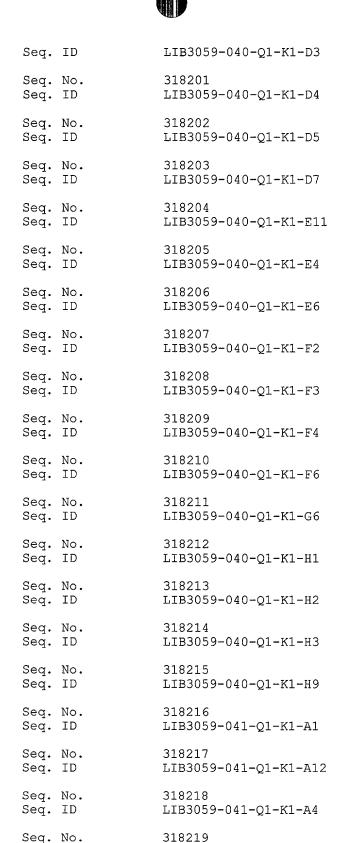
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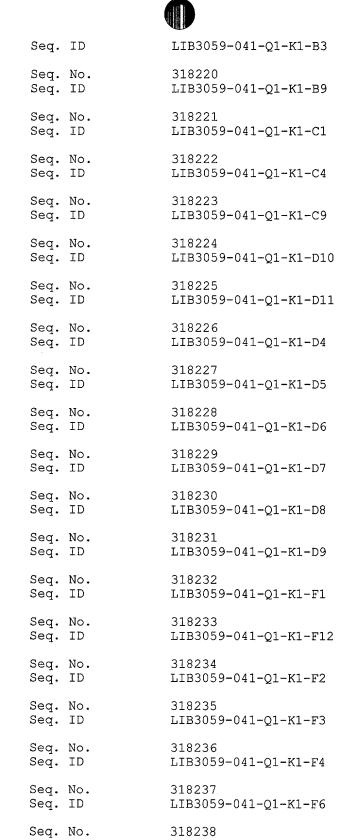
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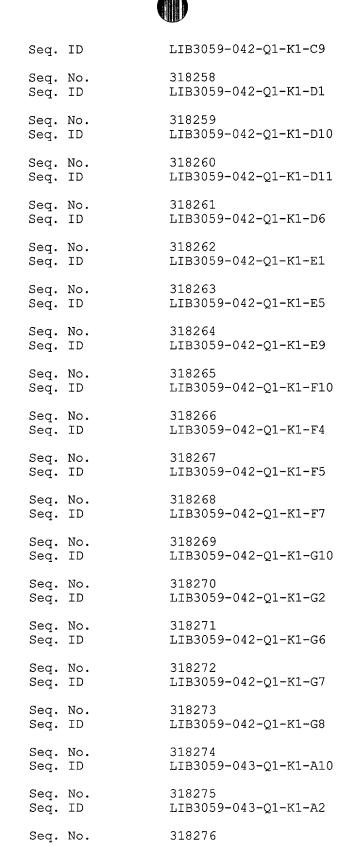
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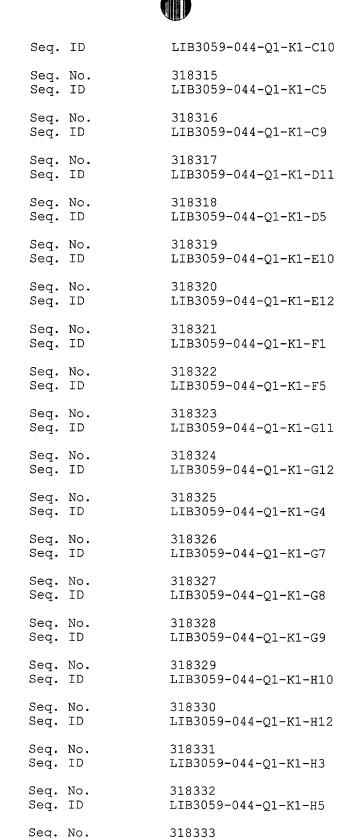




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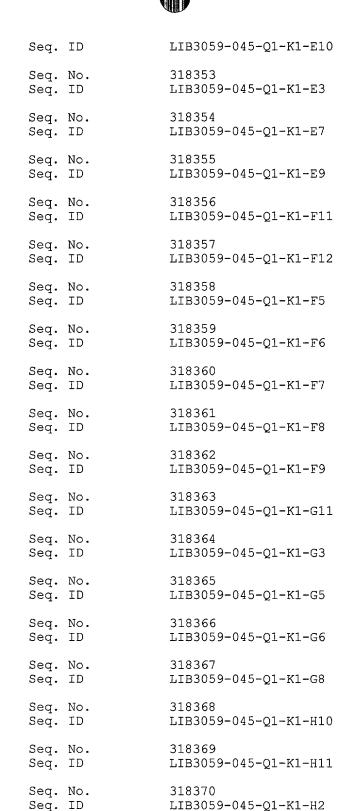


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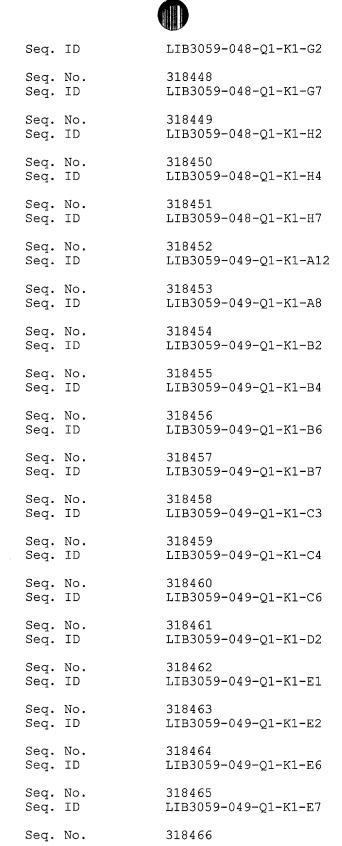
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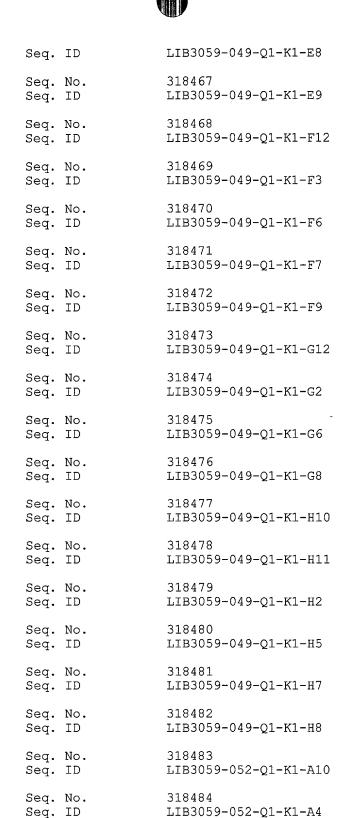
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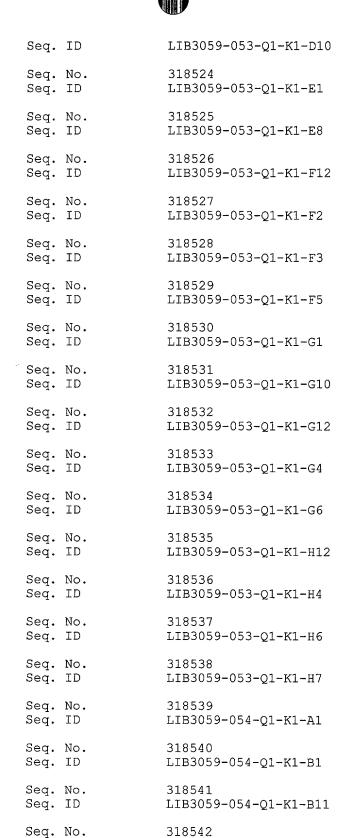


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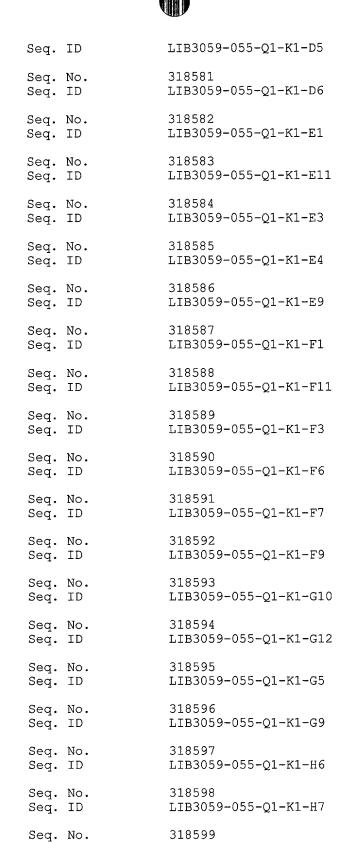


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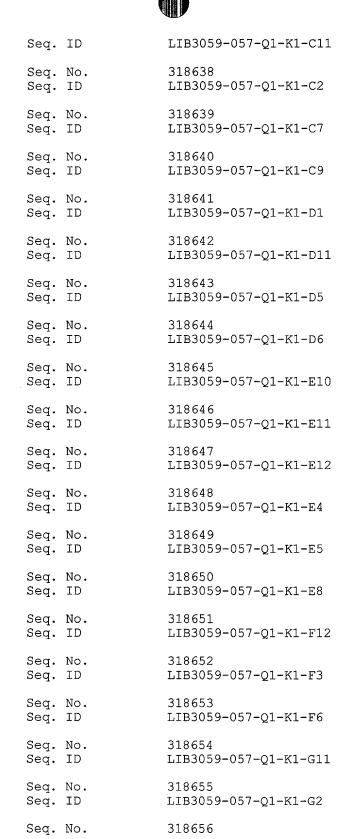


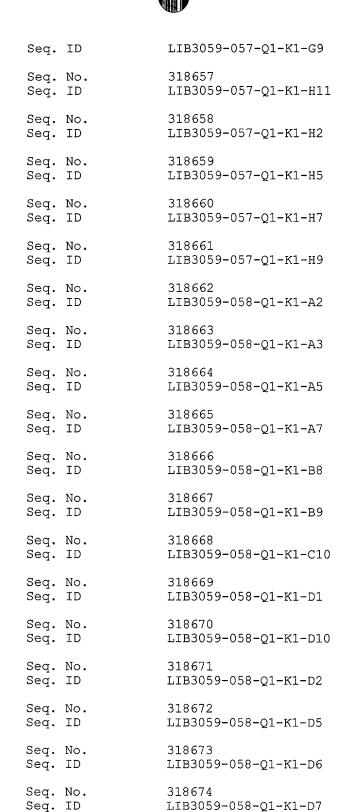


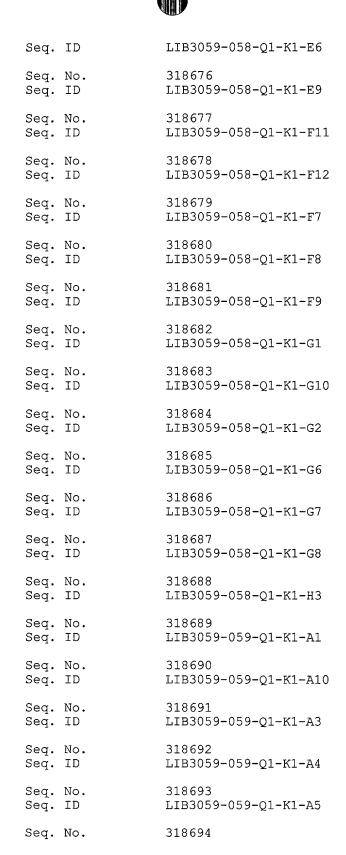
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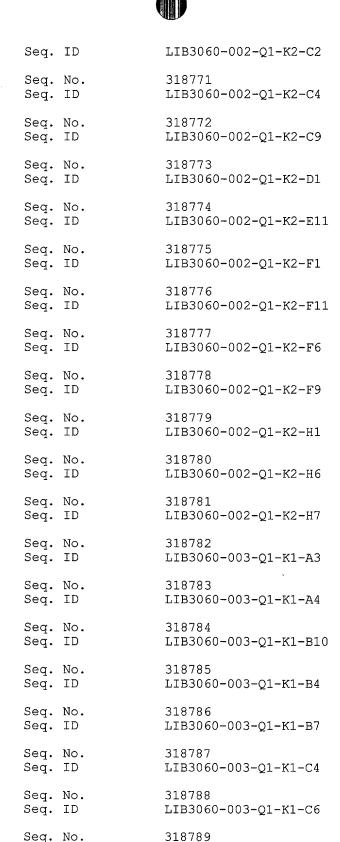
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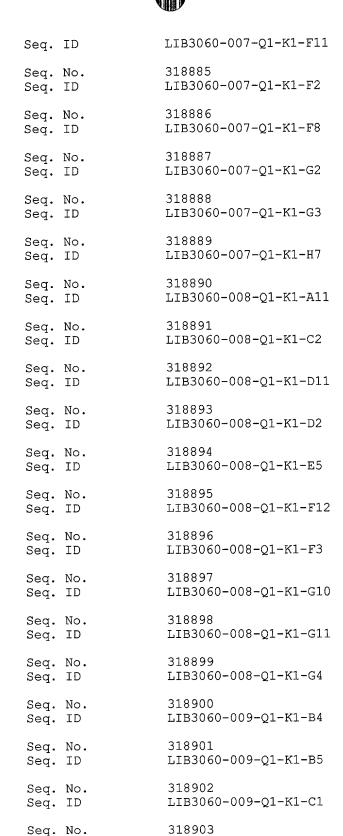
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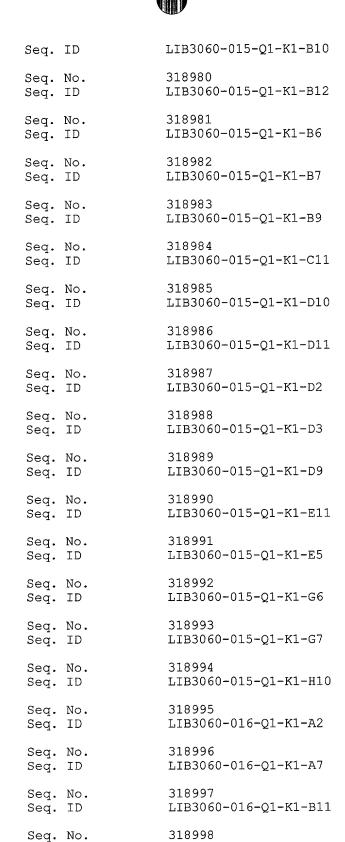
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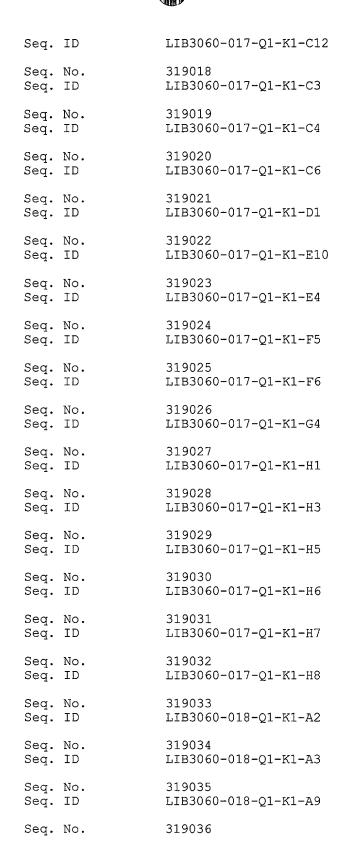
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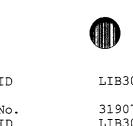
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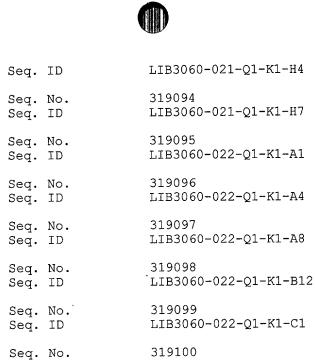
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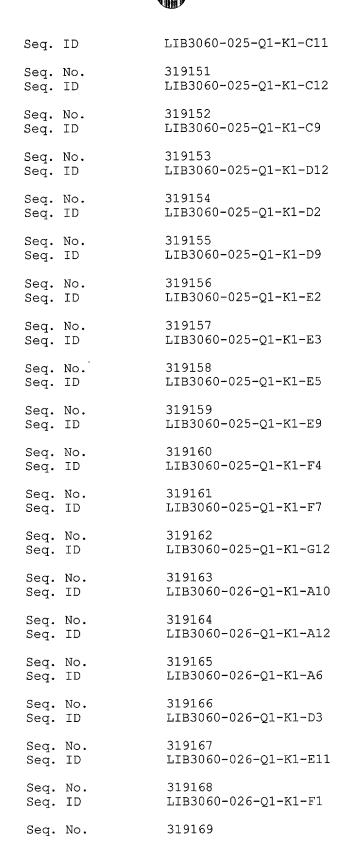
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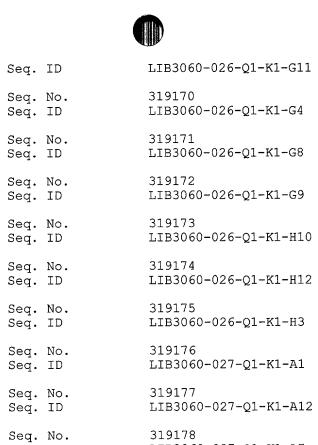


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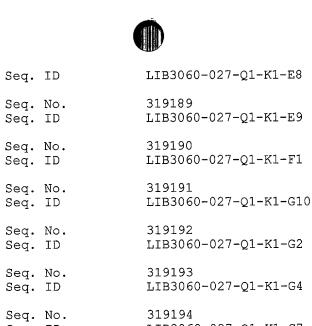
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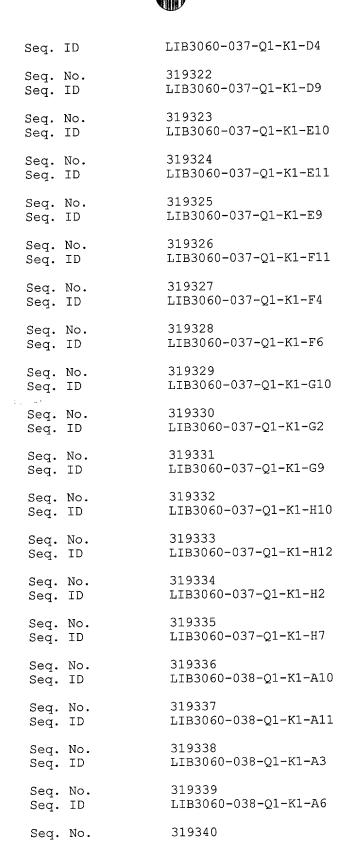


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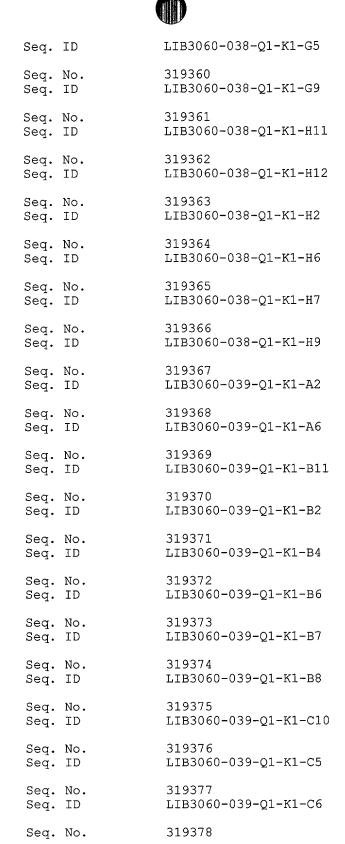
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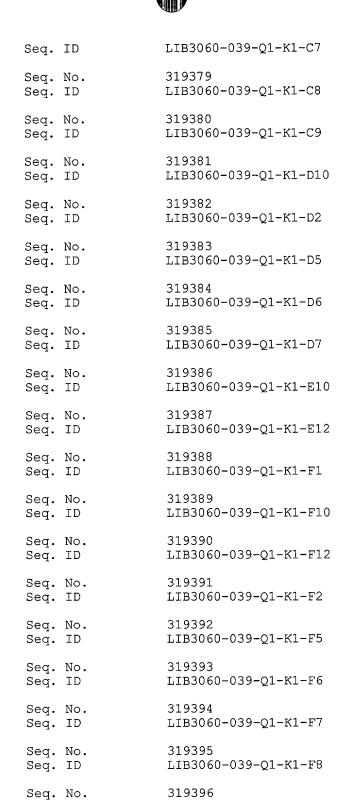


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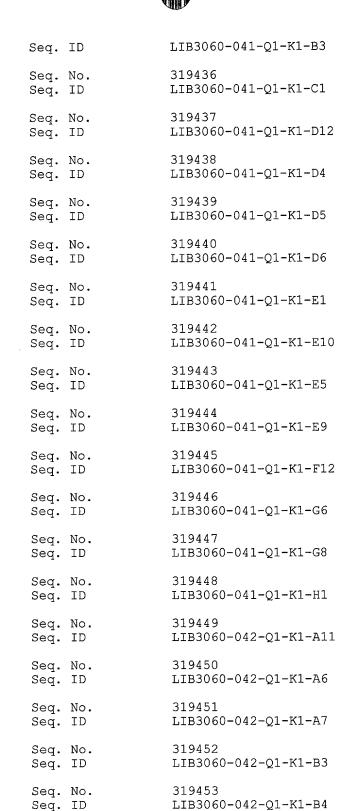


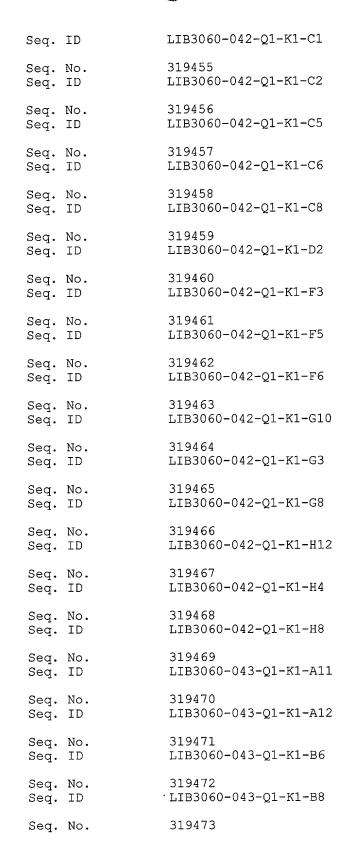
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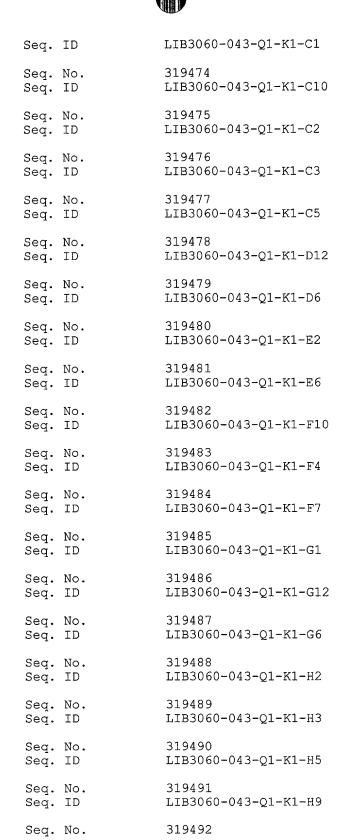


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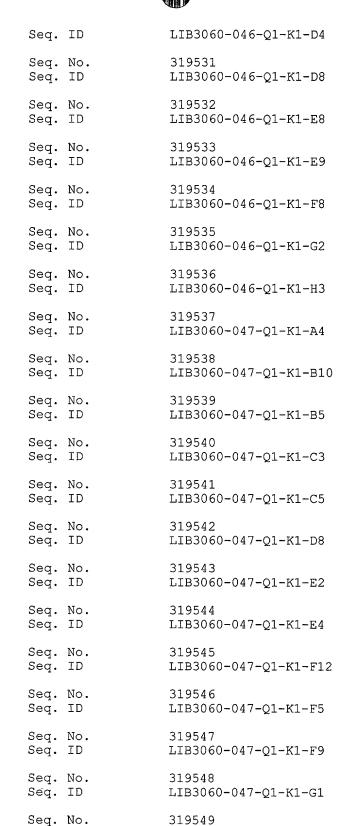






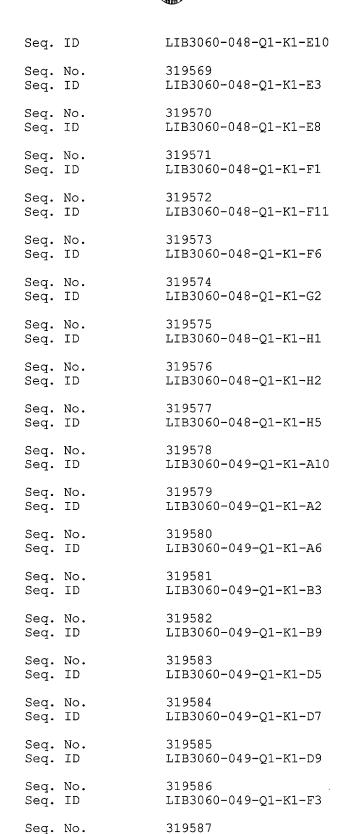
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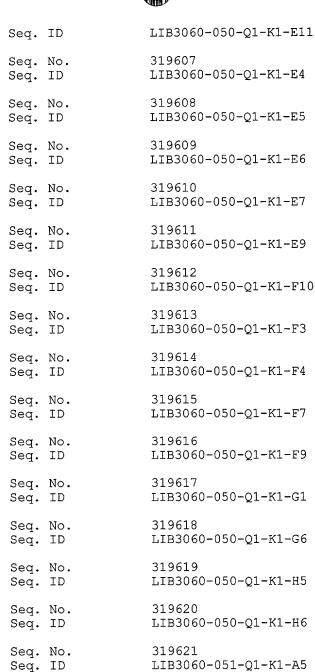




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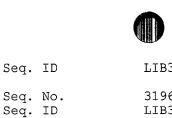
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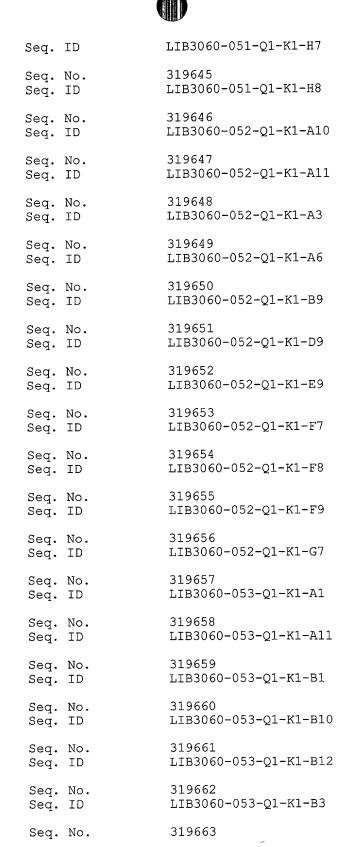
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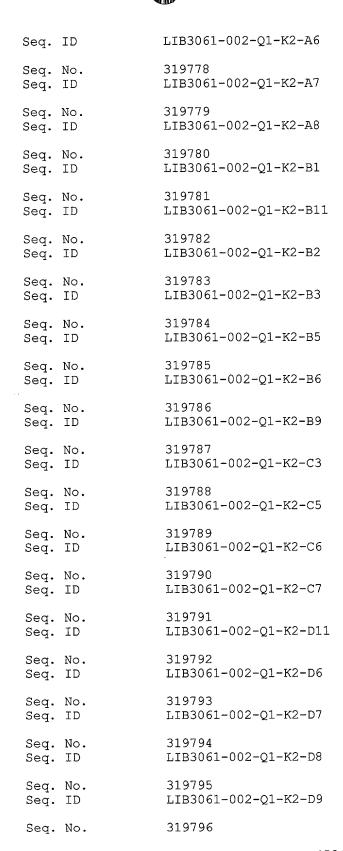
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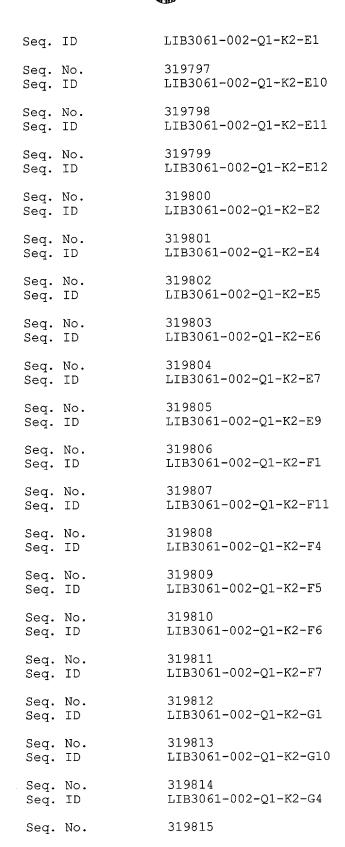


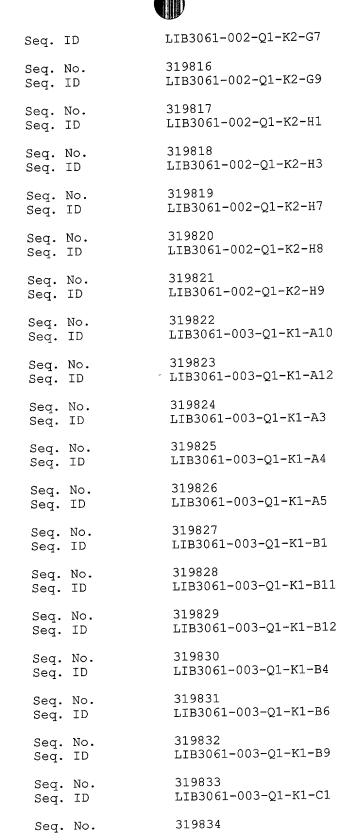
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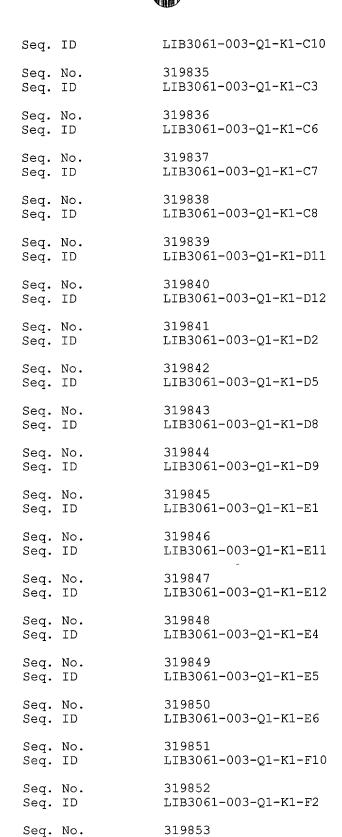
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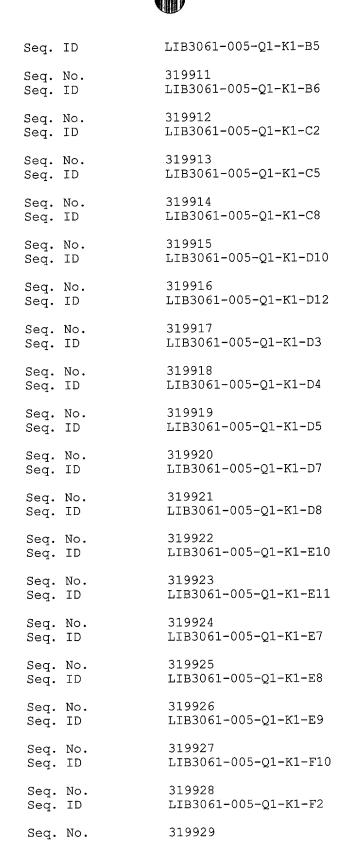
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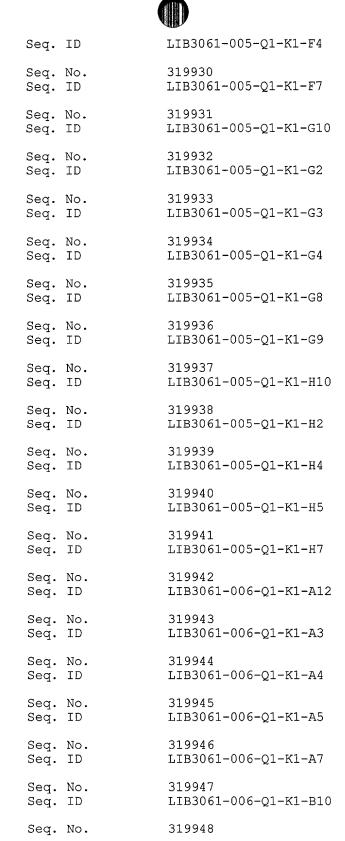


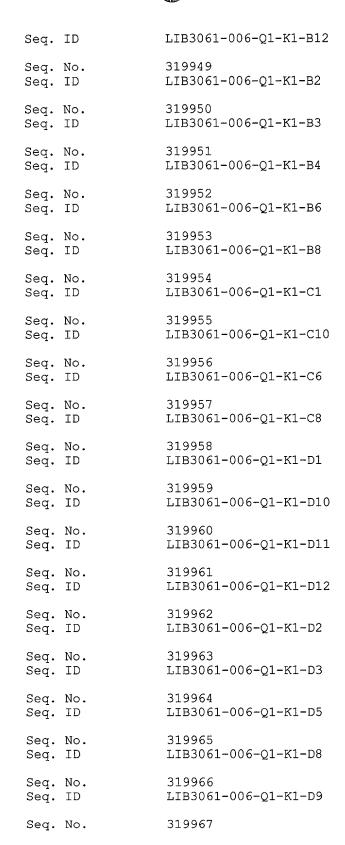
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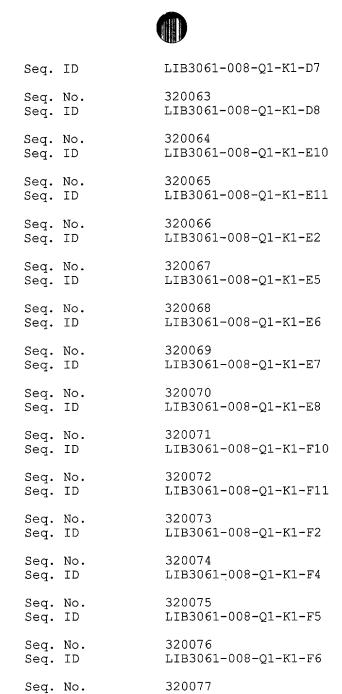
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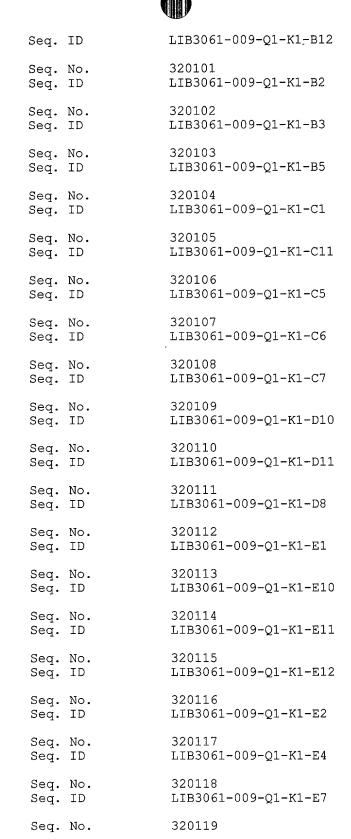
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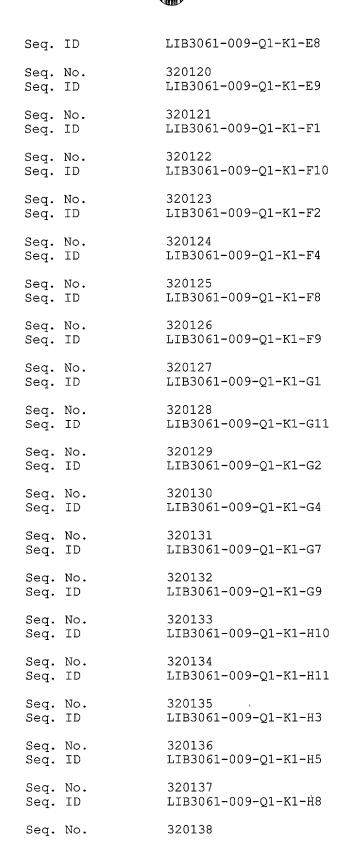
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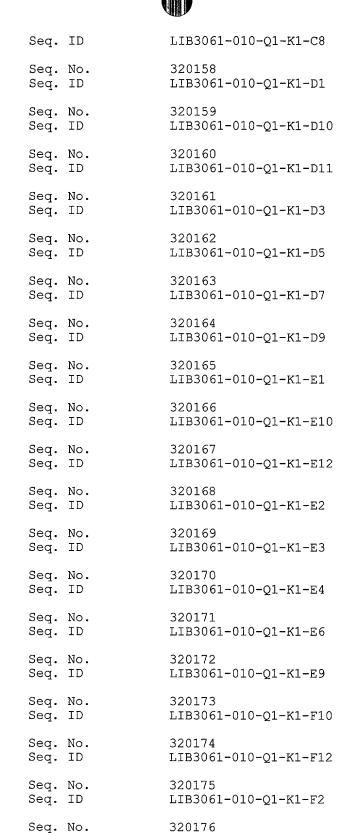
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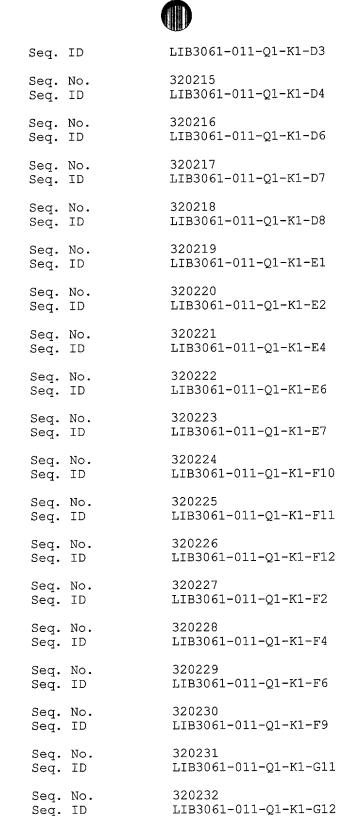


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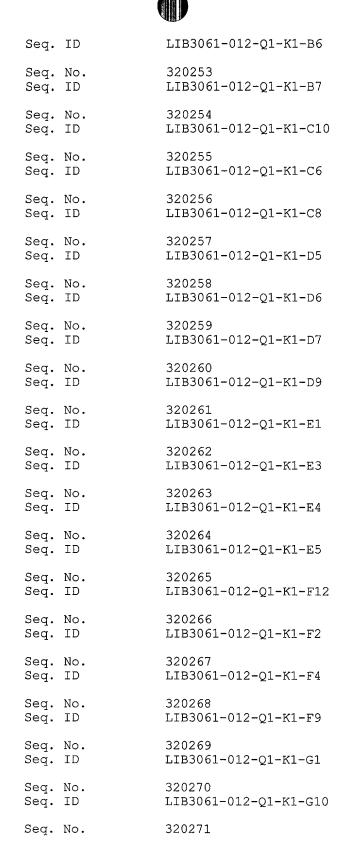


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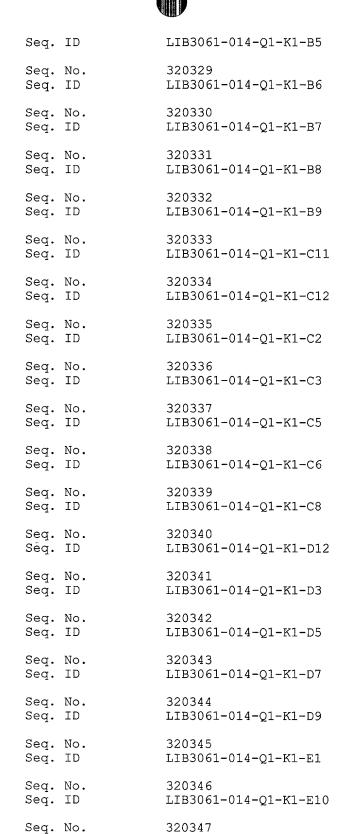
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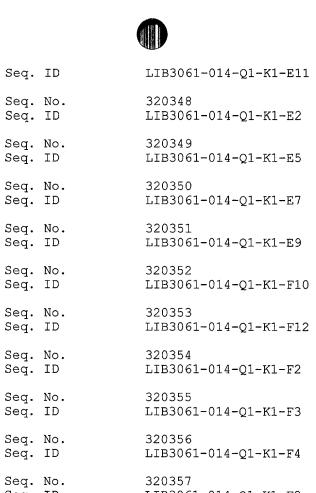


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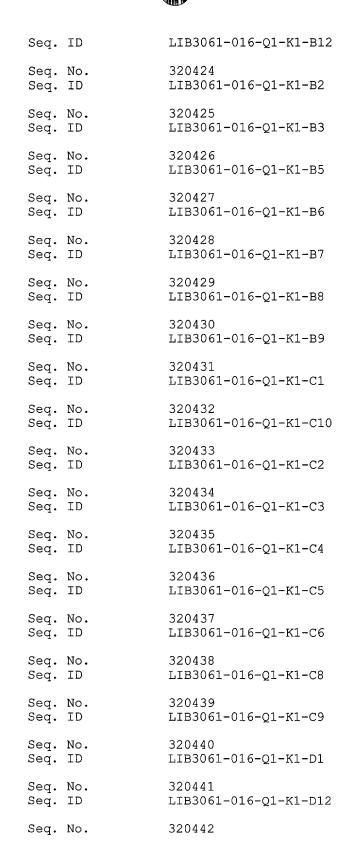
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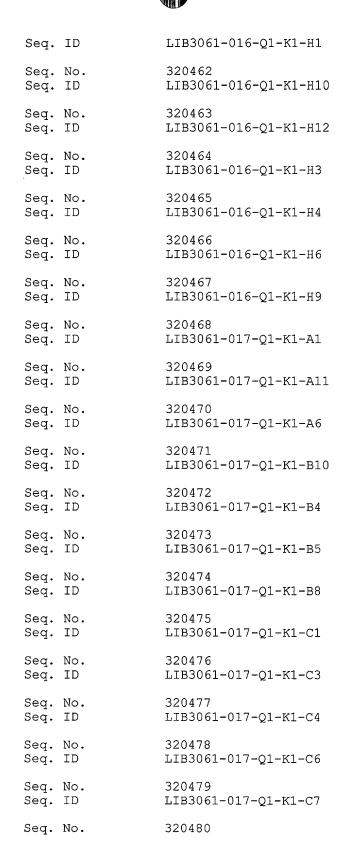


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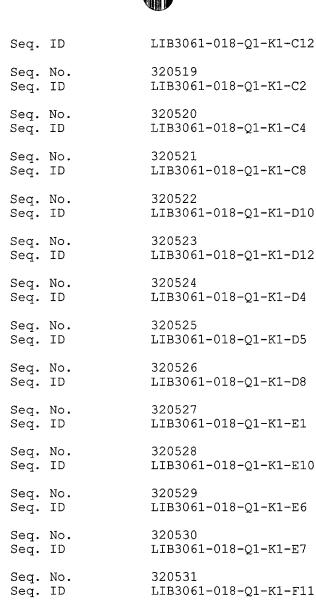


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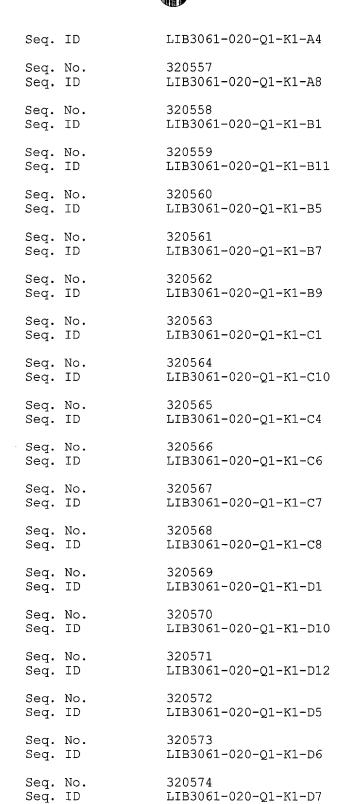
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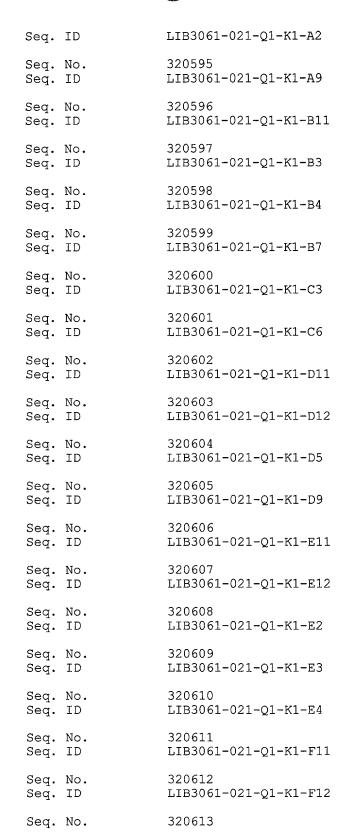
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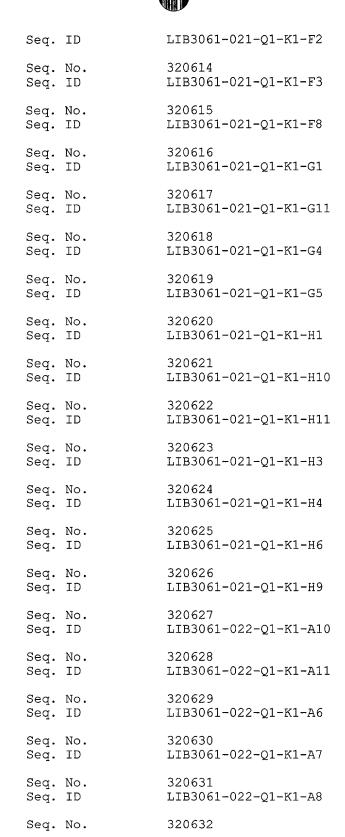
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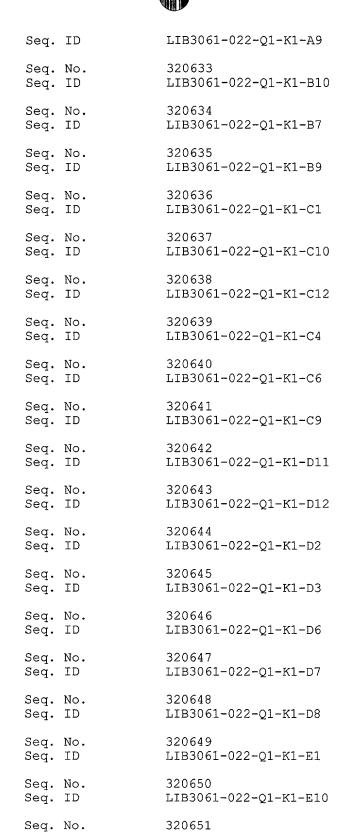




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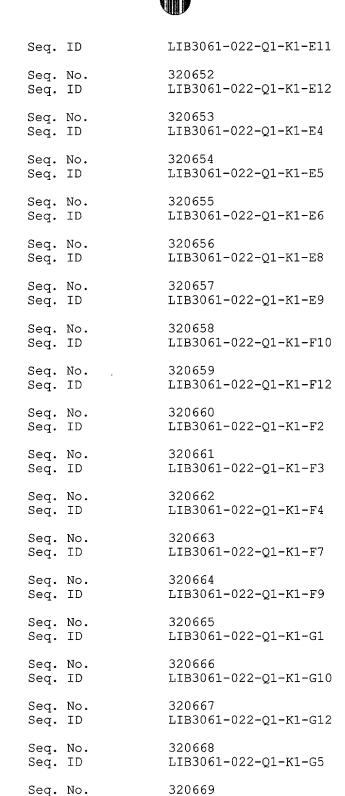






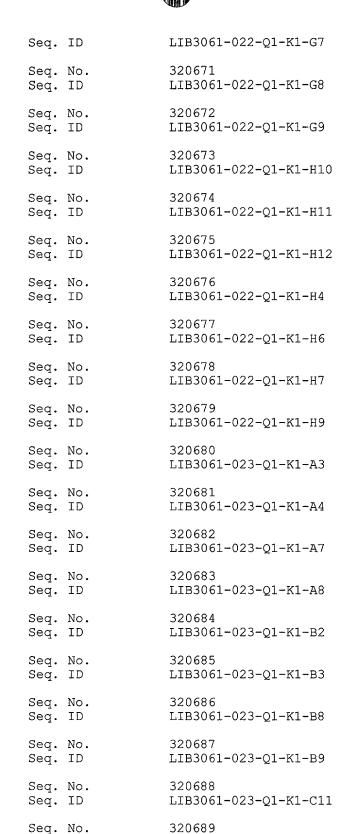
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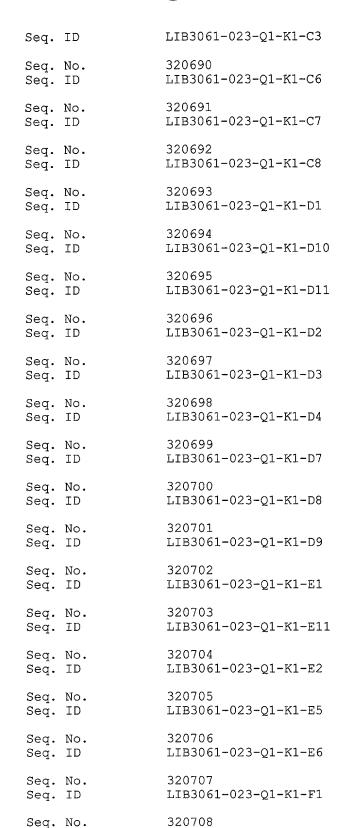
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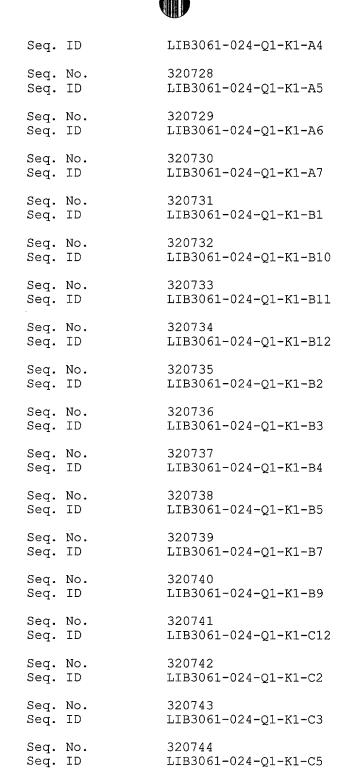
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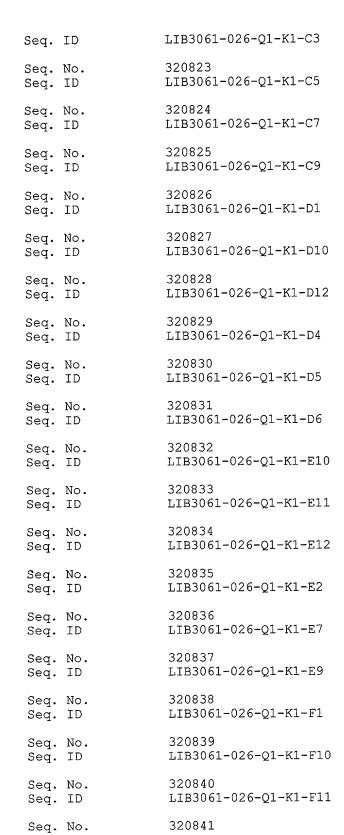
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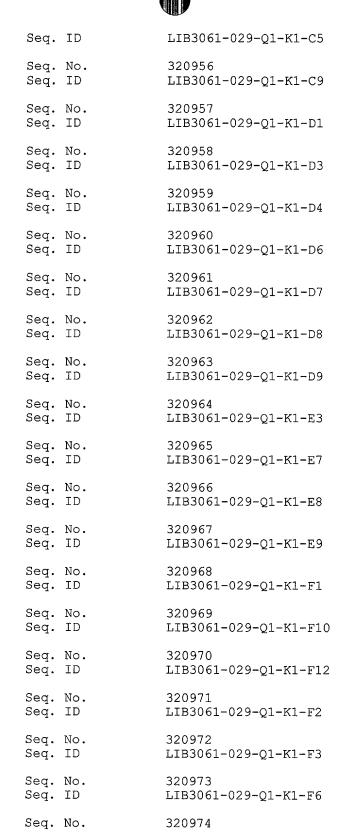


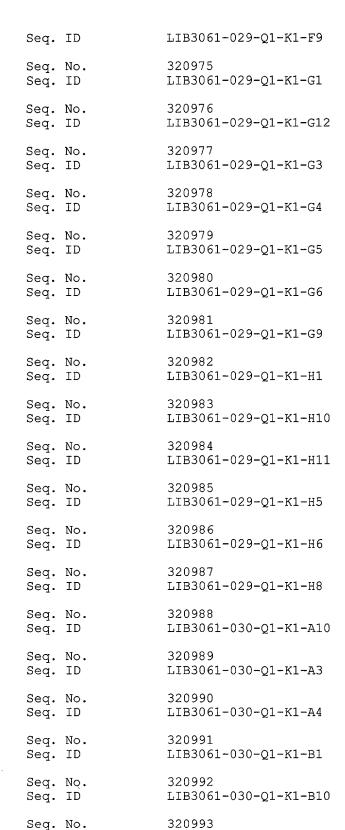
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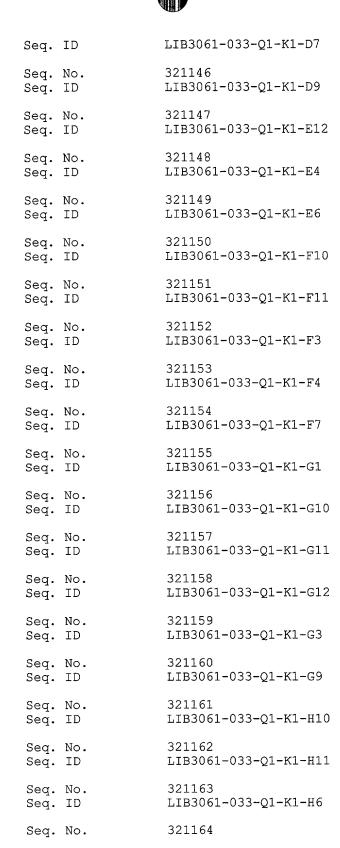
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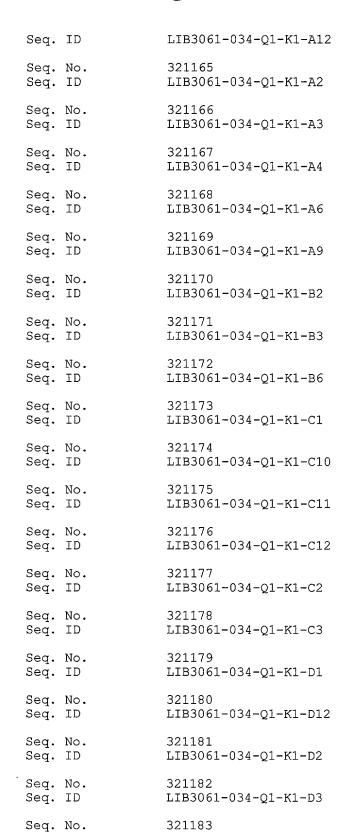
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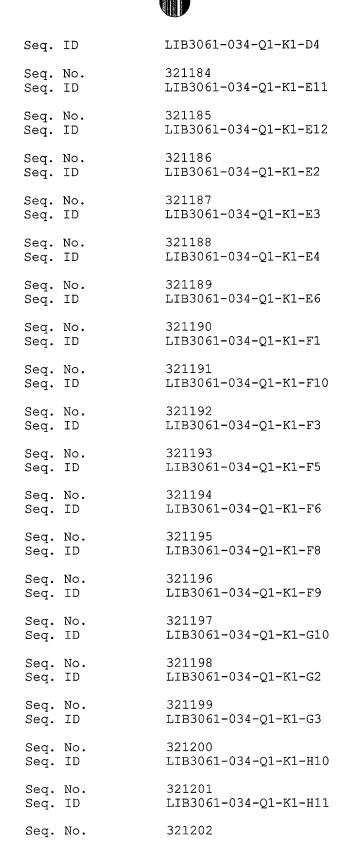
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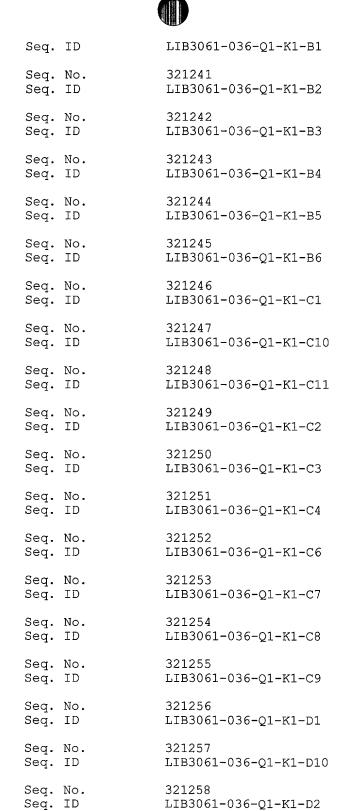




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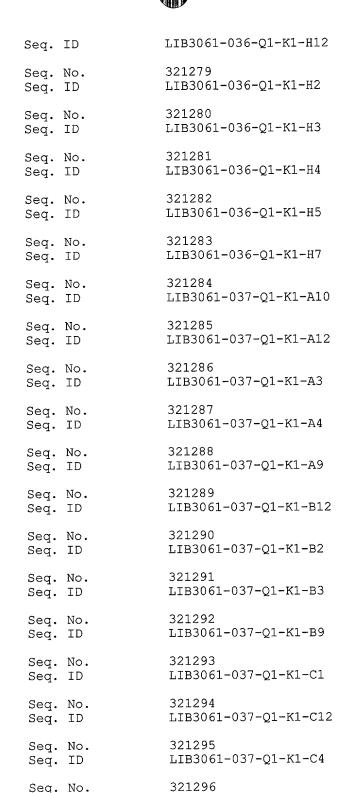


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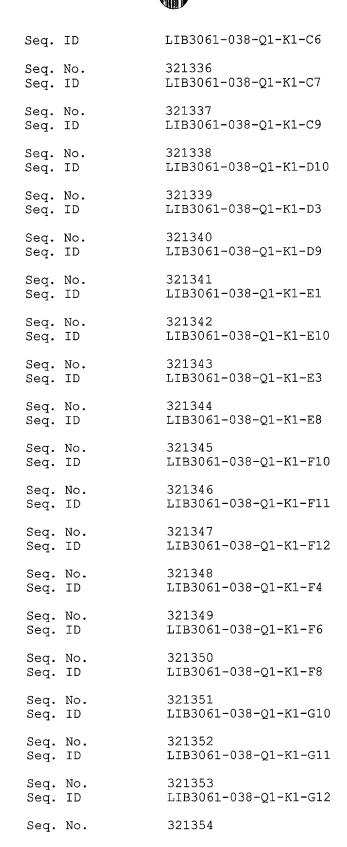
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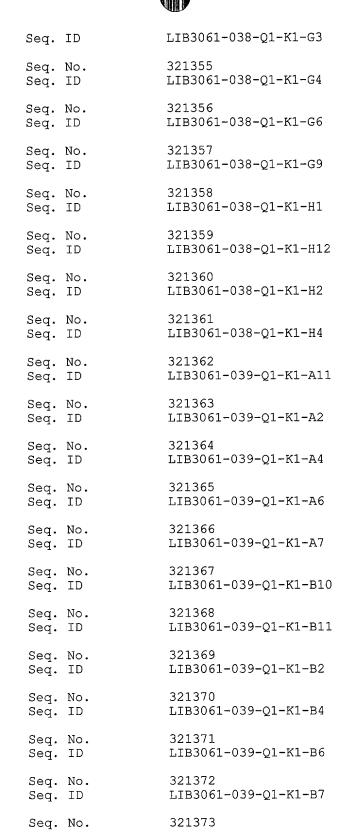
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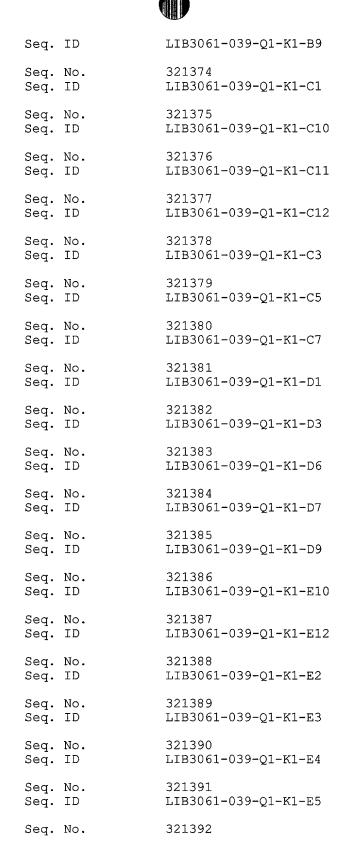
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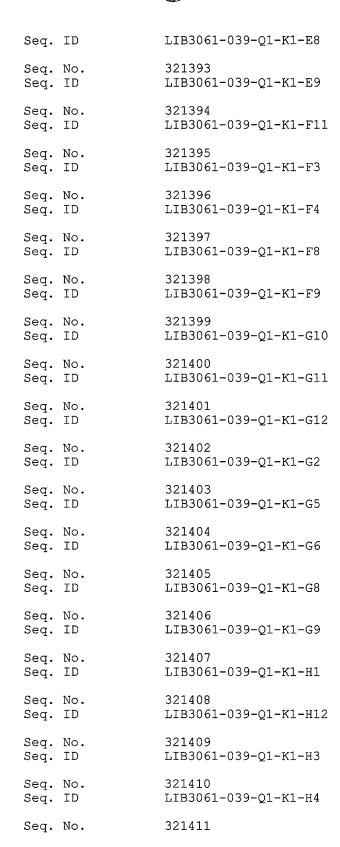


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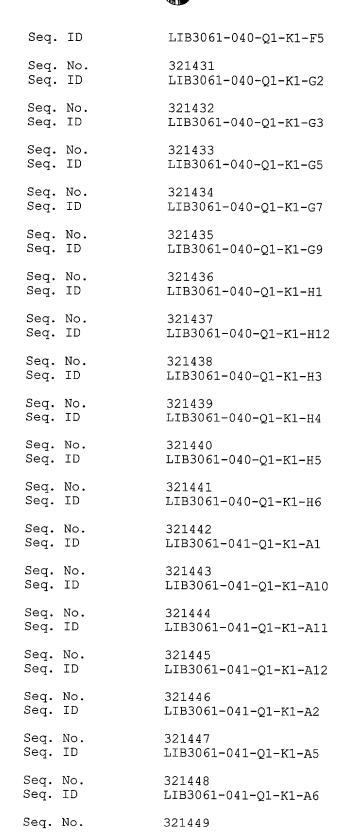








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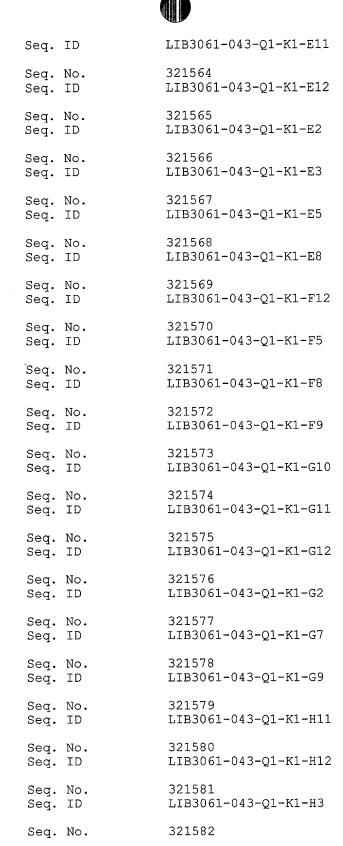


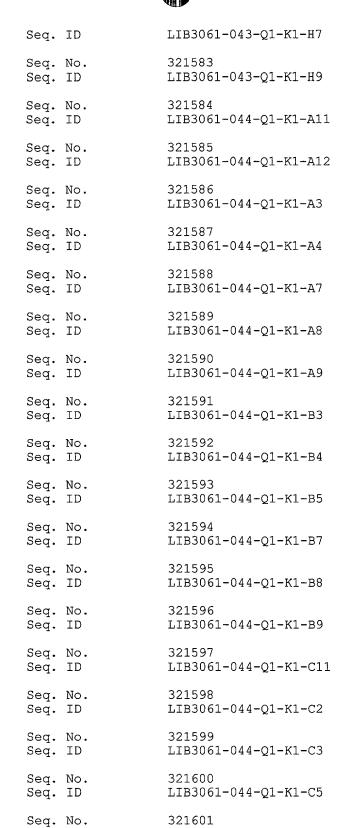
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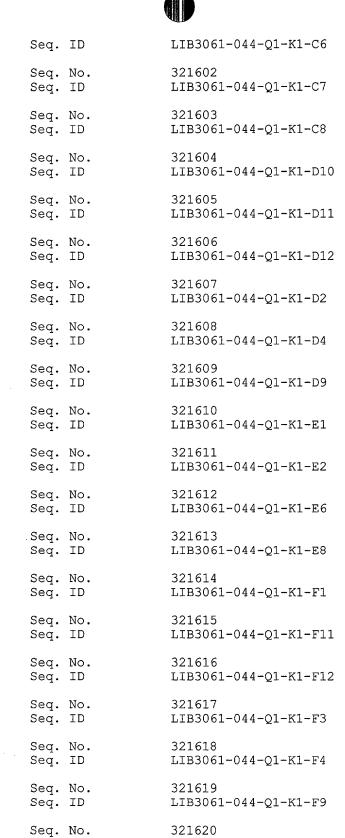
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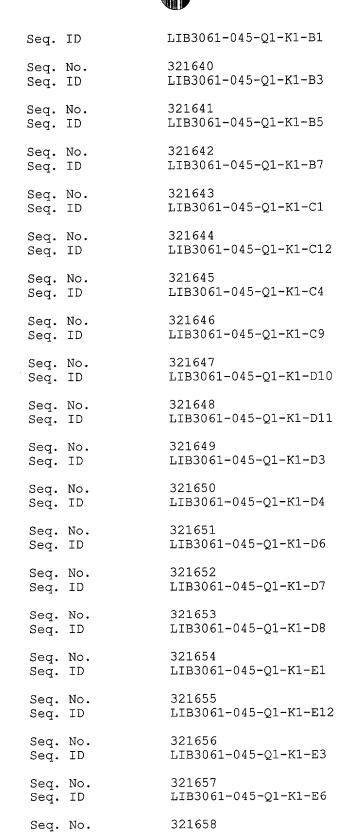


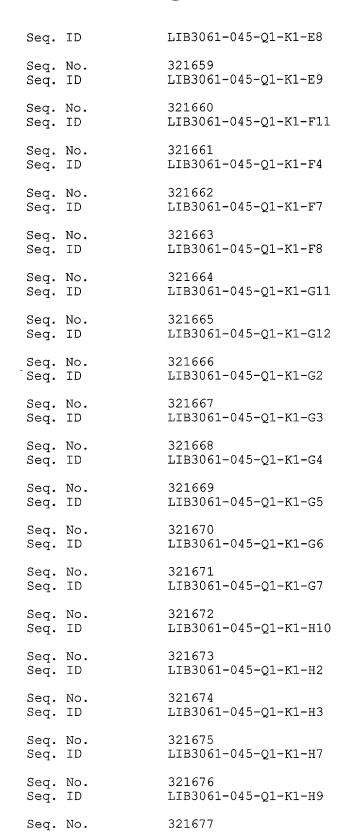


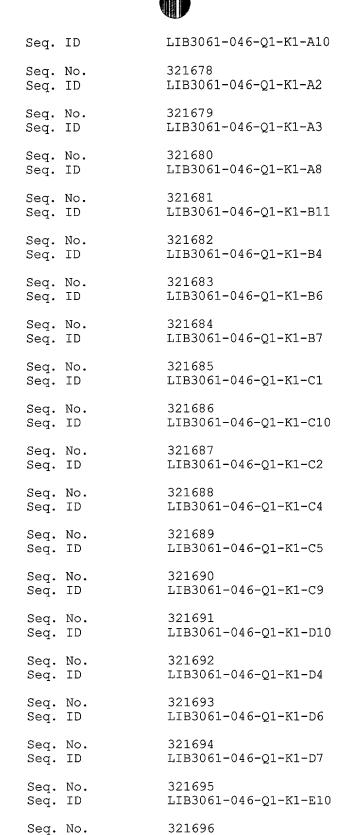


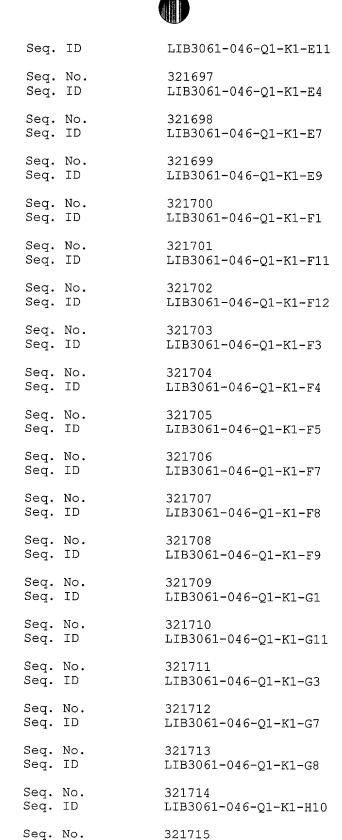
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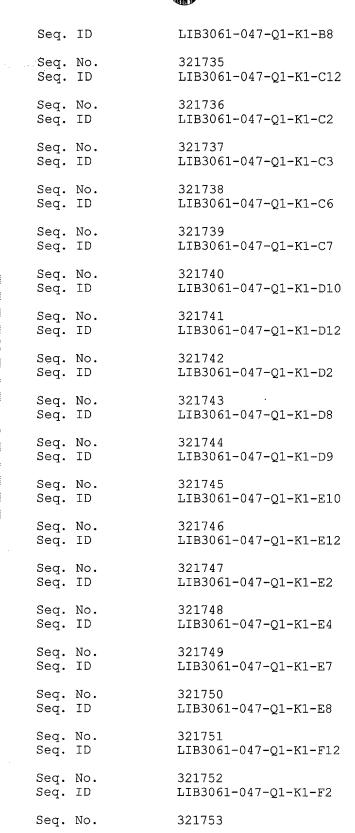






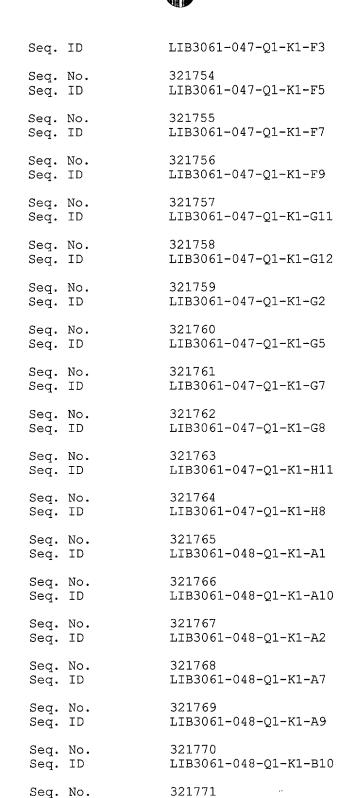


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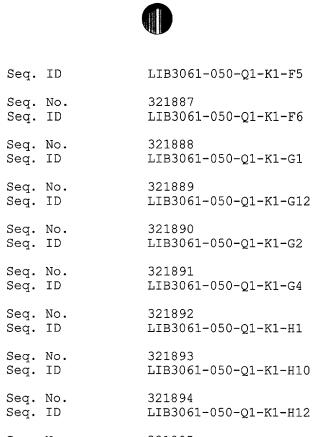
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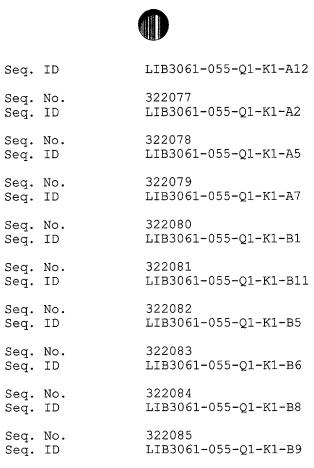
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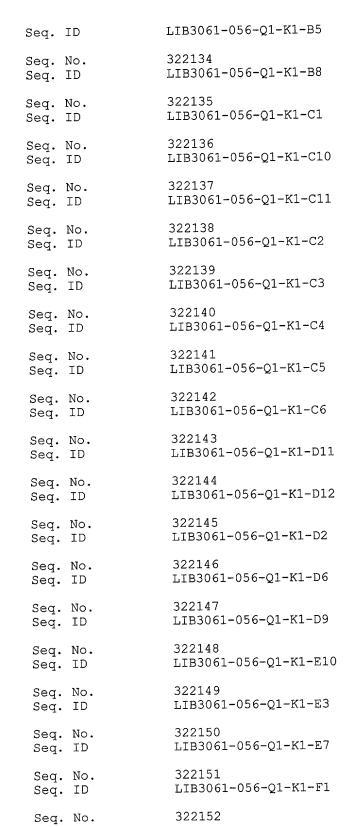
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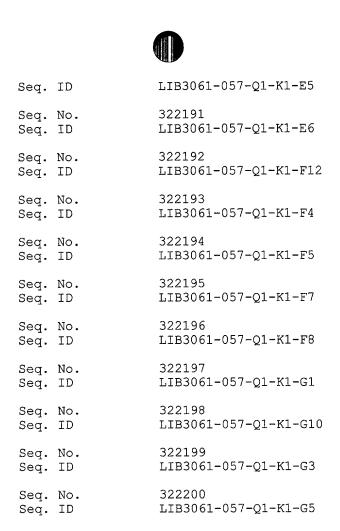
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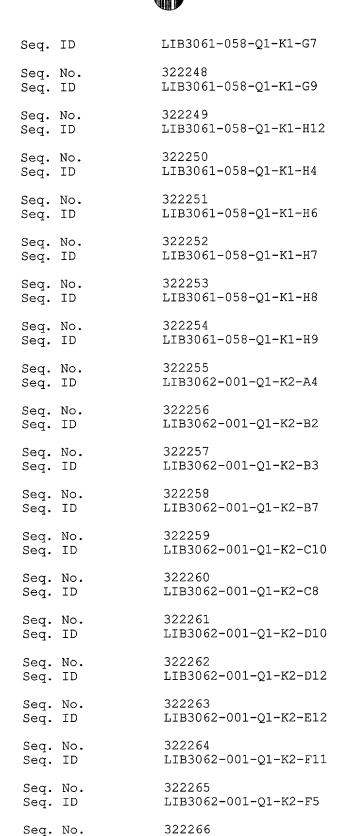
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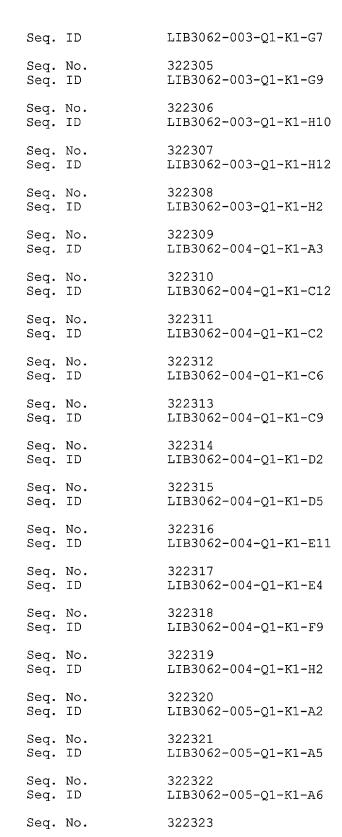
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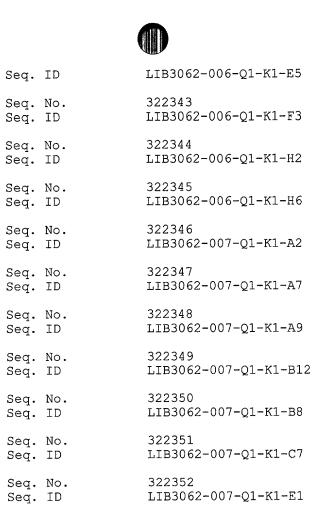
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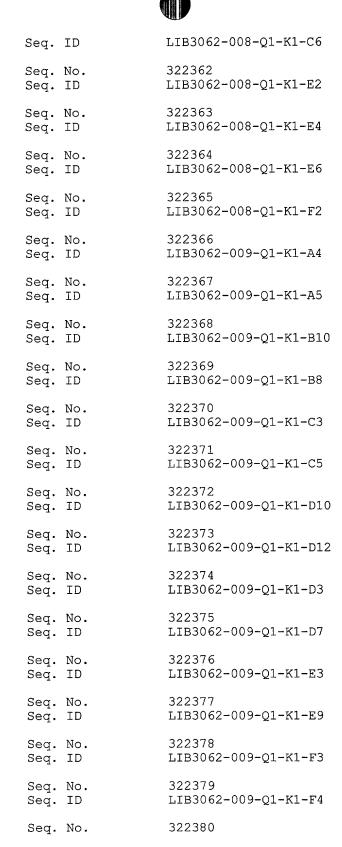
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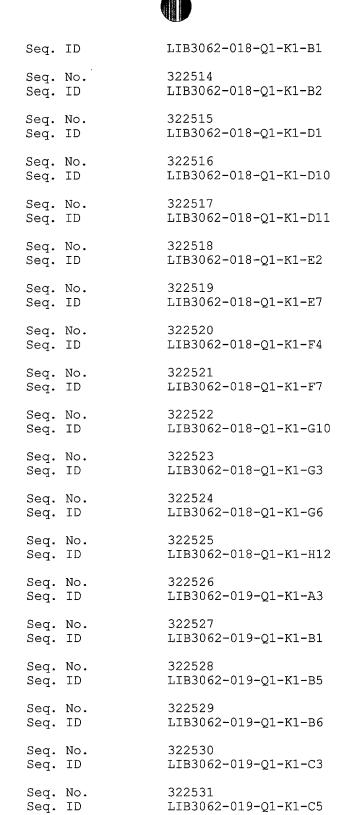


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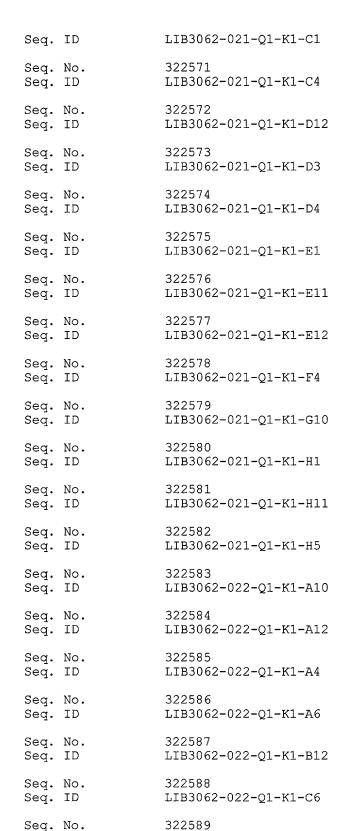


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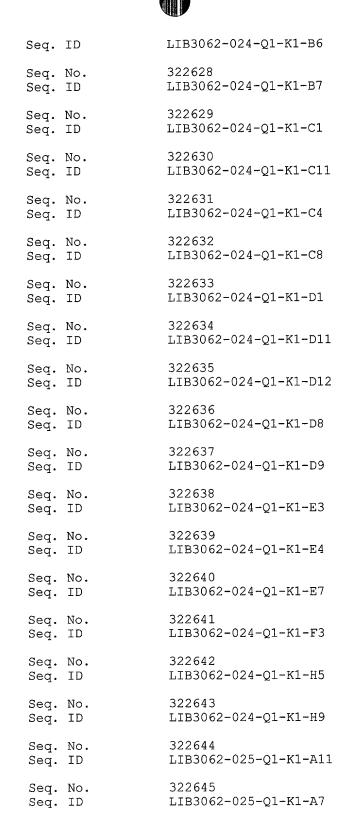
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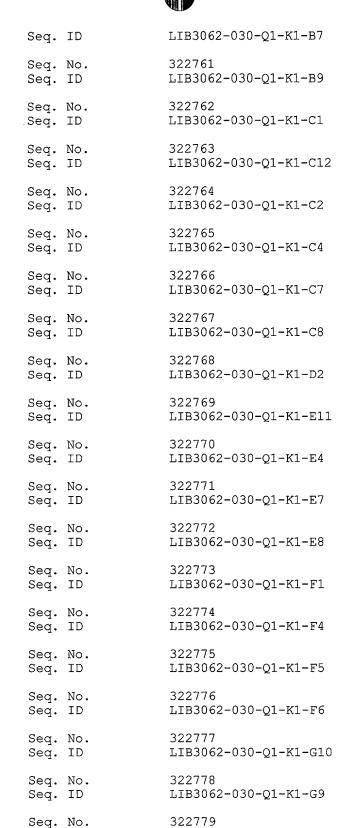
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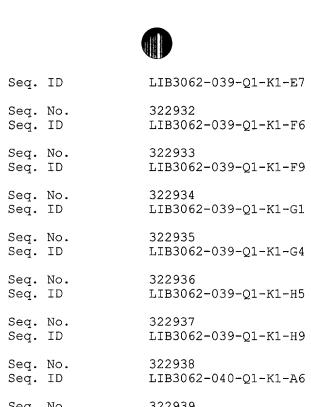


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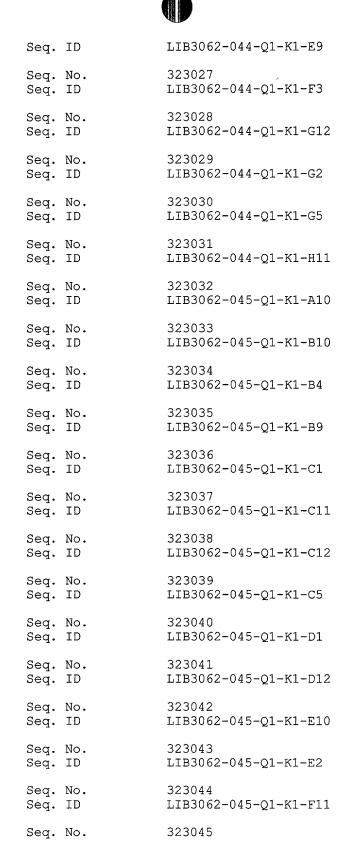
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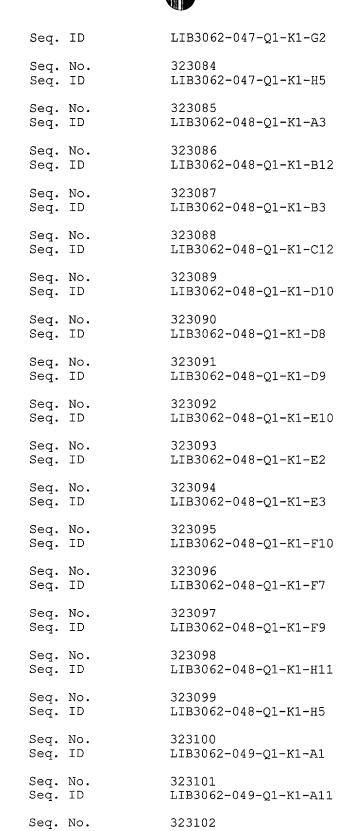
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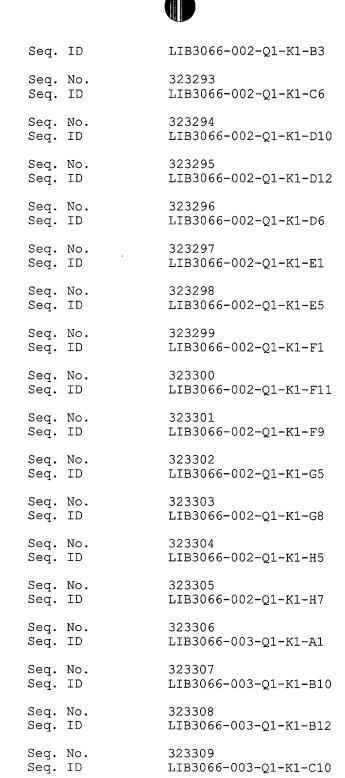
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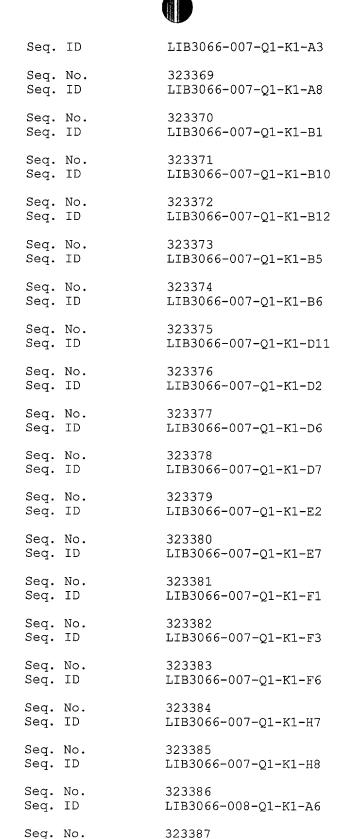
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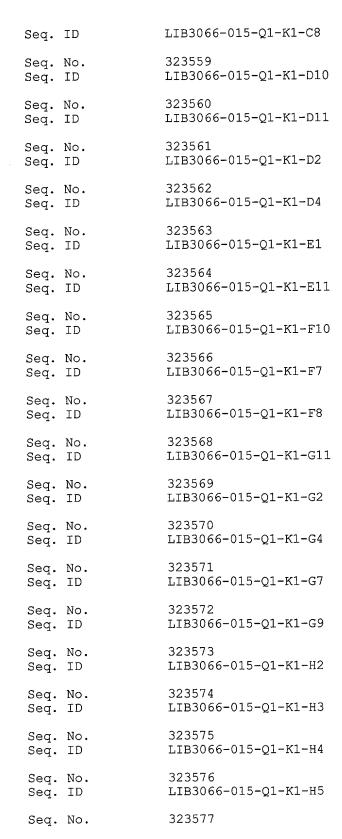
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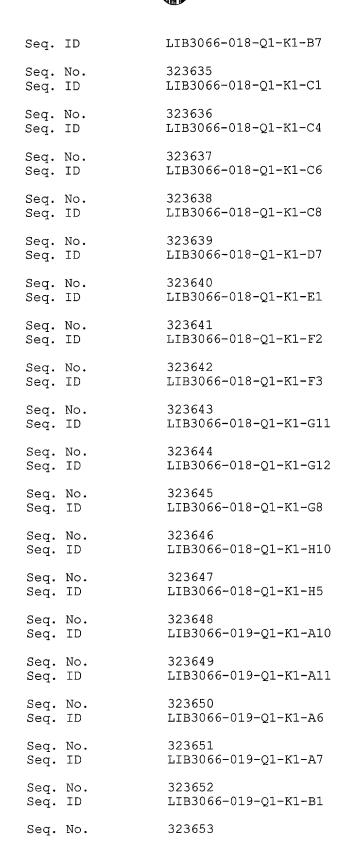


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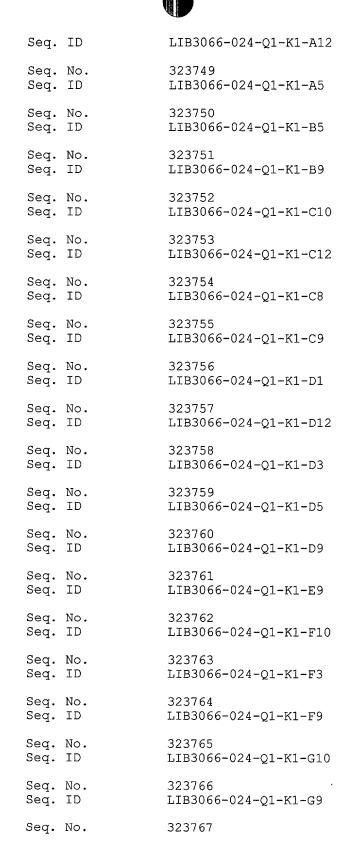
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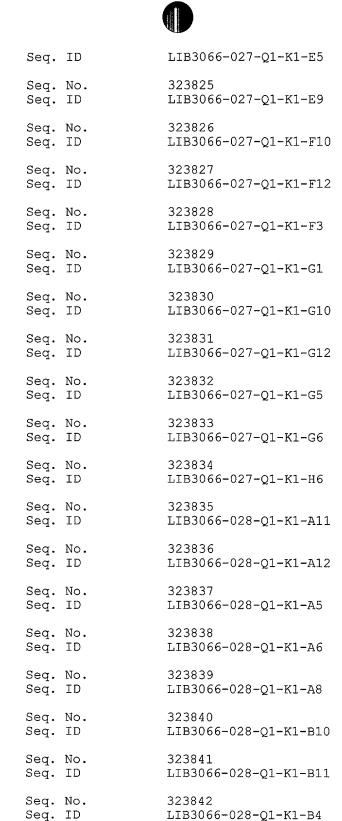


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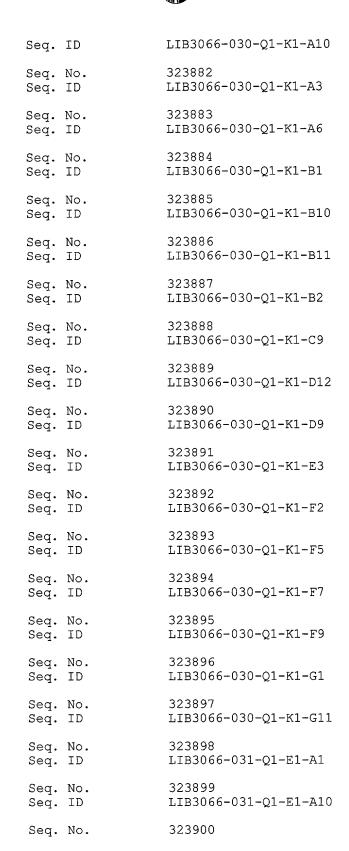
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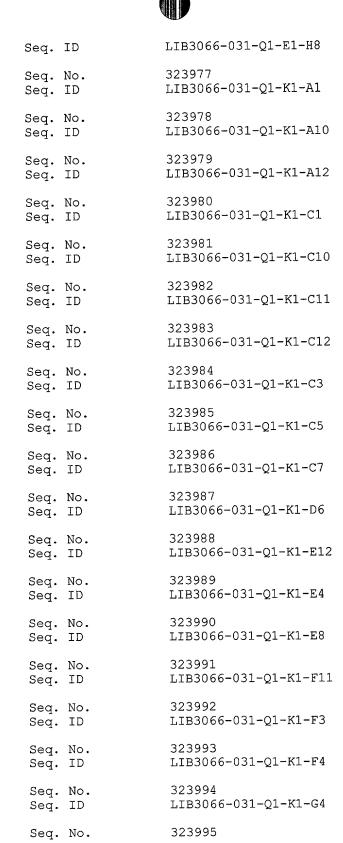


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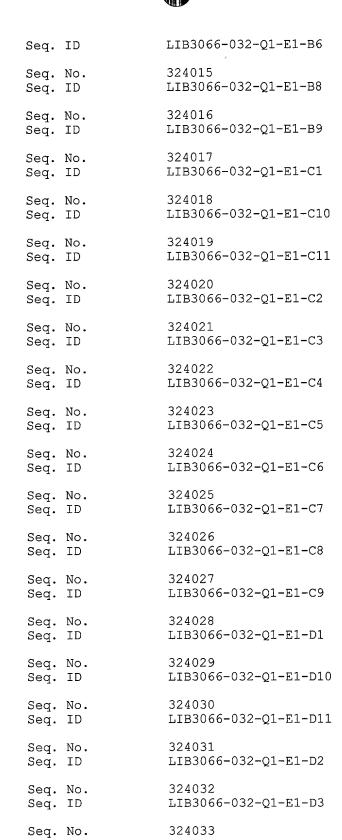
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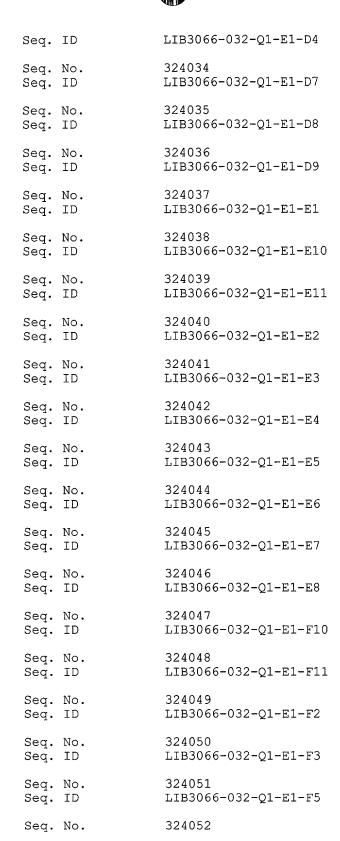




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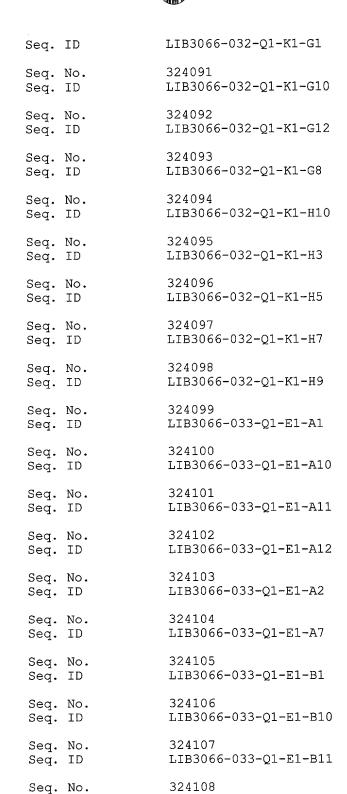
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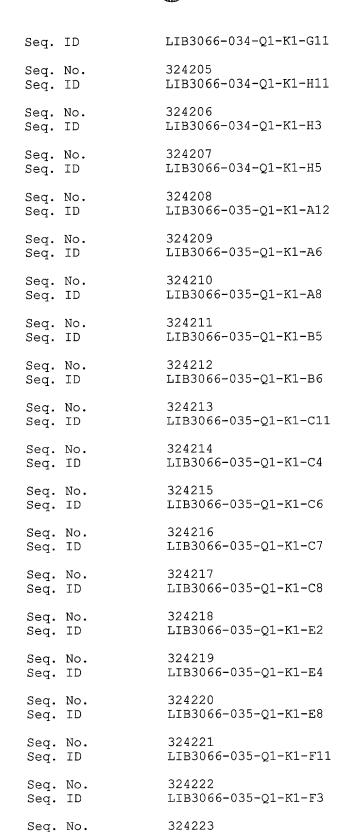


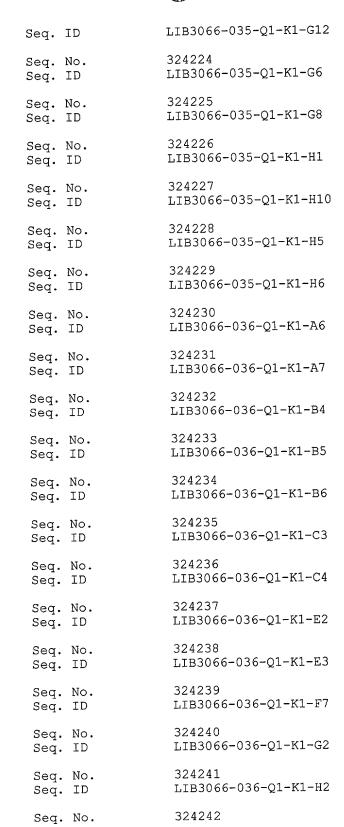
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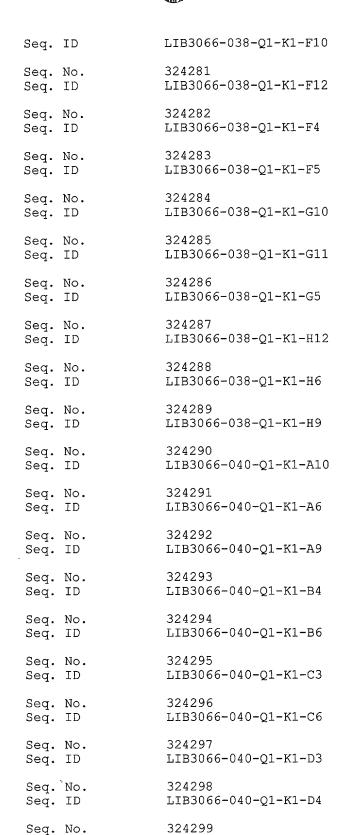




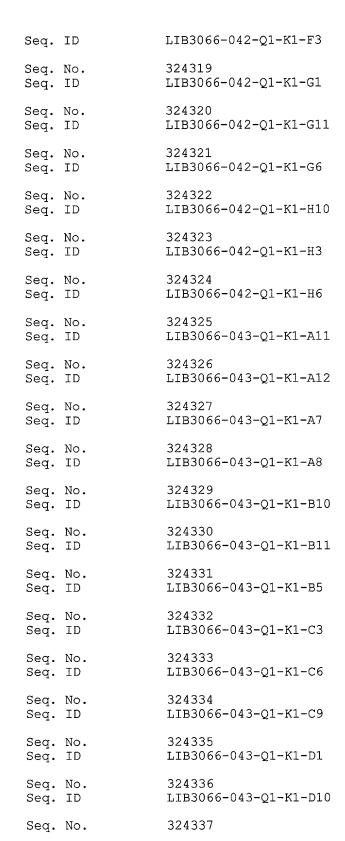
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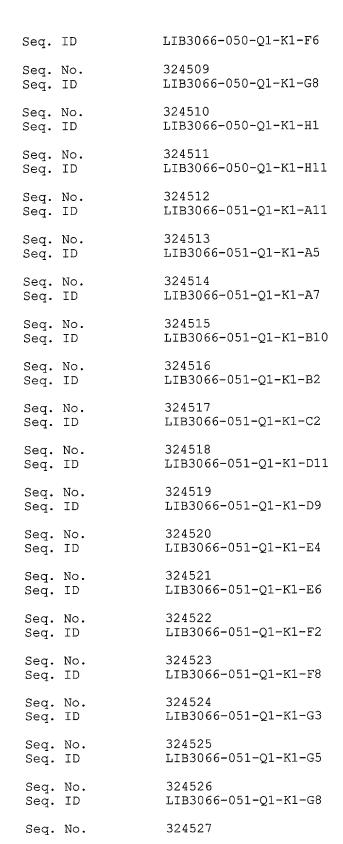
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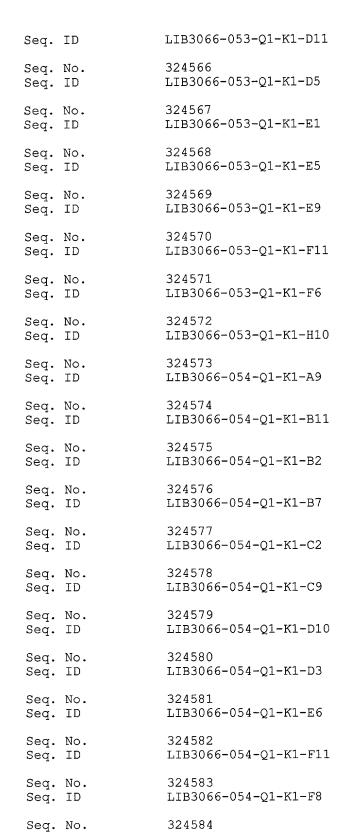




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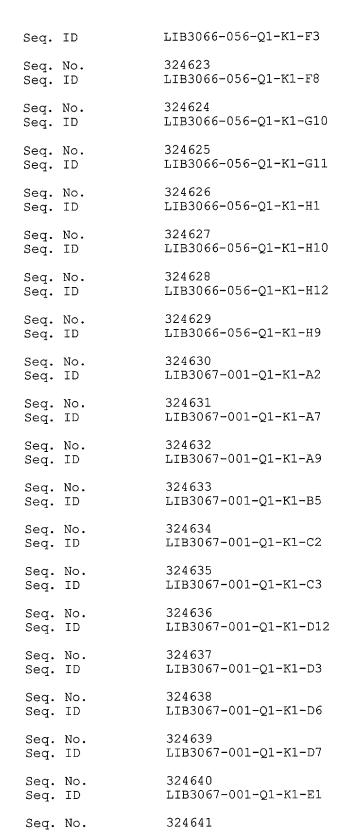


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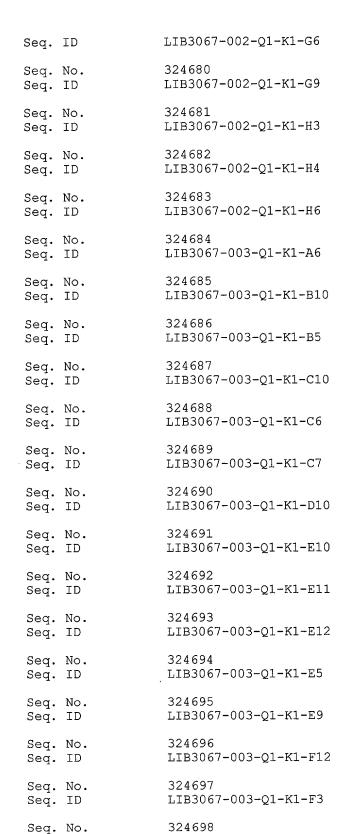
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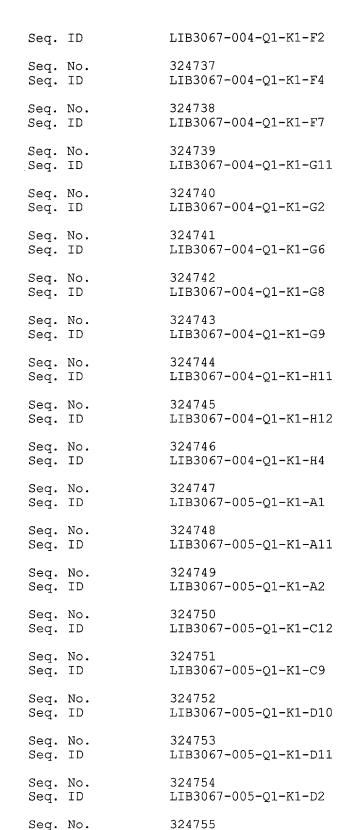


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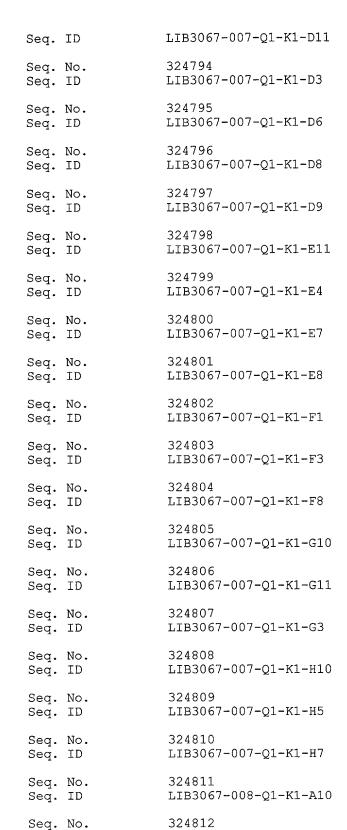
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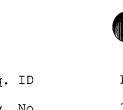
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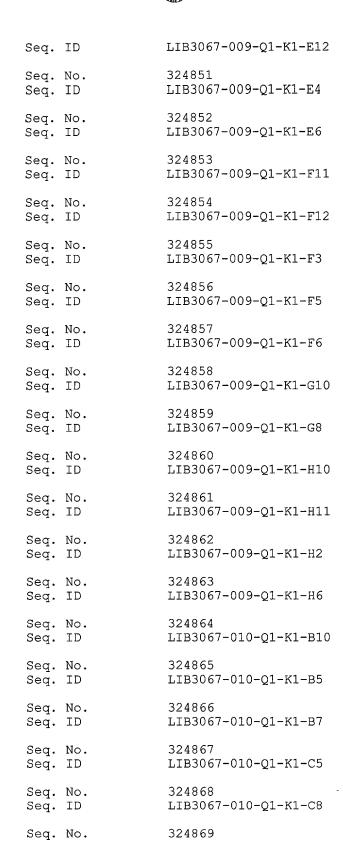
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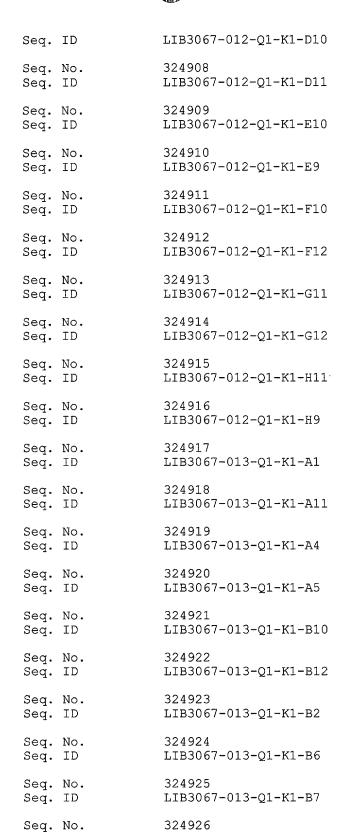
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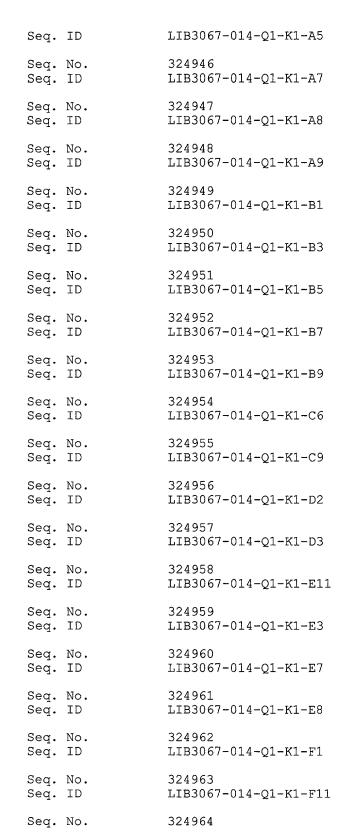


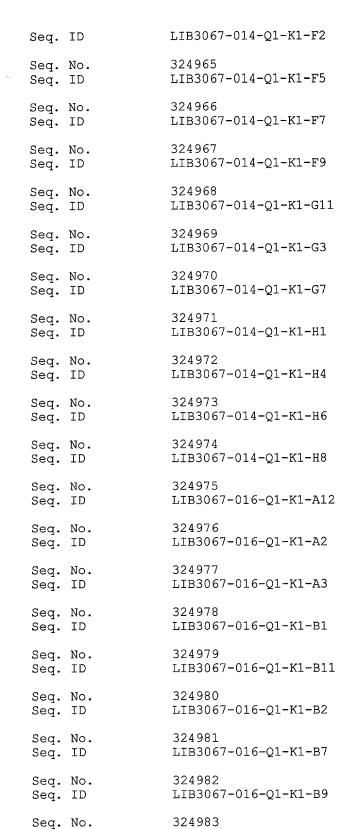
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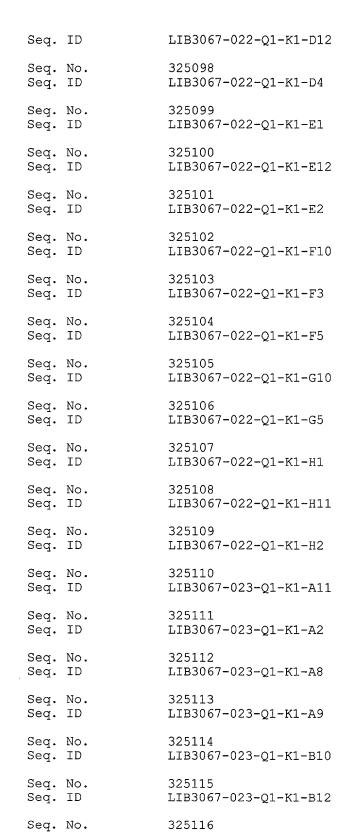
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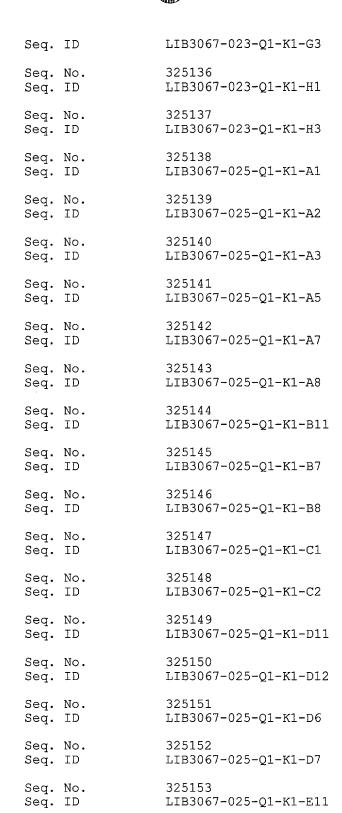
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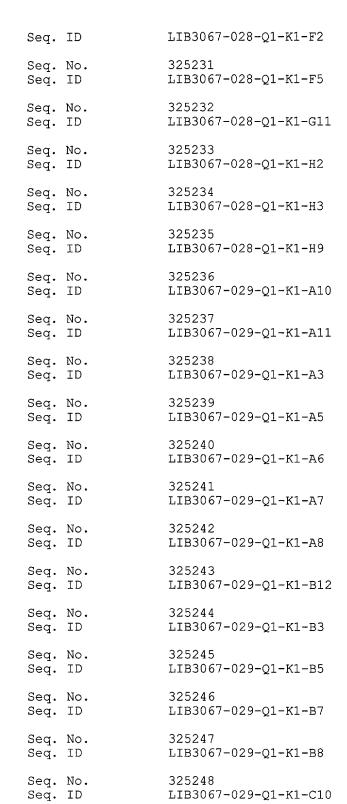
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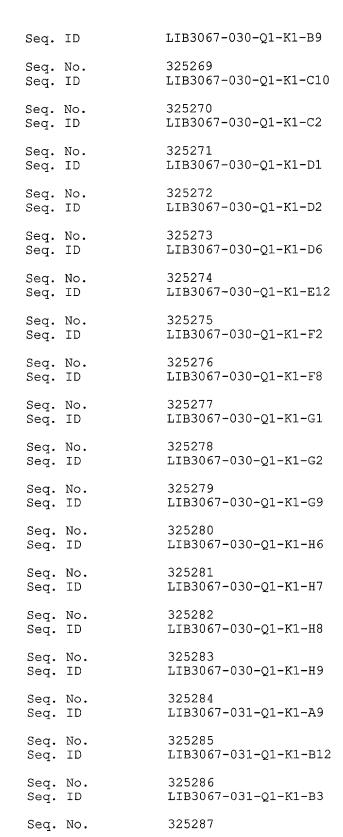
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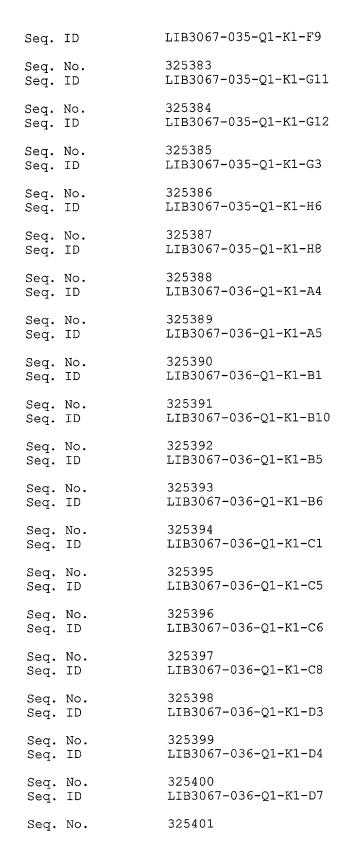
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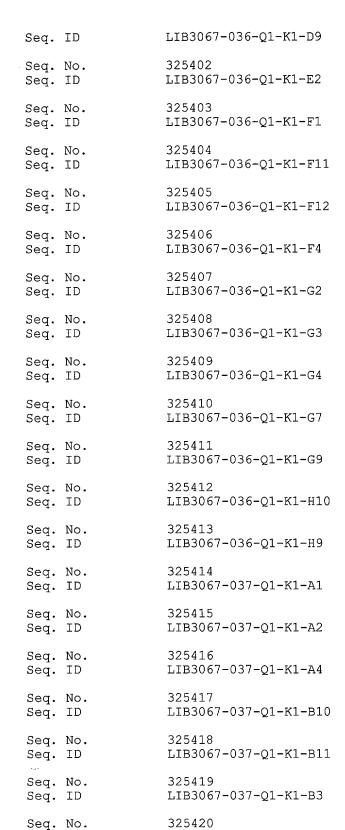
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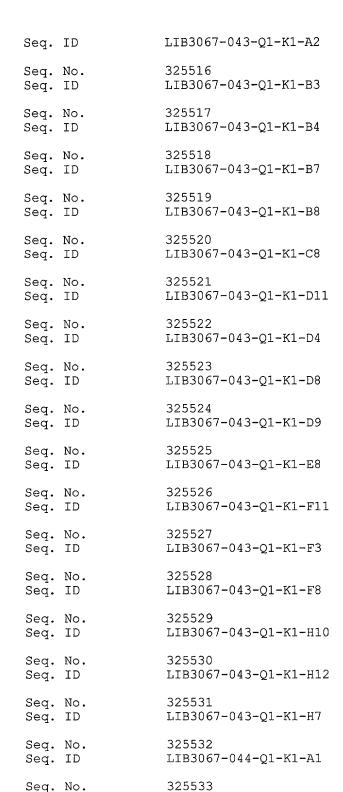
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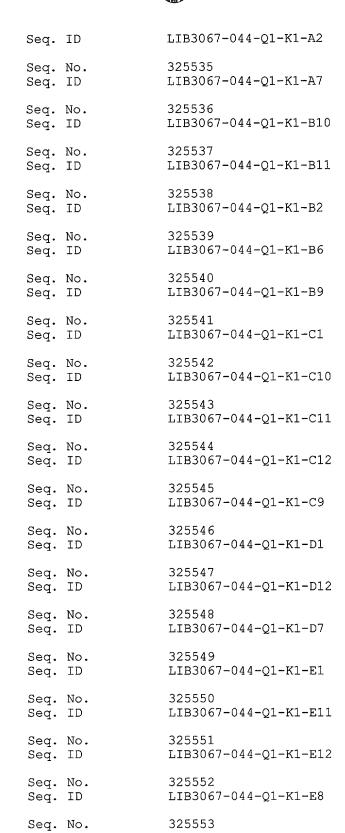
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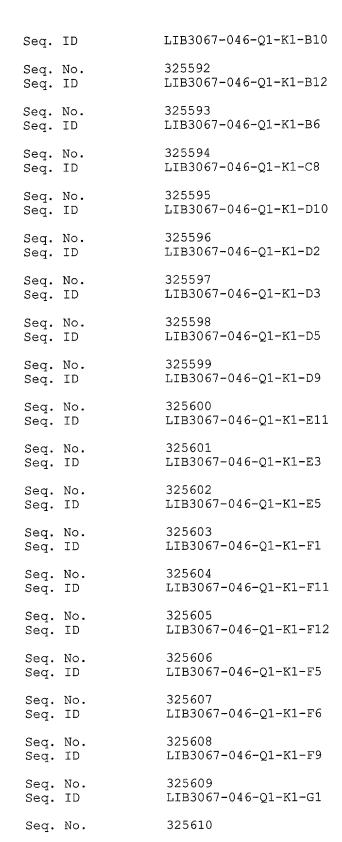
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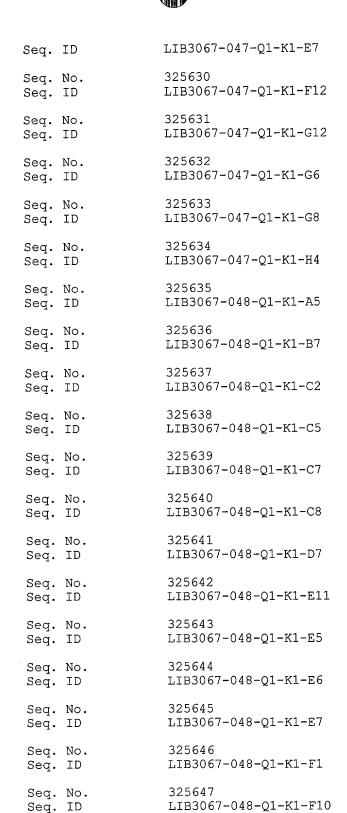
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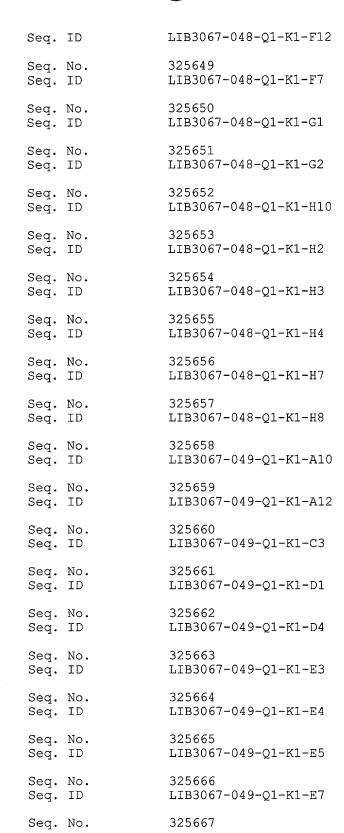


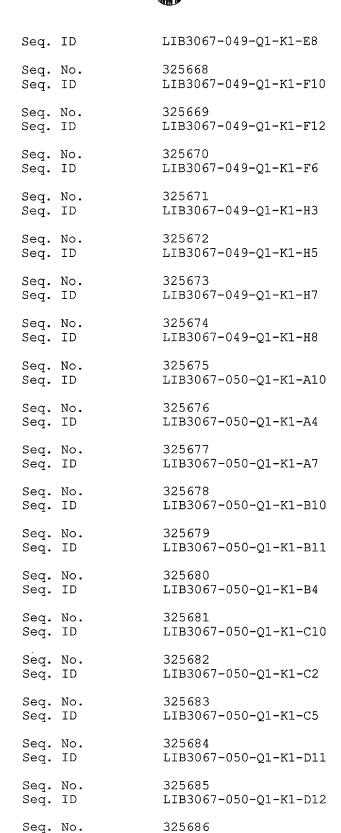


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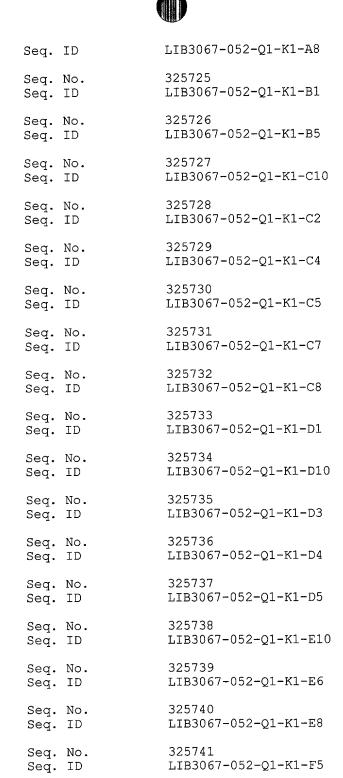






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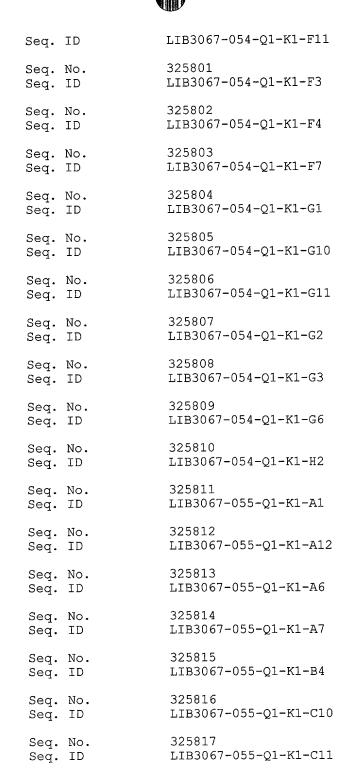


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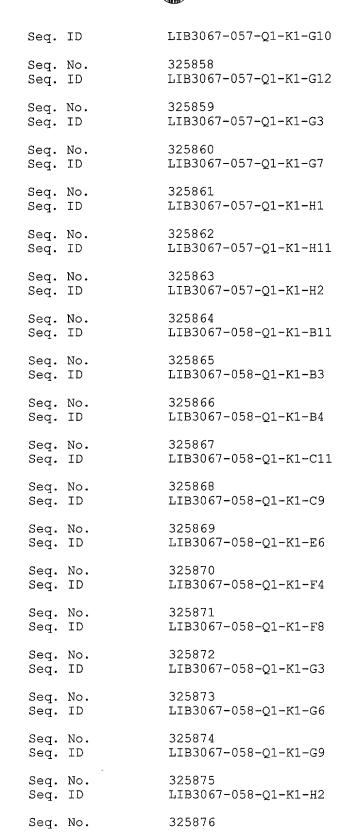


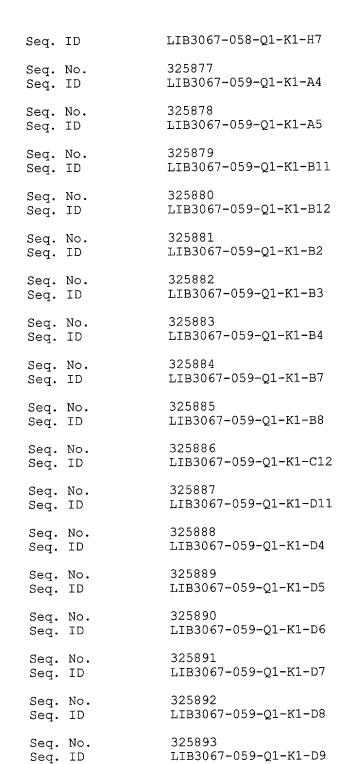
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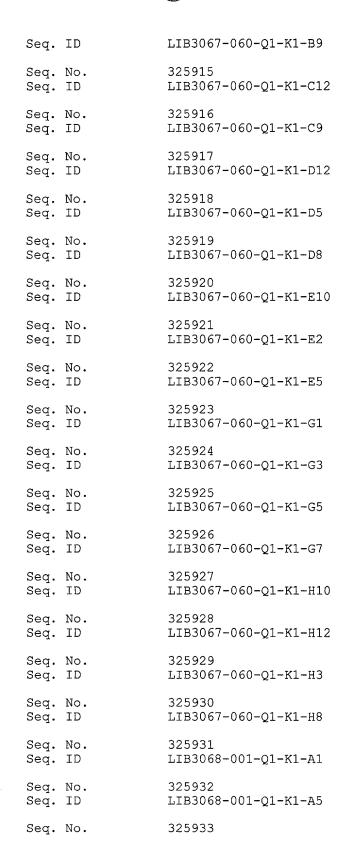
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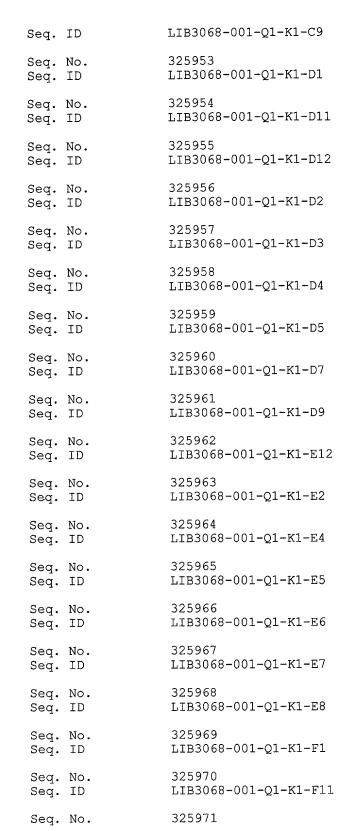


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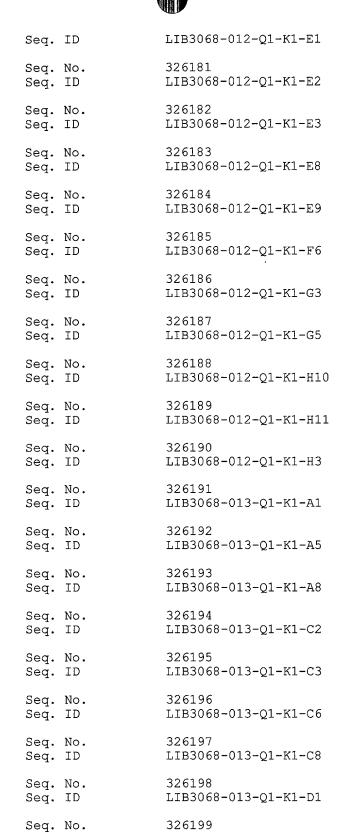
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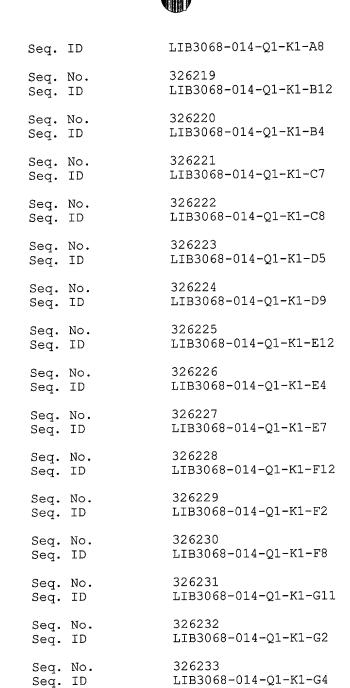
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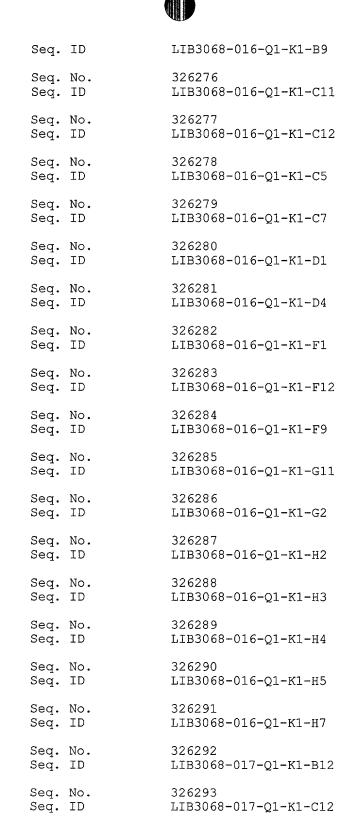


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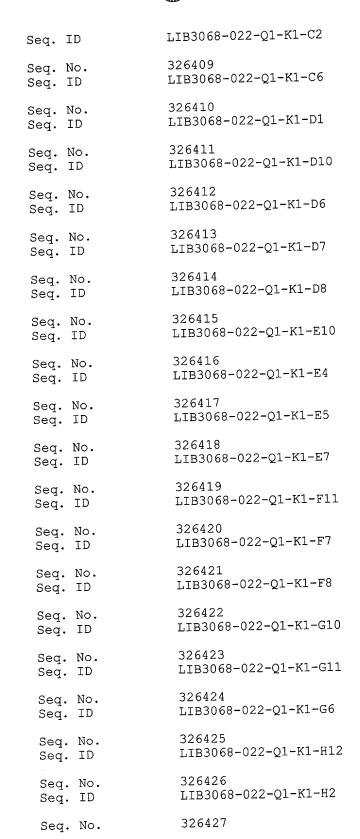
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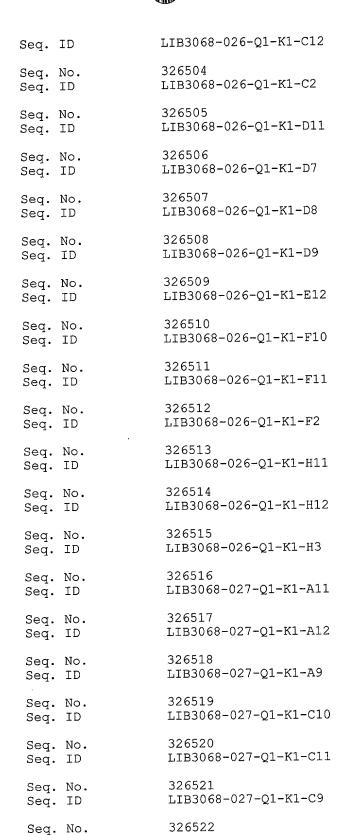
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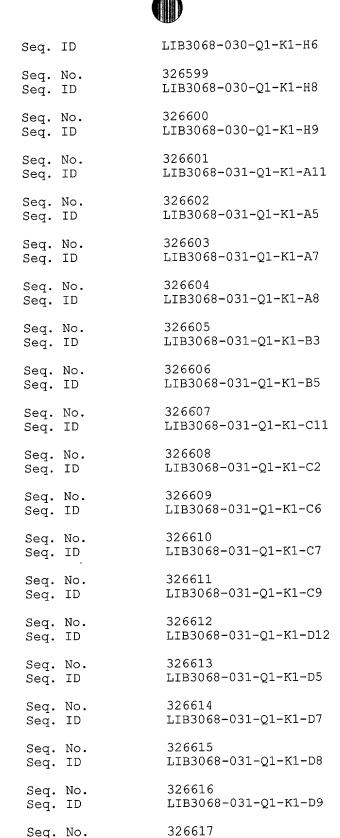


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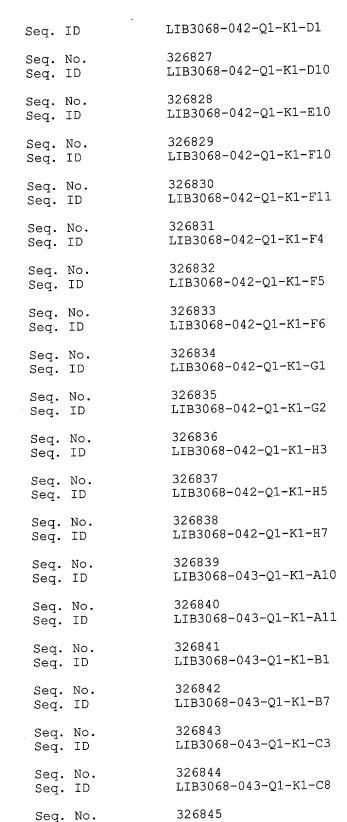


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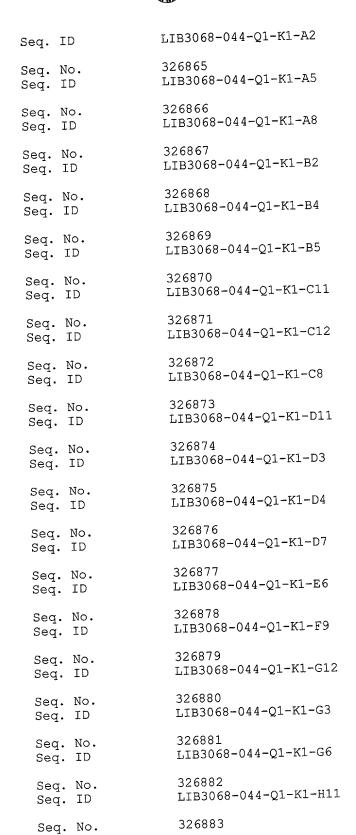
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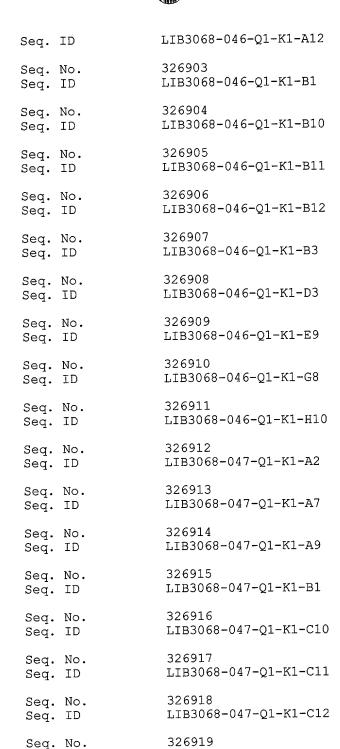
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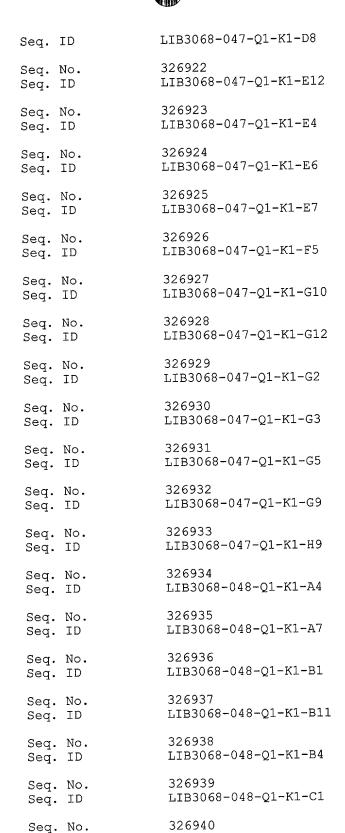


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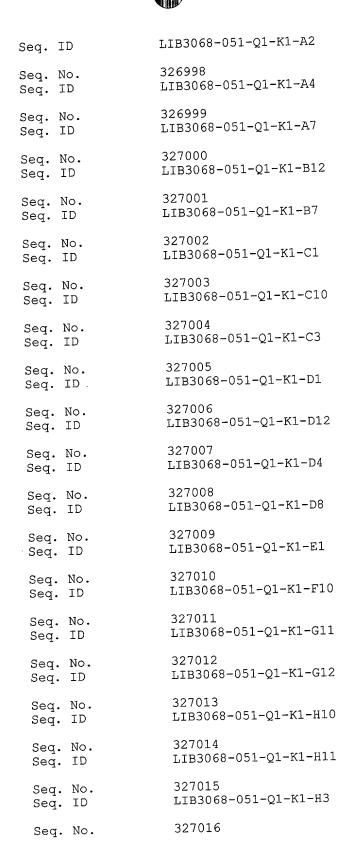


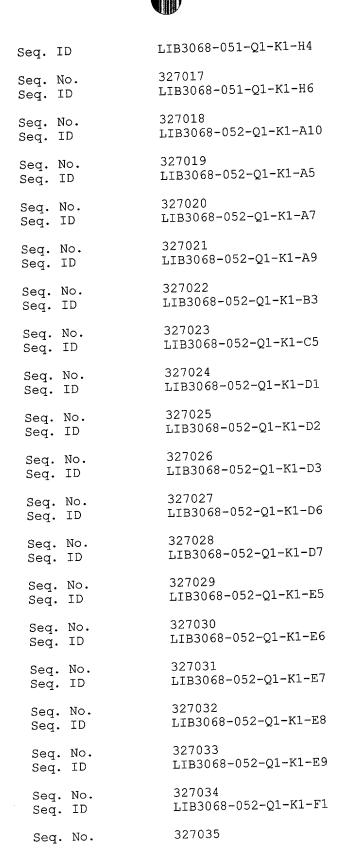


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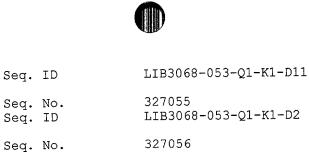
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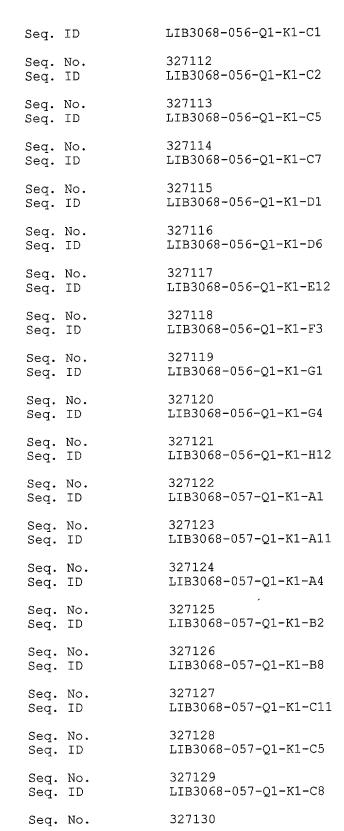
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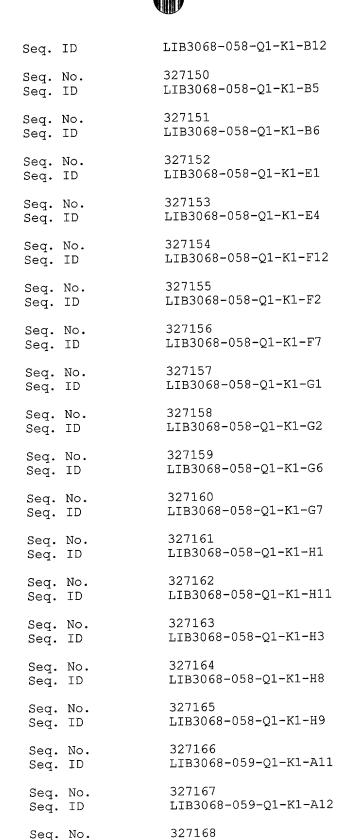


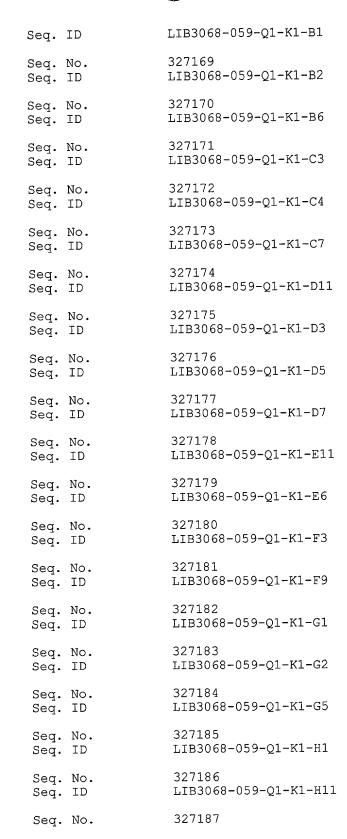
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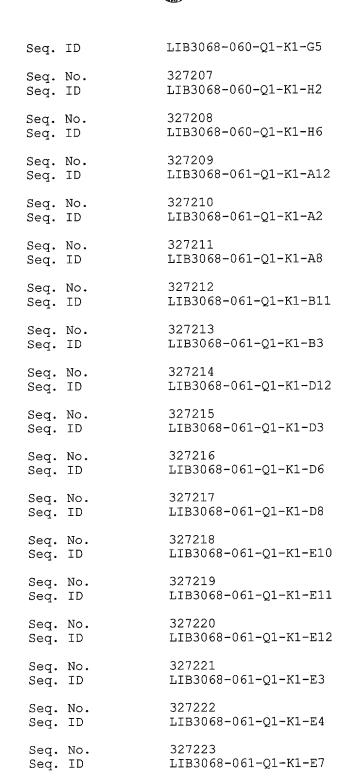


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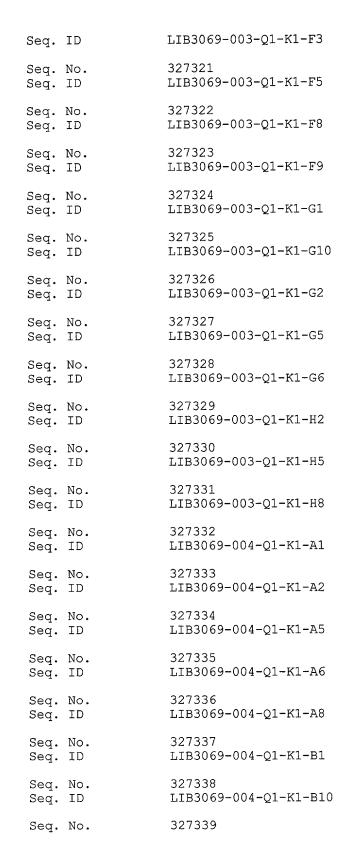
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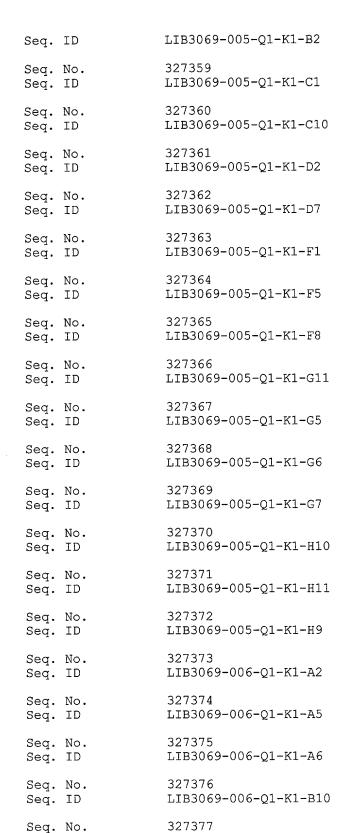


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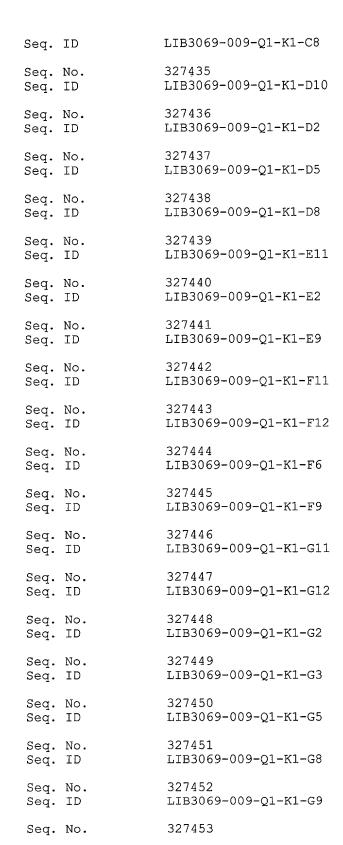
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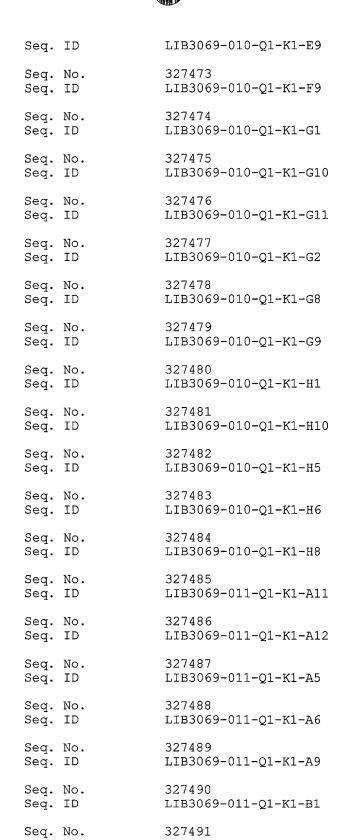


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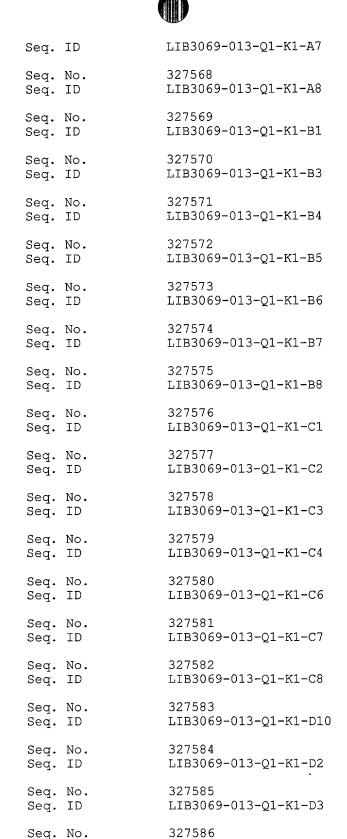


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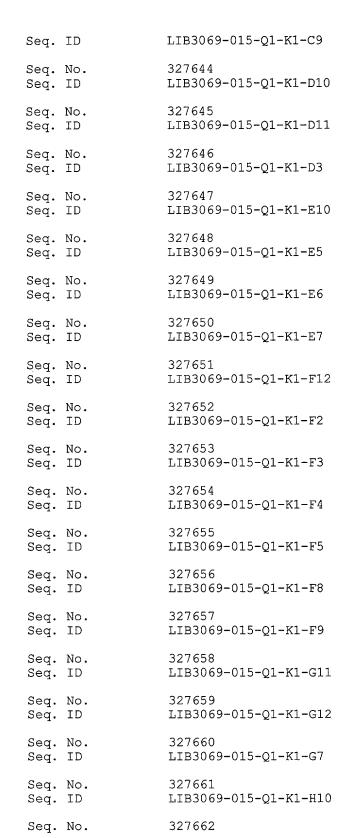


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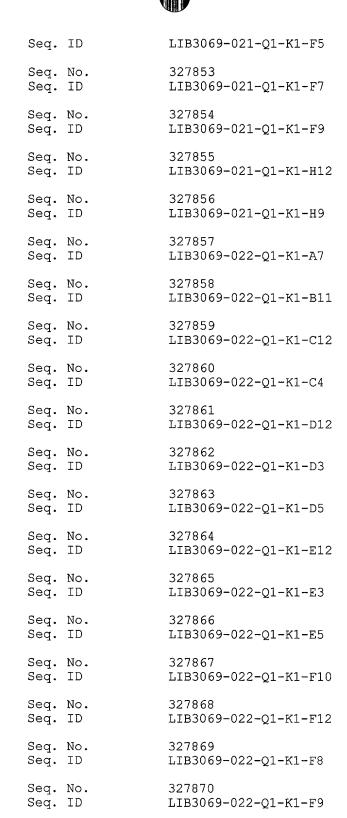
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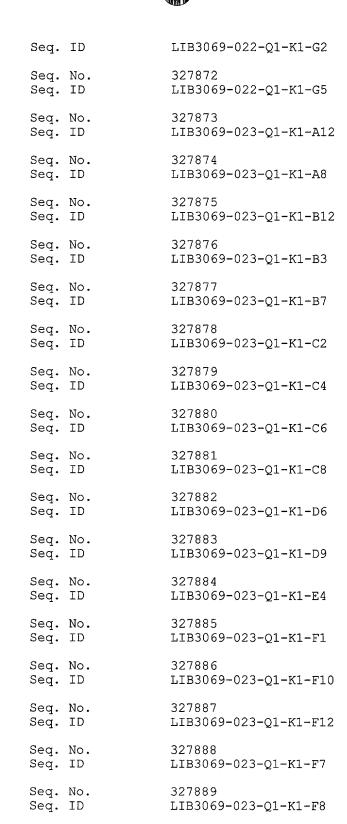


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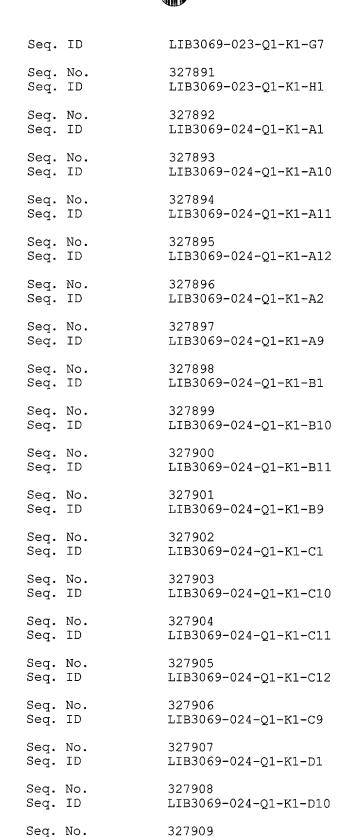
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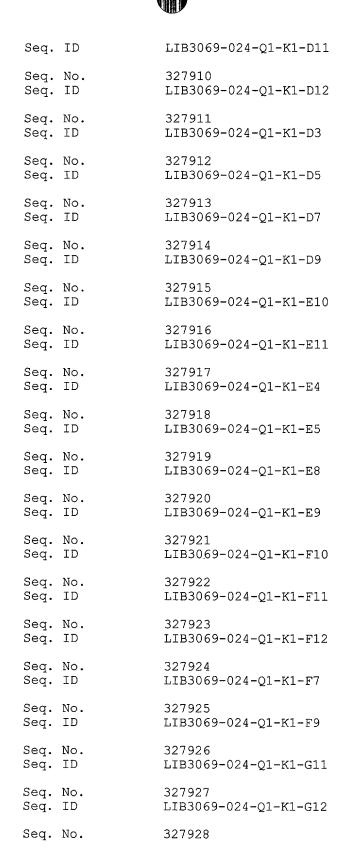


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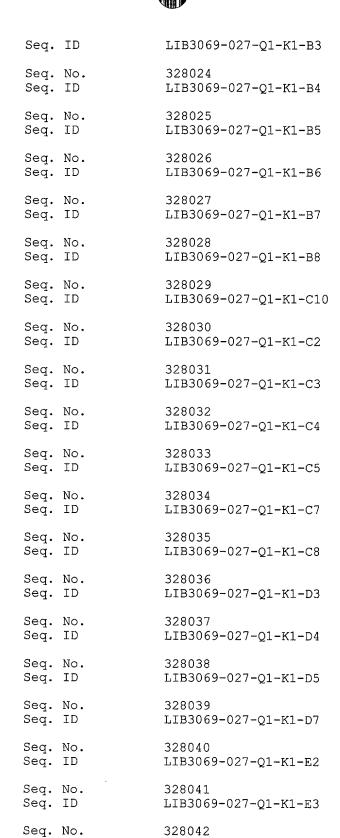


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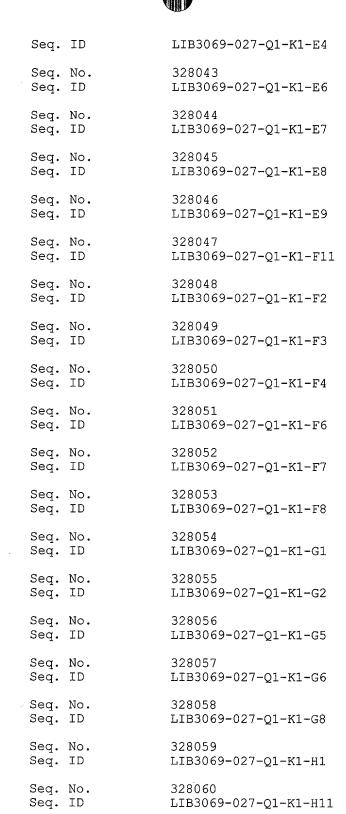
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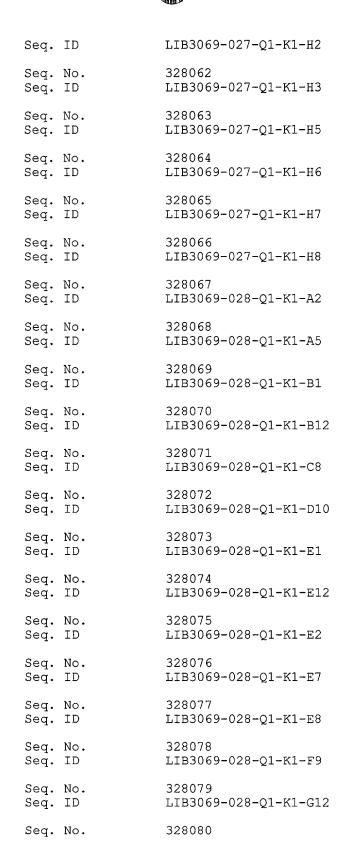


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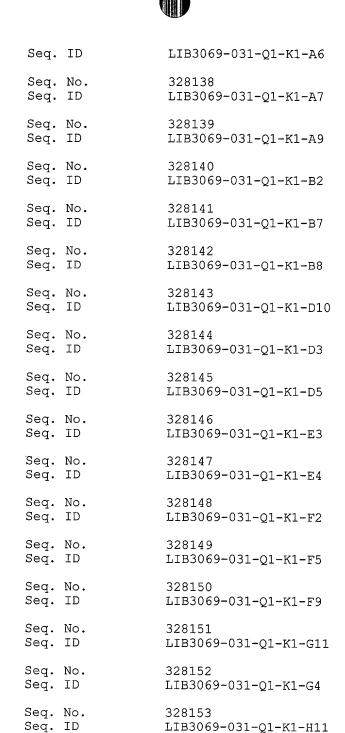




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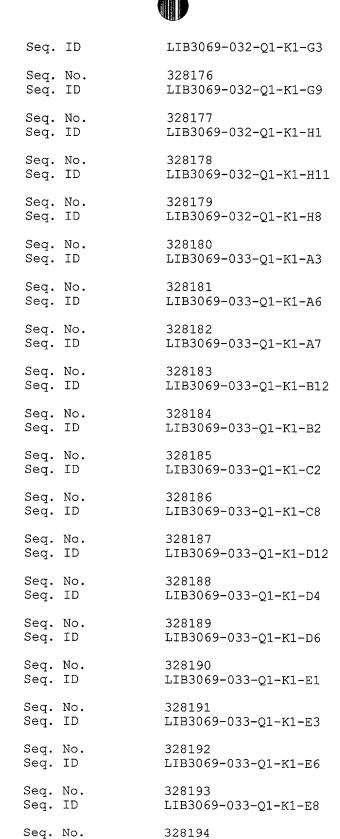
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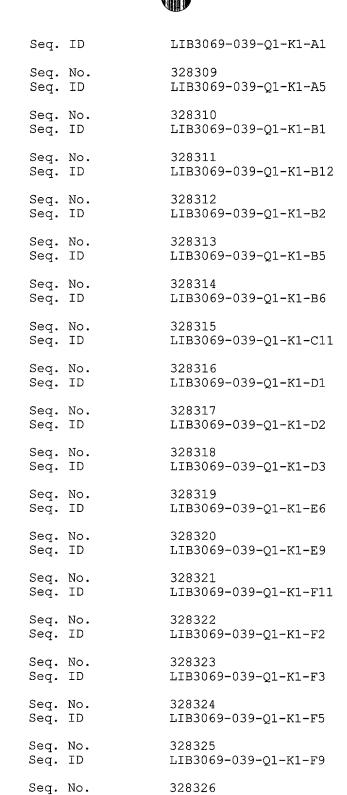
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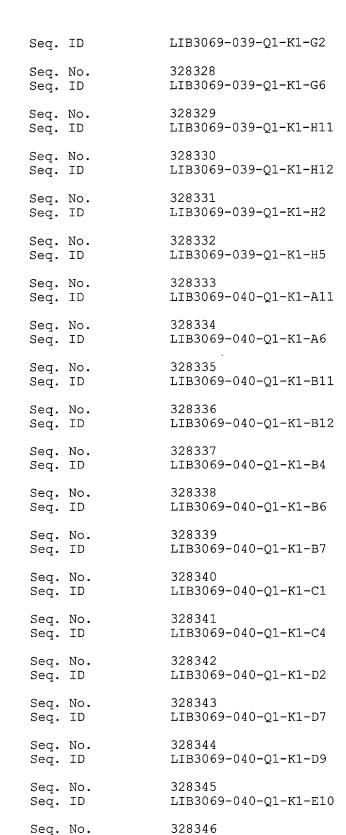
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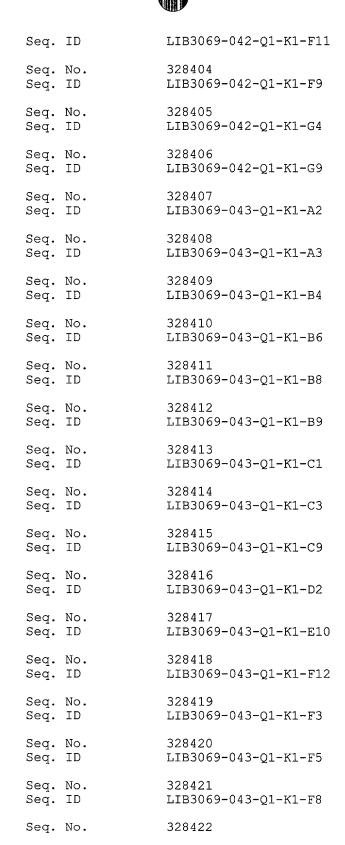
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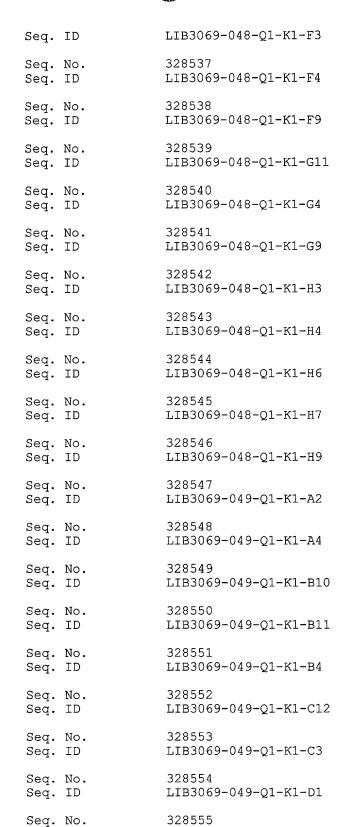


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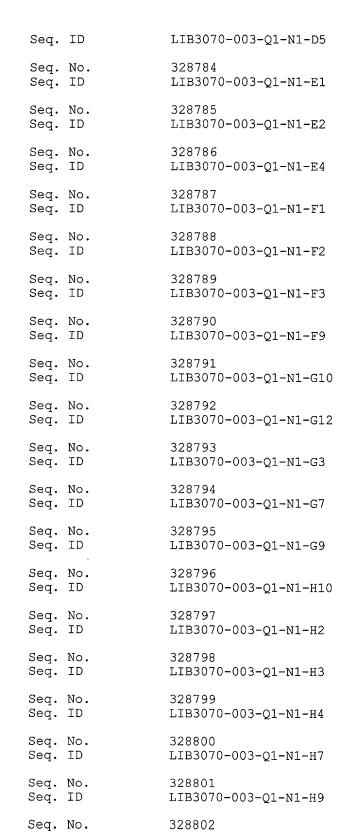
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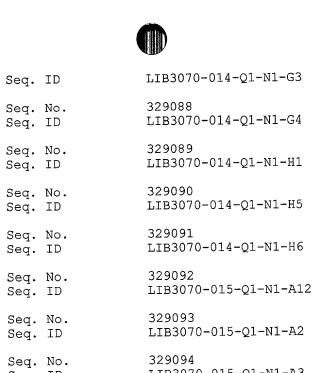


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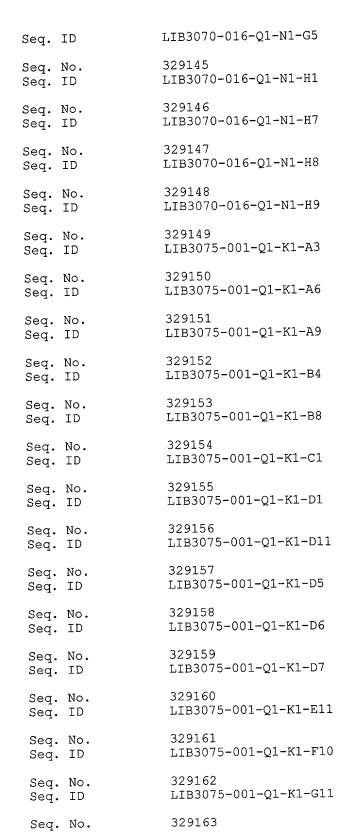
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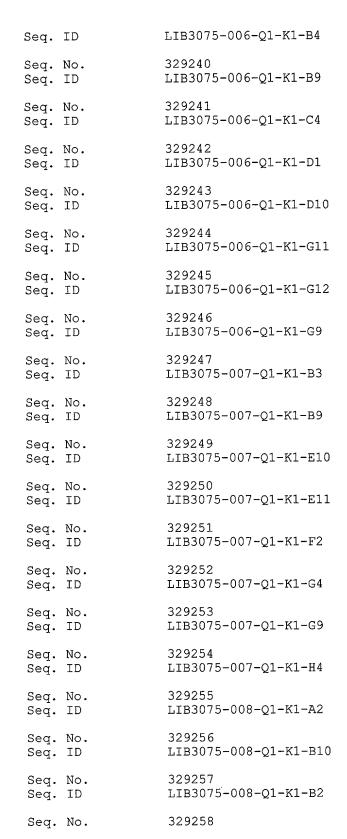
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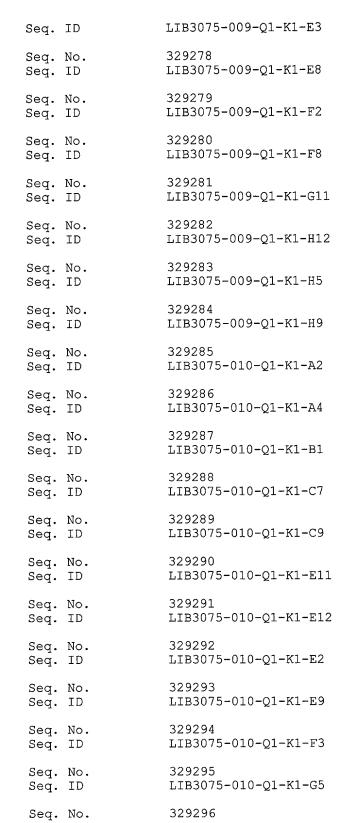


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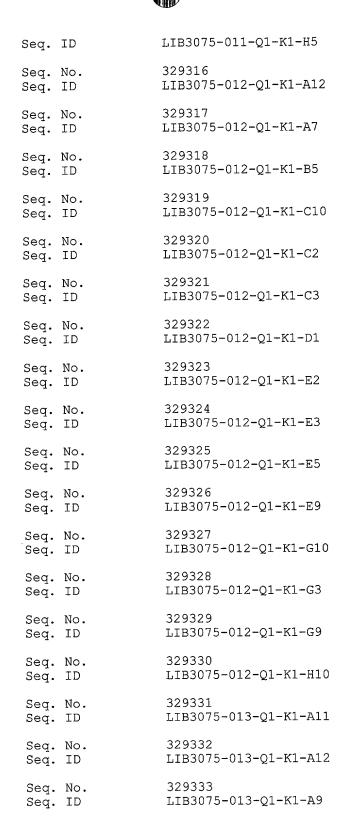


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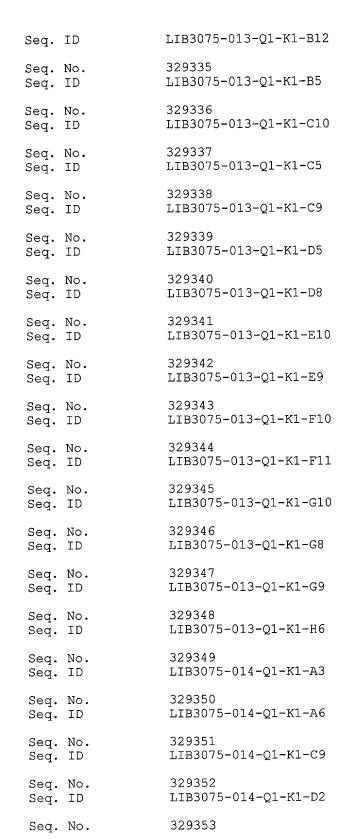


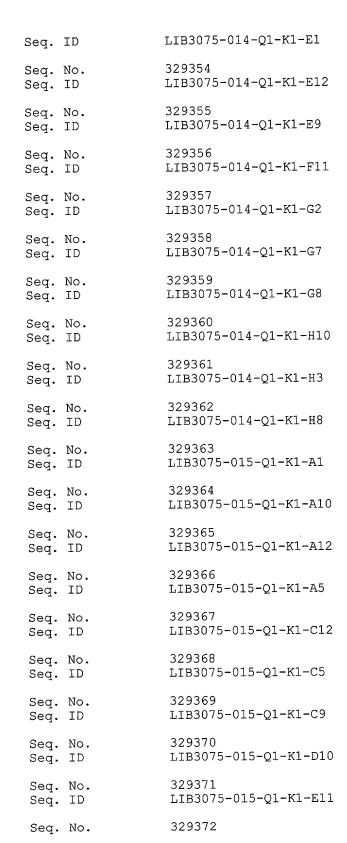
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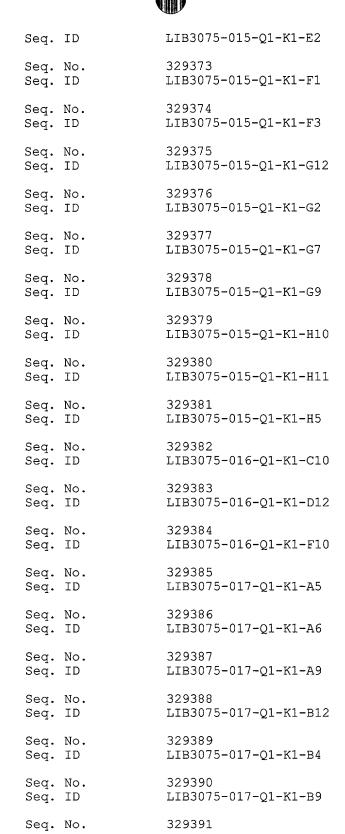
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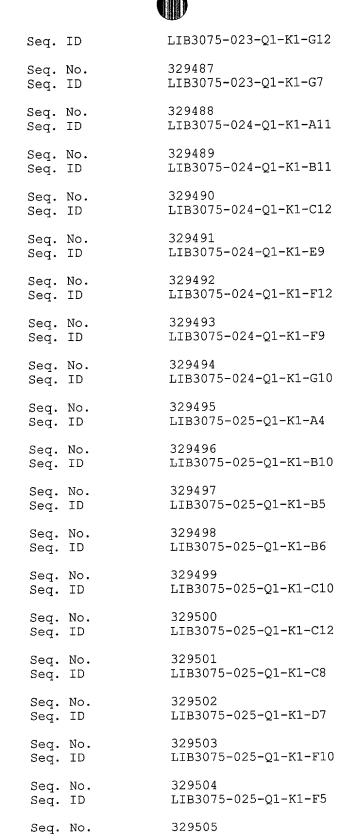
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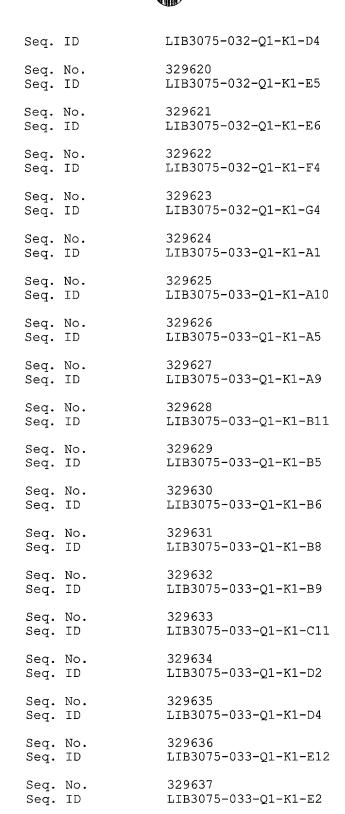
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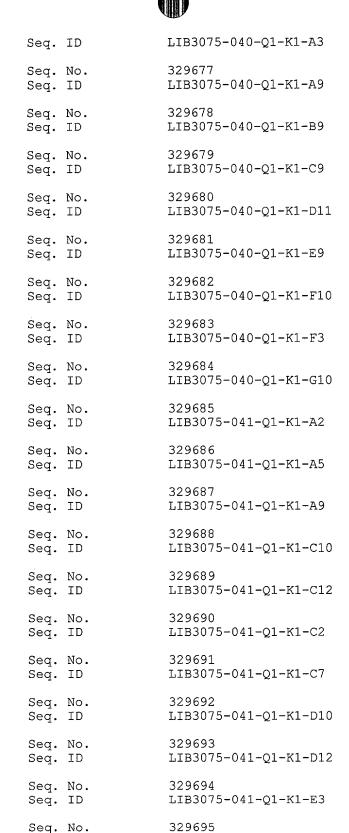
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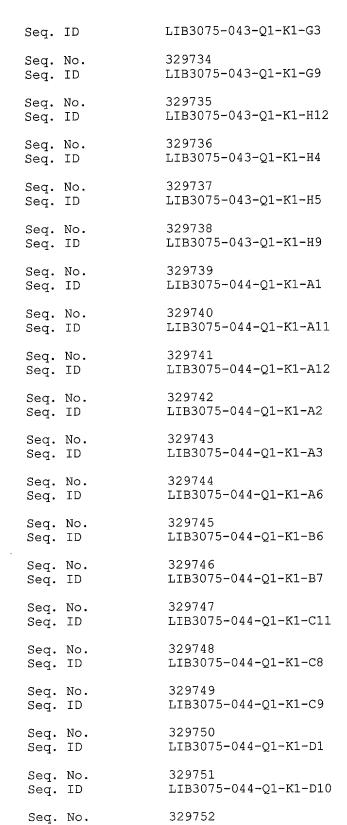




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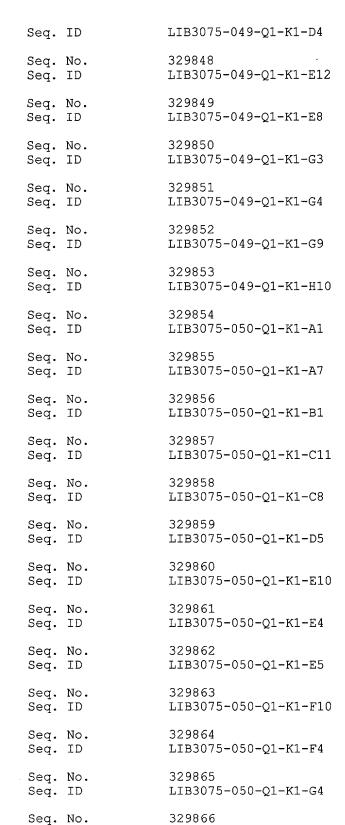
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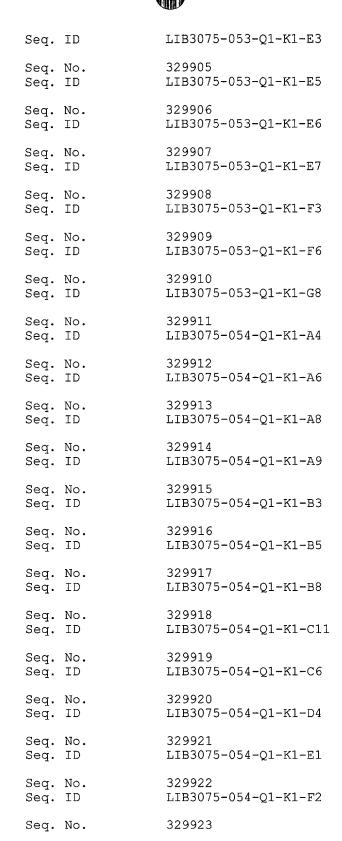




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